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June 24, 2003, 18:43:46; Search time 91 Seconds (without alignments) 2776.299 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                       | Novel human protei | Mouse ischaemic co | Drosophila melanog | Human Plexin prote | Human Plexin-B2. | Human plexin-B1/SE | Novel human diagno | Human plexin-B1/SE | Human Plexin-D1. | Human Plexin-B3. |
|-----------------------------------|--------------------|--------------------|--------------------|--------------------|------------------|--------------------|--------------------|--------------------|------------------|------------------|
| SUMMARIES                         |                    | ABB57196           | ABB65449           | AAU00019           | AAU00015         | ABB11818           | ABG21017           | ABB11709           | AAU00017         | .AAU00016        |
| DB                                | 23                 | 23                 | 22                 | 22                 | 22               | 22                 | 22                 | 22                 | 22               | 22               |
| %<br>Query<br>e Match Length DB I | 1909               | 1884               | 1945               | 2135               | 1838             | 1849               | 1870               | 1992               | 1925             | 1788             |
| *<br>Query<br>Match               | 67.9               | 67.7               | 36.4               | 27.1               | 25.8             | 25.7               | 25.2               | 24.7               | 24.7             | 18.4             |
| Score                             | 6786               | 6764               | 3641               | 2710               | 2580             | 2565               | 2521.5             | 2471               | 2463.5           | 1838.5           |
| Result<br>No.                     | -                  | 7                  | ٣                  | 4                  | 5                | 9                  | 7                  | æ                  | თ                | 10               |

| Human NOV/plexin-A | Human polypeptide, |          | Amino acid sequenc | Human PRO235 prote | Human PRO235 prote |          | 1 PR0235 | g        | Human VESPR. Homo | Viral-encoded sema | Viral encoded sema | Human VESPR. Homo | Amino acid sequenc | Human Pro peptide | Human Plexin A-4. | Drosophila melanog | Human Plexin prote | Human protein segu | Human ovarian anti | Human prostate tum | Gene 16 human secr | Human secreted pro |          | Human RON receptor | Human brain expres | Peptide #11582 enc | peptide  | Novel human diagno | gene 1   | Human albumin fusi | Human PRO1480 (UNQ | ројуј | Protein of the inv | Human protein sequ |
|--------------------|--------------------|----------|--------------------|--------------------|--------------------|----------|----------|----------|-------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|----------|--------------------|----------|--------------------|--------------------|-------|--------------------|--------------------|
| ABB11753           | AAM93421           | AAM93435 | AAY13373           | AAB33420           | AAB24400           | AAU12337 | AAB80241 | AAY13462 | AAB28522          | AAU00239           | AAU00435           | AAB70131          | AAB31693           | ABG34075          | AAU00018          | ABB66230           | AAU00020           | AAB93812           | ABP41337           | AAY74169           | AAB39454           | AAB39455           | AAB57044 | AAW82791           | AAM64598           | AAM37545           | ABG46408 | ABG04109           | AAE03818 | ABG64522           | AAY99410           |       | AAB66159           | . ABB97964         |
| 22                 | 22                 | 22       | 20                 | 21                 | 21                 | 22       | 22       | 20       | 21                | 22                 | 22                 | 22                | 22                 | 23                | 22                | 22                 | 22                 | 22                 | 23                 | 20                 | 21                 | 21                 | 21       | 20                 | 22                 | 22                 | 23       | 22                 | 22       | 23                 | 21                 | 22    | 22                 | 23                 |
| 362                | 716                | 484      | 552                | 552                | 552                | 552      | 552      | 1568     | 1568              | 1568               | 1568               | 1568              | 1568               | 280               | 199               | 816                | 729                | 164                | 226                | 179                | 146                | 146                | 399      | 1400               | 89                 | 89                 | 89       | 276                | 832      | 832                | 837                | 837   | 837                | 893                |
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| 1573.5             | 1486               | 1376     | 1351.5             | (,,                | (,,                | 1351.5   | 1351.5   | 1349     | 1349              | 1349               | 1349               | 1349              | 1349               | 1275              | 1076.5            | 920                | 678                | 653                | 634.5              | 494                | 484                | 484                | 471      | 427                | 9                  | 367                | 367      | ٠<br>ش             | 8        | 328.5              | 8                  |       | 328.5              |                    |
| 11                 | 12                 | 13       | 14                 | 15                 | 16                 | 17       | 18       | 19       | 20                | 21                 | 22                 | 23                | 24                 | 25                | 56                | 27                 | 28                 | 29                 | 30                 | 31                 | 32                 | 33                 | 34       | 35                 | 36                 | 37                 | 38       | 39                 | 40       | 41                 | 42                 | 43    | 44                 | 45                 |

## ALIGNMENTS

antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy; neuroprotective; antiparkinsonian; protein therapy; EST; Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; Ren F; Zhao QA, Liu C, Zhou P, Asundi V, Zhang J, Yang Y, Wehrman T, Drmanac RT; ABB97486 standard; Protein; 1909 AA Novel human protein SEQ ID NO: 754. 10-SEP-2001; 2001WO-US26015. 11-SEP-2000; 2000US-0659671 (first entry) expressed sequence tag WPI; 2002-292408/33. N-PSDB; AJN32672. (HYSE-) HYSEQ INC WO200222660-A2. Homo sapiens. 21-MAR-2002. 27-JUN-2002 Tang YT, Xue AJ, RESULT 1 ABB97486  엄 ò g ò 셤 Š

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The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate call growth, to regulate the haematopoiesis e.g. to treat applastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention.
An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis -
                                                                               Claim 20; SEQ ID NO 754; 509pp; English
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1909 AA; Sequence

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                                                                     FGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVASMIKI
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                                                                                                         GFNHLVVDERTGH1YLGAVNR1YKLSSDLKVLVTHETGPDEDNPKCYPPR1VQTCNEPLT
                           44;
Length 1909;
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 67.9%; Score 6786; DB 23;
66.9%; Pred. No. 0;
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                                                                        EFRDIASHVKVAGVECSPLVDGYIPAEQIVCEMGEAKPSQHAGFVEICVAVCRPEFMARS
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SYSYEGMEINNLPVELTVVWNGHFNI DNPAQNKVHLYKCGAMRESCGLCLKADPDFACGW
                                                       CQGPGQCTLRQHCPAQESQWLELSGAKSKCTNPRITEIIPVTGPREGGTKVTIRGENLGL
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                                       LTKNSEADGMFAXVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEM
                                                                 VSPPG---STTKEQVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes [1] in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABB9912, to ABB9912, encoding the protein sequences in ABB57020 to ABB97374) or by determining the expression profile of a gene group comprising these genes. The expression profile of a gene group comprising these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
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                                                                                                                                                                                                                                                                Mouse ischaemic condition related protein sequence SEQ ID NO:480
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                                                                                                                                                                                                                                                                                                      Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease
1845 NTMSALSEIFSYVGKYSEEILGPLDHDDQCGKQKLAYKLEQVITLMSLDS
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                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL016176) and the encoded proteins
                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                        Disclosure, SEQ ID NO 23139; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                    36.4%; Score 3641; DB 22;
llarity 42.0%; Pred. No. 4.5e-307;
Conservative 320; Mismatches 637;
          WPI; 2001-656860/75.
N-PSDB; ABL09552.
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1708 KHHDSDMQKEGERVNKLVSEIYLTRLLATKGTLQKFVDDLFETIFSTAHRGSALPLAIKY 1767
                                                                                                                                                                                                                                                                                                                                                                                       Human, Plexin, semaphorin domain, hyperplasia, neoplasia, cancer,
neurodegenerative disease, autoimmune disease, lupus, multiple sclerosis,
inflammatory bowel disease, diabetes type I; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a Human Plexin. Plexins are large transmembrane proteins whose extracellular domain shares homology with Scatter factor receptors and contain an approximately 500 amino acid Semaphorin domain. The plexin polymuclectides and polypeptides, and plexin-specific binding agents are useful in diagnosis, therapy and in the biopharmaceutical industry. In particular, the plexin polymuclectides and polypeptides are useful for generating compounds (e.g. plexin-specific binding agents or antibodies) for treating or diagnosing a disease or disorder involving aberrant cell growth (e.g. hyperplasia, neoplasia, cancer or neurodegenerative disease), or diseases or disorders involving aberrant immune regulation (e.g. autoimmune diseases such as lupus, inflammatory
                                                                                                                                                                        1828 QTFWDSCSTSDHRLGKDSPSSKLLYAKDIPEYRKWVDRYYRDIRDMSPISDQDWNAMLAE
                                                                                             QTFMDSCSTSEHRLGKDSPSNKLLYAKDIPSYKNWVERYYSDIGKMPAISDQDMNAYLAE
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                                                                                                                                                        OSRMHWNEPNTMSALSEIFSYVGKYSEEILGPLDHDDQCGKQKLAYKLEQVITLMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Encoded by AAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Encoded by ACC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 72-77; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                AAU00019 standard; Protein; 2135
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(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                            Human Plexin protein.
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Tamagnone L;
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                                                                                                                                                                                                                                                                                                                            948 PGEQMYRNGKIVVQI-----GDYRGESKEDYEFVDPKILDFNPKFGPTSGGTEIHITGK 1001
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                                                                    SEORVPAL -- RFNSSSVQCQNTSYSYEGMEINNLPVELTVVWNGHFNIDNPAQNKVHLYK
                                                                                                                              NLNAGSNVVVMFGKQ-PCLFHRRSPSYIVCNTTSSDEVLEMKVSVQVDRA-KIHQDLVFQ
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                                                                                                                                                                                                                                                                                             -GEAKPSQHAGFVEICVAVCRPEFMARSSQLYYFWTLTLSDLKPSRGPMSGGTQVTITGT
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                                                                                                                                                                                      CREMADSCGICLALSEKYNCGWCSSTNTCEVEEQCNKNKEGKTDWLNRS---EICPNPEI
                                                                                                                                                                                                                                  TEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGYIPAEQIVCEM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLNATEMTCQAPALALGPDHQSDLTERP--EEFGFILDN----VQSLLILNKTNFTYYPNP
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                                              SFQEGRVKLPEDCPQLLRV---DKILVPVEVIKPITLKAKNLPQPQSGQRGYECILNIQG
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|--|----------|---|---------------------------------------|---|--|------------------------------|----|------------|---|--------|-----|-----|--|--|--------|-----|---|---|----------------------|--|---------------|--|-----|---|-----|--|-----|---|
| ease or Diabetes Type I), or immunosuppressive diseases such a | 2135 AA; | / Match<br>Local Similarity 30.6%; Pred. No. 9.1e-226;<br>nes 690; Conservative 353; Mismatches 701; Indels 508; Gaps 6 | SOKORSFVTFRGEPABGFNHLVVDERTGHIYLGAV 6 | 69 NRIYKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLITTNNVNKMLLIDYKENRLI 12: | ACGSLYQGICKLIRLEDLFKLGEPYHKKEHYLSGVNESGSVFGVIVSYSNLDD 18 | SSRKLTKNSEADGMFAYVFHDEFVASMI |    | മവ         | TAENSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFS | AAPPTV | E)  | m   | SALLIIDDNFCGLDMN-APLGVSDMVRGIPVFTEDRDRMTSVIAVVKARSLAFVGT 4 | CAQLEVOLIDATECGSURIESETIMSENVERBERTETREFENENTE |        |     | 483 AQHLDCASCLAHRDPYCGWCVLLGRCSRRSECSRGQGPEQWLWSFQPEL-GCLQVAAMSP 54 | NNISVSQYNVLLVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQIQCYSPAAKEV | SPALLTGSGVMCPSPDPSEA | 621 PRIITENGDHHVVOLQLKSKETGMTFASTSFVFYNCSVHNSCLSCVESFYRCHW 67   .: | VCTHDPKTCSFQE | ::::   <br>  654 CVWQHLCTHKASCDAGPMVASHQSPLVSPDPPARGGPSPSPPTAPKALATPAPDTLPVEP 71 | 693 | 714 GAPSTATASDISPGASPSLLSFWGPWAGSGSISSPGSTGSPLHEEPSPPSPQNGPGTAVP 77 | 993 | 774 APIDFRPSATPEDLLASPLSPSEVAAVPPADPGPEALHPTVPLDLPPATVPATTFPGAMG 8 |     | 834 SVKPALDWLTREGGELPEADEWTGGDAPAFSTSTLLSGDGDSAELEGPPAPLILPSSLDY 89 |
| bowel dis  | Sequence | Query Ma<br>Best Loc<br>Matches   |                                       |   | •  |                              |    |            |   |        |     |     |  |  |        |     |   |   |                      | ,  |               |  |     |   |     |  |     |   |
| S. 6   | 3 \$ 8   | M Be  | oy<br>D                               | දු ද  | 8 8  | 8 &                          | qq | <u>ک</u> و | ò   | qq     | È   | q   | 8  | g ;  | 중<br>음 | ò   | qq  | ò   | qq                   | \$ 8<br>8  | ð             | QQ   | δ   | QQ  | ò   | qu   | ò   | đ   |

1862 QDYVPG-----ERTPMLEDVDEGGIRPWHLVKPSDEPEPPRPRRGSLRGGERERAKAIP 1915 EIYLTRLLATKGTLQKFVDDLFETIFSTAHRGSALPLAIKYMFDFLDEQADKHGIHDPHV 1734 1390 IMTVLQSKLEYATDVLKQLLADLIDKNLESKNHPKLLLRRTESVAEKMLTNWFTFLLXKF 1449 1450 LKECAGEPLFSLFCAIKQQMEKGPIDAITGEARYSLSEDKLIRQQIDYKTLVLS---CVS 1506 1699 VRDSVGEFLYMLFRGIKHQVDKGPVDSVTGKAKYTLNDNRLLREDVEYRPLTLNALLAVG 1758 DEDITIKIENDWKRINTLAHYQVPDGSVVALV---SKOVTAYNAVNNSTVSRTSASKYEN 1623 1624 MIRYTGSPDSLRSRTPMITPDLESGVKWWHLVKNHEHGDQKEGDRGS------KMVS 1674 1237 TERRLQRGQ-----FKYTLDPNITSAGPTKSFLSGGREICVRGQNLDVVQTPRIRVTVV 1290 1165 -- ARVGGMEYSPGMYXIAPDSPLSLP--AIVSIAVAGGLLIIFIVAVLIAYKRKSRESDL 1269 1330 EDHPVLRDLEVPGYRQERVEKGLKLFAQLINNKVFLLSFIRTLESQRSFSMRDRGNVASL 1389 969 GTQVTITGTNLNAG--SNVVVMFGKQPC-LFHRRSPSYIVCNTTSSDEVLEMKVSV---- 1021 ::| | | | : :| | | | : :| | | : :| | | : :| | | : :| | : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : :| : 1013 BGLHVVLYDCSVGHGDCSRCOTAMPQYGCVWCEGERPRCVTREACG------EARAVAT 1065 913 953 --ILVPVEVIKPITLKAKNLPQPQSGQRGYECI 740 794 1641 LTVALHGKLEYFTDILRTLLSDLVAQYV-AKN-PKLMLRRTETVVEKLLTNWMSICLYTF 1270 TLKRLOMOMDNIESRVALECKEAFAELOTDIHELTSDIDGAGIPFIDYRTYTMRVLFPGI 854 KCTNPRITEIIPVTGPREGGTKVTIRGENIGLEFRDIASHVKVAGVECSPLVDGYIPAEQ 914 IVCEMGEAKPSQHAGFVEICV----AVCRPEFWARSSQLYYFWTLTLSDLKPSRGPMSG 1022 ---QVDRAKIHQDLVFQYVEDPTIVRIEPEWSIVSGNTPIAVWGTHLDLIQNPQIRA---1110 DLTERPEEFGFILDN-VQSLLILNKTNFTYYPNPVFEAFGPSG---ILBLKPGTPIILKG 741 LNIQGSEQRVPAL-----RFNSSSVQCQNTSYSYEGMEINNLPVELTVVWNGHFNIDNP 795. AQNKVHLYKÇGAMRESÇGLÇLKADPDFACGWÇQGP-GQCTLRQHÇPAQESQWLELSGAKS ----KHGGKEHINICEVLNATEMTCQAPALALGPDHQS KNLIPPVAGGNVKLNYTVLVGBKPCTV-TVSDVQLLCBSP--NLIGRHKVM-----700 --DCPQLLRVDK-1819 1567 1076 1166 1214 g ઠે g Š g ઠે g ò g ò 엄 ò 요 상 원 8 8 8 8 8 8 9 % a 6 B 6 g à 면 상 <sup>연</sup> ò 셤 Š

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SNKLLYAKDIPSYKNWVERYYSDIGKMPAISDQDMNAYLAEQSRMHMNEFNTMSALSEIF 1854
                                                                                                                                                                                                                                                                        Human; Plexin-B2; semaphorin domain; hyperplasia; neoplasia; cancer; burorodegenerative disease; autoimmune disease; lupus; multiple sclerosis; inflammatory bowel disease; diabetes type I; rheumatory atthritis; immunogen; antibody; MET related sequence; MRS.
                                            2033 INKLLYARDIPRYKRMVERYYADIRQTVPASDQEMNSVLAELSWNYSGDLGARVALHELY
                               RHTWKSNCLPLRFWVNMIKNPQFVFDIHKNSITDACLSVVAQTFMDSCSTSEHRLGKDSP
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/label= "Tertiary MET related
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/label= "Semaphorin domain"
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/label= "G-P repeat region"
1196..1215
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|abel= "Mature Plexin-B2"
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Tamagnone L;
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                                                                                                       The sequence represents Human Plexin-B2. Plexins are large transmembrane proteins whose extracellular domain shares homology with Scatter factor receptors and contain an approximately 500 amino acid Semaphorin domain. The plexin polymucleotides and polypeptides, and plexin-specific binding agents are useful in diagnosis, therapy and in the biopharmaceutical industry. In particular, the plexin polymucleotides and polypeptides are useful for generating compounds (e.g. plexin-specific binding agents or antibodies) for treating or diagnosing a disease or disorder involving aberrant cell growth (e.g. hyperplasia, neoplasia, cancer or aberrantive disease), or diseases or disorders involving aberrant immune régulation (e.g. autoimmune diseases such as lupus, inflammatory bowel disease or Diabetes Type 1), or immunosuppressive diseases such as multiple sclerosis or rheumatoid arthritis.
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Best Local Similarity 33.2%; Pred. No. 1.5e-214;
Matches 654; Conservative 344; Mismatches 713;
                                                        79pp; English.
                                                           4; Page 52-56;
autoimmune diseases)
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; pathma; arthritis; chronic inflammatory condition; proliferative retinopathy; bone disorder; osteoporosis; vascular disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; cell culture; drug screening; gene therapy; antinflammatory; antiacture; drug screening; gene therapy; antinflammatory; antiacthmatic; antiarthritic; haemostatic; antiatreriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences ABB10981-ABB12330 represent 1150 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides of identifying compounds which bind to polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities; including cytokine, cell proliferation or cell differentiation activities; seem cell growth factor activity; immunomodulatory activity; tissue growth activity; immunomodulatory activity: or inhibin-related activities;
                                     1657 FFDFLDEQAEKHNIQDEDTIHIWKTNSLPLRFWVNILKNPHFIFDVHVHEVVDASLSVIA 1716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                       1836 QSRMHMNEFNTMSALSEIFSYVGKYSEFILGPLDHDDQCGKOKLAYKLEQV 1886
                                                                                                                                            Human plexin-B1/SEP receptor homologue, SEQ ID NO:2188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 259-260; 1963pp; English.
                                                                                                                                                                                                                                                                     ABB11818 standard; peptide; 1849 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                   11-JAN-2002 (first entry)
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chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliocating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers), chronic inflammantory conditions (e.g., arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal repair (or nucleic acids encoding them) may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound crepair (or nucleic acids encoding them) may be used to promote wound crepair (or nucleic acids encoding them) may be used to promote wound crepair (or nucleic acids encoding them) may be used to promote coll growth. For example, such polypeptides with growth factor activity may be used in call cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The presents a novel human collypeptide of the invention.

equence 1849 AA;

78 VATGPVLDNKKCTPPIEASQCHE-AEMTDNVNQLLLVDPPRKRLVECGQLLKGICALRAL 136 137 SNISLRLFYEDGSGEKSFVASNDEGVATVGLVSSTGPGGDRVLFVGKGNGPHDNGIIVST 196 202 RKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQP 261 197 KLLDRTDSREAFEAYTDHATYKAGYLSTNTQQF------VAAFEDGPYVFFVFNQQ 246 EMVSPPGSTTKEQVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAV 321 DK-HPARNRT-----LLARMCREDPNYYSYLEMDLQCRDPDIH----AAAF---GTC 290 LGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCYRGEGTL 381 DLAWLKVK----DIPCSSALLTIDDNF-CGLD-MNAPLGVSDMVRGIPVFTEDRDRMTSV 435 347 EARDIFYKPFHGDIQCGGHAPGSSKSFPCGSEHLPYPLGSRDGLRGTAVLQRGGLNLTAV 406 436 IAYVYKNHSLAFVGTKSGKLKKIRVDGPRGNALQYETVQVVDPGPVLRDMAFSKDHEQLY 495 465 554 663 584 ICNSPSS--IP--VTPPGQDHVAVTIQLLLRRGNIFLTSYOYPFYDCRQAMSLEENLPCI 639 144 ED--LFKLGEPYHKKEHYLSGVNESGSVFGVIVSYSNLDDKLFIATAVDGKPEYFPTISS 201 24 TLLTRQPAPLSQKQRSFVTFRGEPAEGFNHLVVDERTGHIYLGAVNRIYKLSSDLKVLVT 83 Query Match 25.7%; Score 2565; DB 22; Length 1849; Best Local Similarity 33.1%; Pred. No. 3.2e-213; Matches 652; Conservative 343; Mismatches 716; Indels 260; Gaps 84 HETGPDEDNPKCYPPRIVQTCNEPLTTINNVNKMLLIDYKENRLIACGSLYQGICKLLRL TVAAENNHTVAFLGTSDGRILKVYLT-PDGTSSEYDSILVEINKRVKRDLVLSGDLGSLY IMSEROLTRVPVESCGOYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPRRPA-SE OCYSPAAKEVPRITTENG-DHHVVQLQLKSKETGMTPASTSFVFYNCSVHNS-----CL MKQCVRLT-VHPNNIS-VSQYNVLLVLETYNVPELSA--GVNCTFEDLSEMDGLVVGNQI 262 322 291 382 407 247 요 셤 ð 8 ઠ

| ò        | 664  | CYBSPYRCHWCKYRHVCTH-DPKTCSFQBGRVKLPEDCPQLLRVDK1LVPVEVIKP           |
|----------|------|--|
| qq       | 640  |  |
| ò        | 721  | TLKAKNLPQPQSGQRGYECILNIQGSEQRVPALRFNSSSVQCQNTSYSYEGMEINN 776       |
| Dp       | 697  | NFQGKNLDTVKGSSLHVGSDLLKFMEPVTMQESGTFAFRTPKLSHDA 743                |
| ò        | 777  | LPVELTVVWNGHFNIDNPAQNKVHLYKCGAMRESCGLCLKADPDFACGWCQGPGQ 831        |
| Dþ       | 744  | NETLPLHLYVKSYĞK-NIDSKLHVTLYDCSFGRSDCSLCRAANPDYRCAWCGGQSR 798       |
| ò        | 832  | CTLRQHCPAQESQWLELSGAKSKCTNPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIA 891   |
| QQ       | 799  | CVYEALCNTTSECPPVITRIQPETGPLGGGIRITILGSNLGVQAGDI- 846               |
| ζ        | 892  | SHVKVAGVECSPLVDGYIPAEQIVCEMGEAKPSQHAGFVEICVAVCRPEFMARSS 946        |
| Db       | 847  | QRISVAGRNCSFQPERYSVSTRIVCVI-EAAETPFTGGVEVDVFGKLGRSPPNV 899         |
| č        | 947  | QLYYFMTLTLSDLKPSRGPMSGGTQVTITGTNLNAGSNVVVMFGKQPCLFHRRSPSYIVC 1006  |
| qq       | 900  | QFTFQQPKPLS-VEPQQGPQAGGTTLTHGTHLDTGSQEDVRVTLNGVPC 948              |
| Š        | 1001 | NTISSDEVLEMKVSVQVDRAKIHQDLVFQYVEDPTIVRIEPEWSIVSG 1054              |
| Db       | 949  | CVTGPQATRGOMLLEVSYGGSPVPNPGIFFTYRENPVLRAFEPLRSFAS                  |
| λŏ       | 1055 | NTPIAVWGTHLDLIQNPQIRAKHGGKEHINICEVLNATEMTCQAPALALGPDH 1107         |
| qu       | 1009 | GRSINVTGQGFSLIQRFAMVVIAEPLQSWQPPREAESLQPMTVVGTDYVFH 1059           |
| ò        | 1108 | QSDLTERPEEFGFILDNVQSLLILNKTNFTYYPNPVFEAFGPSGILEL 1155              |
| qq       | 1060 | NDTKVVFLSPAVPEEPEAYNLTVLIEMDGHRALLRTEAGAFEYVPDPTFENF 1111          |
| ò        | 1156 | KPGTPIILKGKNLIPPVAGGNVKLNYTVLUGEKPCTV-TVSDVQLLCESPNLIGR 1209       |
| qq       | 1112 | TGGVKKQVNKLIRARGTNLNKAMTLQBABAFVGAERCTMKTLTETDLYCEPPEVQPP 1168     |
| λ̈́o     | 1210 | HKPAIVSIAVAG 1246  |
| qq       | 1169 | PRRRQKRDTTHNLPEFIVKFGSREWVLGRVEYDTRVSDVPLSLILPLVIVPMVVVIAVS- 1227  |
| λõ       | 1247 | GLIIFIVAVLIAYRRKSRESDLTLKRLQMQMDNLESRVALBCKEAFAELQTDIHELTSD 1306   |
| DP<br>DP | 1228 | VYCYWRKSQQAEREYEKIKSQLEGLEESVRDRCKKEFTDLMIEMEDQTND 1277            |
| δγ       | 1307 | 1.DGAGI PFLDYRTYTWRVLPPGI EDHPVLRDLEVPGYRQERVEKGLKLFAQLINNK 1362   |
| дg       | 1278 | . HEAGIPVLDYKTYTDRVFFLPSKDGDKDVMITGKLDIPEPRRPVVEQALYQFSNLLNSK 1337 |
| ò        | 1363 | VFLLSFIRTLESQRSFSMRDRGNVASLIMTVLQSKLEYATDVLKQLLADLIDKNLESKNH 1422  |
| Db       | 1338 | SFLINFIHTLENQPEFSARAKVYFASLLTVALHGKLEYYTDIMHTLFLELLEQYVVAKN- 1396  |
| ۵۷       | 1423 | PKLILRRTBSVAEKMLTNWFTFLLYKFLKECAGEPLFSLFCAIKQQMEKGPIDAITGEAR 1482  |
| op<br>Q  | 1397 | PKIMLRRSETVVERMLSNWMSICLYQYLKDSAGEPLYKLFKAIKHQVEKGPVDAVQKKAK 1456  |
| ۵,       | 1483 | YSLSEDKLIRQQIDYKTLVLSCVSPDNANSPEVPVKILNCDTITQVKEKILDAIFKNVPC 1542  |
| Ωp       | 1457 | YTINDIGLIGDDVEYAPLIVSVIVQDE-GVDAIPVKVINCDIISQVKEKIIDQVYRGQPC 1515  |
| ò        | 1543 | SHRPKAADMDLEWRQGSGARMILQDEDITTKIENDWKRLNTLAHYQVPDGSVVALVSKQV 1602  |
| QΩ       | 1516 | SCWPRPDSVVLEWRPGSTAQ-ILSDLDLTSQREGRWKRVNTLMHYNVRDGATLIL 1569       |
| ò        | 1603 | RTPM   |
| Ωp       | 1570 | : :     : :     : :     : :     :   :                              |

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              MFDFLDEQADKHGIHDPHVRHTWKSNCLPLRFWVNMIKNPQFVFDIHKNSITDACLSVVA
                                                                                                   QTFMDSCSTSEHRLGKDSPSNKLLYAKDIPSYKNWVERYYSDIGKMPAISDQDMNAYLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                  QSRMHMNEFNTMSALSEIFSYVGKYSEEILGPLDHDDQCGKQKLAYKLEQV 1886
                                                                                                                                                                                                                                                                                                                                            Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 51376; 103pp; English
                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #21008
                                                                                                                                                                                                                                            ABG21017 standard; Protein; 1870 AA
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23-AUG-2000; 2000US-0649167
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   OKEGDRGS
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   721 TLKAKNIPQPQSGQRGYECILNIQGSEQRVPA--LRFNSSSVQCQNTSYSYEGMEINN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              764 NETLPLHLYVKSYGK-NID----SKLHVTLYNCSFGRSDCSLCRAANPDYRCAWCGGOSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVYEALC-----NTTSECPPPVITRIQPETGPLGGGIRITILGSNLGVQAGDI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKQCVRLT-VHPNNIS-VSQYNVLLVLETYNVPELSA--GVNCTFEDLSEMDGLVVGNQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546 SKSÇVAVTSAQPONMSRRAQGEVQLTVSP--LPALSEEDELLCLFGESPPHPARVEGEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LPVELTVVWNGHFNIDNPAQNKVH--LYKCGAMRESCGLCLKADPDFACGWCQGPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496 IMSERQLIRVPVESCGOYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPRRFA-SE
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                                                                                                                                                                                                                                              24 TLLTROPAPLSQKQRSFVTFRGEPAEGFNHLVVDERTGHIYLGAVNRIYKLSSDLKVLVT
                                                                                                                                                                                                                                                                               98 VATGPALDNKKCTPPIEASQCHE-AEMTDNVNPLLLVDPPRKRLVECGQLLKGICALRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKLIKMSEADGMFAYVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 RLLDRTDSREAFEAYTDHATYKAGYLSTNTQQF------VAAFEDGPYVFFVFNQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 DK-HPARNRT-----LLARMCREDPNYYSYLEMDLQCRDPDIH----AAAF----GTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 LGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCYRGEGTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                              144 ED--LFKLGEPYHKKEHYLSGVNESGSVFGVIVSYSNLDDKLFIATAVDGKPEYFPTISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 IAYVYKNHSLAFVGTKSGKLKKIRVDGPRGNALQYETVQVVDPGPVLRDMAFSKDHEQLY
                                                                                                                                                  Length 1870;
                                                                                                                                               Query Match 25.2%; Score 2521.5; DB 22; Length 1870
Best Local Similarity 32.9%; Pred. No. 2e-209;
Matches 648; Conservative 342; Mismatches 721; Indels·261;
                                                                                                         1870 AA;
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1422
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                                    920 QFTFQQPKPLS-VEPQQGPQAGGTTLTIHGTHLDTGSQEDV-----RVTLNGVPC
                                                                                                                                                                                    1055 NTPIAVWGTHLDLIQNPQIRAKHGGKEHINICEVLNATEMTCQA----PALALGPDH---
                                                                                                                                                                                                                                                                                                                                                                                                                     -----QSDLTERPEEFGFI----LDNVQSLLILNKTNFTYYPNPVFEAFGPSGILEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1156 KPGTPIILKGKNLIPPVAGGNVKLNYTV----LVGEKPCTV-TVSDVQLLCESPNLIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1210 HK-------PAIVSIAVAGMEYSPGMVYI---APDSPLSL-----PAIVSIAVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1247 GLLIIFIVAVLIAYKRKSRESDLTLKRLQMQMDNLESRVALECKBAFAELQTDIHELTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1307 LDGAGIPFLDYRTYTMRVLF----PGIEDHPVLRDLEVPGYRQERVEKGLKLFAQLINNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1363 VFLLSFIRTLESQRSFSMRDRGNVASLIMTVLQSKLEYATDVLKQLLADLIDKNLESKNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1716 MFDFLDEQADKHGIHDPHVRHTWKSNCLPLRFWVNMIKNPQFVFDIHKNSITDACLSVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTFMDSCSTSEHRLGKDSPSNKLLYAKDIPSYKNWVERYYSDIGKMPAISDQDMNAY-LA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSLSEDKLIRQQIDYKTLVLSCVSPDNANSPEVPVKILNCDTITQVKEKILDAIFKNVPC
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ABB11709 standard; peptide; 1992 AA **ABB11709** 

RESULT 8

ABB11709;

(first entry) 11-JAN-2002

Human plexin-B1/SEP receptor homologue, SEQ ID NO:2079.

Human; cytokine; cell proliferation; cell differentiation; growth factor; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer. haematopoiesis regulation, tissue growth, immunomodulator; activin, inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; etlissue regeneration; wound healing; infection; immune disorder; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;

Homo sapiens

09-AUG-2001

05-FEB-2001; 2001WO-US03800

03-FEB-2000; 2000US-0496914 27-APR-2000; 2000US-0560875

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

2001-457740/49.

N-PSDB; ABA08953

treating or ameliorating a medical condition in a mammalian subject Human proteins and DNA encoding sequences useful for preventing e.g. arthritis and cancer -

Claim 20; Page 231-232; 1963pp; English

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA05574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of identifying compounds which corp polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention have homology to known proteins, thereby clypeptides of the invention have homology to known proteins, thereby comparing a insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may complete activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; have various activities; arem cell growth factor activity; chaematopolesis regulatory activity; tissue growth activity; chaematopolesis regulatory activity; tissue growth activity; chaematopolesis regulatory activities; haemostatic, thrombotic or chemokinetic activities; haemostatic, thrombotic or chemokinetic activities; haemostatic, thrombotic or chemokinetic activities; polypeptides and nucleotides of involved in oncogenesis, cancer cell proliferation or metastasis.

Complication are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions and use useful for preventing, treating or parthrities, conditions, e.g., by protein or gene therapy. Such conditions and abnormal confidences, haematopoletic disorders (e.g., myeloid or lymphoid cell actorier growth. Polypeptides involved with tissue regeneration and regineral ischaemia, bone disorders (e.g., osteoporosis), and abnormal crepair (or nucleic acids encoding them) may be used to promote wound immunomodulatory activities may be used in the treatment of viral, immunomodulatory activities may be used in the treatment of viral,

Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to amoment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and mucleotides screening techniques. The present sequence represents a novel human polypeptide of the invention. and fungal infections in addition to immune disorders 8888888888888

1992 AA; Sequence

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61; 859 417 627 WCVLHNTCTRKERCERSKEPRRFASEMK---QCVRLTVHPNNISVSQ-YNVLLVLETYNV 584 639 | | | : : : | | | | | : : BSLSGMEMACDYGNNIRTVARVPGPAFGHQIAYCNLLPRDQFPPFPPNQDH--VTVEMSV 745 RVNGRNIVKANFIIYDCSRIAQVYPHTACISCLSAQWPCFWCSQQHSCVSNQSRCEASPN 805 RVKLPEDCPOLLRVDKILVPVEVIKPITLKAKNLPQPQSGQRGYECILNIQGSEQRVPAL 753 RENSSSVQC-QNTSYSYEGMEINNLPVELTVVWNGHFNIDNPAQNKVHLYKCGAMRESCG 812 -----KEQVYTSKLVRLCKEDTA-----FNSYVEVPIGCERSGVEYRLLQAAYLSK 317 ----LÓCÁGGAG 410 AGAVLGRILGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCY-- 375 171 PAPDVVAVLDSVVQGTGPACERKLNIQ-LQPEQLDCGAA-------HLQHPLSILQ 518 MVRGIPVFTEDRDRMTSVIAYVYKNHSLAFVGTKSGKLKKIRVDGPRGNALQYETVQVVD 477 LLLLGAARAGALEIQRRPPSPTPT--------NNFALDGAAGTVYLAAVNRL 139 ----PTISSRKLTKNSEADGMFAYVFHD --RGEG-----TLDLAWLKVKDIPCSSALLTIDDNFCGLDMNAPLGVSD RRVVTVAXGEPVHHVMQFDPADSGXLYLMTSHQMARVKVAAACNVHSTCGDCVGAADAYCG WCALETRCTLOODCTNSSOOHFWTSASEGPSRCPAMTVLPSEIDVROEYPGMILQISGSL PELSA-GVNCTF----EDLSEMDGLVVGNQIQCYSPAAKEVPRIITENGDHHVVQLQLKS KETGMTPASTSFVFYNCS------VHNSCLSCVESPYRCHWCKYRHVCTHDPKTCSFQEG PTS-PODCPRTILLSPLAPVPTGGSQNILVPLANTAFFQGA--ALECSF---GLEBIFEAV 200 CGSIYOGFCOLRRRGNISAVAVRFPPAAPPAEPVTVFPSMLNVAANHPNASTVGLVLPPA PLKATPVFR--APGLTSVAVASVNNYTAVFLGTVNGRLLKINLN------ESMQVVS -----PGPVLRDMAFS-KDHEQLYIMSERQLTRVPVESCGQYQSCGECLGSGDPHCG YKLS-SDLKVLVTHETGPDEDNPKCYPPRIVQ-TCNEPLTTTNNVNKMLLIDYKENRLIA 260 AGAGGSRLLVGATYTGYGSSFFPRNRSLEDHRFENTPEIAIRSLDTRGDLAKLFTFDLN-BFVASMIKI PSDTFTIIPDFDIYYVYGFSSGNFVYFLT--LQPEMVSPPGSTT-----LLMVG----MGSSTLLTRQPAPLSQKQRSFVTFRGEPAEGFNHLVVDERTGHIYLGAVNRI CGSLYQGICKLLRLEDLFKLGEPYHKKEHYLSGVNESGSVFGVIVSYSNLD------Gaps Indels 312; Length 1992; Ouery Match 24.7%; Score 2471; DB 22; Best Local Similarity 31.8%; Pred. No. 5.8e-205; Matches 647; Conservative 336; Mismatches 742; ----DKLFIATAVDGKPEYF---519 268 640 746 754 529 628 585 588 15 96 72 130 181 221 272 318

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1774 VAQTEMDSCSTSEHRLGKDSPSNKLLYAKDIPSYKNWVERYYSDIGKMPAISDQDMNAYL 1833 1479 VSKQVTAYNAVNNSTVSRTSASKYENMIRYTGSPDSLRSRTPMITPDLESGVKMWHLV-K 1656 NNKVFLLSFIRTLESQRSFSMRDRGNVASLIMTVLQSKLEYATDVLKQLLADLIDKNLES 1419 -----DLDT-EKYFHLVLP 1746 1078 871 964 931 KYMPDPLDEQADKHGIHDPHVRHTWKSNCLPLRFWVNMIKNPQFVFDIHKNSITDACLSV NHEHGDOKEGDRGS---KMVSEIYLTRLLATKGTLOKFVDDLFETIFSTAHRGSALPLAI KNHPKLLLRRTESVAEKMLTNWFTFLLYKFLKECAGEPLFSLFCAIKQQMEKGPIDAITG 918 OCLGREDLGHLCMWSDG---CRLRG--PLQ----PMAGT---CPAPEIRAIEPLSGPLD 1079 IDPCTELMRIDISIAC--IMPEGALPAPVPVCVRFERRGCVHGNLTFWYMQNPVITAISP EWSIVSGNTPIAVWGTHLDLIQNPQIRAKHGGKEHINICEVLNATEMTCQAPALALGPDH :: || |: | 1196 PVDFFINGRAYADEVAVAEELLDPEEAQRGSRFRLDYLPNPQFSTAKREKWIKHHPGEPL RESDLTLKRLQMQMDNLESRVALECKEAFAELQTDIHELTSDLD-GAGIPFLDYRTYTMR | :: :: :||:: |||: | :- | | :- || || || || || || || || || || || || RRAERYWQXTILIQMEEMESQIPFLEYKHFVTR ----GIEDHPVLRDLEVPGYRQERVEKGLKLFAQLI TFFPKCSSLYEERYVLPSQTLNSQGSSQAQETHPLLGEWKIPESCRPNMEEGISLFSSLL EARYSLSEDKLIRQQIDYKTLVLSCVSPDNANSPEVPVKILNCDTITQVKEKILDAIFKN 1540 VPCSHRPKAADMDLEWRQGSGARMILQDEDITTKIENDWKRLNTLAHYQVPDGSVVA--L LCL-KADPDFACGWCQGPGQCTLRQHCPAQESQWLELSGAKSKCTNPRITEIIPVTGPRE GGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGYIPAEQIVCEMGEAKPSQHAGFVE KQPCLFHRRSPSYIVCNTTSSDEVLEMKVSVQV---DRAKIHQDLVFQYVEDPTIVRIEP QSDLTERPEEFGFILDNVQSLLIL-----NKTNFTYYPNPVFEAFGPSGILELKPGTPI -LIGRHKVMARVGGMEYSPGMVYIAPDSPLSLPAIVSIAVAGGLLIIFIVAVLIAYKRKS 1137 RRSPVSGGRTİTVAĞERFHMVQNVSMAVHHIGREP-TLCKVLNSTLITCPSPGALSNASA ICVAVCRPEFMARSSOLYYFMTLTLSDLKPSRGPMSGGTQVTITGTNLNAGSNVVVMFG-1162 IL-----KGKNLIPPVAG-----GNVKLNYTVLVGEKPCTVTVSDVQLLCESPN-1722 IDKK------DNTLGRVK---VLFP-----1805 1425 1420 1603 1662 1598 1657 813 872 932 1024 991 1048 1108 1309 1365 1324 1360 1485 1480 1206 1265 ò 셤 ò 셤 a 셤 g ઠ 셤 à 엄 ò ò 염 셤 ð 셤 8 g ò g ð 셤 ò 셤 ð ð 셤 ò g 8 q ò ò

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1865 IAQAFIDACSISDLQLGKDSPTNKLLYAKEIPEYRKIVQRYYKQIQDMTPLSEQEMNAHL 1924
                                                                                                                                                                                                                                                  Human; Plexin-D1; semaphorin domain; hyperplasia; neoplasia; cancer; neurodegenerative disease; autoimmune disease; lupus; multiple sclerosis; inflammatory bowel disease; diabetes type I; rheumatoid arthritis; immunogen; antibody; MET related sequence; MRS.
                            1834 AEQSRMHMNEFNTMSALSEIFSYVGKYSBEILGPLDHDDQCGKQKLAYKLEQVITLM
                                              New plexin polynucleotides and polypeptides, useful in diagnosis, therapy and in producing compounds for treating diseases involving aberrant cell growth (e.g. cancer) or immune regulation (e.g. autoimmune diseases)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= "Secondary MET related sequence, MRS"
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/label= "Transmembrane domain"
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/label= "Primary Met related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mature Plexin-D1"
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label= Signal_peptide
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                                                                                                                                  standard; Protein; 1925 AA
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(REGC ) UNIV CALIFORNIA.
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The sequence represents Human Plexin-D1. Plexins are large transmembrane proteins whose extracellular domain shares homology with Scatter factor receptors and contain an approximately 500 amino acid Semaphorin domain. The plexin polymucleotides and polypeptides, and plexin-specific binding agents are useful in diagnosis, therapy and in the biopharmaceutical

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industry. In particular, the plexin polynucleotides and polypeptides are useful for generating compounds (e.g. plexin-specific binding agents or antibodies) for treating or diagnosing a disease or disorder involving aberrant cell growth (e.g. hyperplasia, neoplasia, cancer or neurodegenerative disease), or diseases or disorders involving aberrant immune regulation (e.g. autoimmune diseases such as lupus, inflammatory bowel disease or Diabetes Type 1), or immunosuppressive diseases such as nultiple sclerosis or rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                               80 YOLSGANLSLEAEAAVGPVPDSPLCHAPQLPQASCEHPRRLTDNYNKILQLDPGQGLVVV
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                                                                                                                                                                                                                                                                         15 LLMVG---MGSSTLLTRQPAPLSQKQRSFVTFRGEPAEGFNHLVVDERTGHIYLGAVNRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL---KGKNLIPPVAGGNVKLNYTVLVGEKPCTVTVSDVQLLCESPN-----LIGRHKVM 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1196 TLVIHKEQDSL-----GLQSHEYRVKIGQVSCDIQIVSDRIIHCSVNESLGAAVGQLPIT 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRTLESQRSFSMRDRGNVASLIMTVLQSKLEYATDVLKQLLADLIDKNLESKNHPKLLLR 1428
                                                                                                                                                                                                                                                                                                                                        1108 QSDLTERPERFGFILDNVQSLLIL-----NKTNFTYYPNPVFEAFGPSGILELKPGTPI 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GIEDHPVLRDLEVPGYRQERVEKGLKLFAQLINNKVFLLSF 1368
                                                                                                                                                                                               RTESVAEKMLTNWFTFLLYKFLKECAGEPLFSLFCAIKQOMEKGPIDAITGEARYSLSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDRGS----KMVSEIYLTRLLATKGTLQKFVDDLFETIFSTAHRGSALPLAIKYMFDFLDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1489 KLIRQQIDYKTLVLSCVSPDNANSPEVPVKILNCDTITQVKEKILDAIFKNVPCSHRPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STSEHRLGKDSPSNKLLYAKDIPSYKNWVERYYSDIGKMPAISDODMNAYLAEQSRMHMN
                                                                                                                            1019 TDPCTBLMRTDTSIAC--TMPEGALPAPVPVCVRFERRGCVHGNLTFWYMQNPVITAISP
                                                                                                                                                                                                                                                                                                                   1048 EWSIVSGNTPIAVWGTHLDLIQNPQIRAKHGGKEHINICEVLNATEMTCQAPALALGPDH
                                                                                                                                                                                                                                                                                                                                                                                                                :: | | | :
1136 PVDFFINGRAYADEVAVAEELLDPEEAQRGSRFRLDYLPNPQFSTAKREKWIKHHPGEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1214 ARVGGMEYSPGMVYIAPDSPLSLPAIVSIAVAGGLLIIFIVAVLIAYKRKSRESDLTLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WVNESVVRCDQVVLHTTRKSQV--FPLSLQLKGRPARFLDSPEPMTVMVYNCAMGSPDCS
                                                       GGTKVT1RGENLGLEFRD1ASHVKVAGVECSPLVDGY1PAEQIVCEMGEAKPSQHAGFVE
                                                                                                                                                                                                                                                 KQPCLFHRRSPSYIVCNTTSSDEVLEMKVSVQV---DRAKIHQDLVFQYVEDPTIVRIEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1274 LOMOMDNIESRVALECKEAFAELQTDIHELTSDLD-GAGIPFLDYRTYTMRVLFP----
                                   LCL-KADPDFACGWCQGPGQCTLRQHCPAQESQWLELSGAKSKCTNPRITEIIPVTGPRE
                                                                                                                                                                            932 ICVAVCRPEFMARSSQLYYFMTLTLSDLKPSRGPMSGGTQVTITGTNLNAGSNVVVMFG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::|: |
---DNTLGRVK------
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                                                                          858
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                                                                                                             872
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Human; Plexin-B3; semaphorin domain; hyperplasia; neoplasia; cancer; neurodegenerative disease; autoimmune disease; lupus; multiple sclerosis; inflammatory bowel disease; diabetes type I; rheumatoid arthritis; immunogen; antibody; MET related sequence; MRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New plexin polynuclectides and polypeptides, useful in diagnosis, therapy and in producing compounds for treating diseases involvinaberrant cell growth (e.g. cancer) or immune regulation (e.g.
         Tesier-Lavigne M;
EFNIMSALSEIFSYVGKYSEEILGPLDHDDQCGKQKLAYKLEQVITLM
                                                                                                                                                                                                                                                                                         1100..1119
/label= "Transmembrane domain"
                                                                                                                                                                                                                                             "Extracellular domain"
                                                                                                                                                                                                                                                                         4..507
|abel= "Semaphorin domain"
                                                                                                                                                                                                                                                                                                                                                                                                                          Goodman CS,
                                                                                                                                                                                                                          label= Signal_peptide
..1099
label= "Extracellular"
                                                                 Ź
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 58-62; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    growth (e.g. cancer)
                                                                 AAU00016 standard; Protein; 1788
                                                                                                                                                                                                                                                                "Mature
                                                                                                                                                                                                                                                                                                                                                                              9908-0150576
                                                                                                                                                                                                                                                                                                                                                          2000WO-US23365
                                                                                                                                                                                                                                                                                                                                                                                                                          Comoglio PM,
                                                                                                                                                                                                                                                      24..1788
/label= "I
                                                                                                                                                                                                                                                                                                                                                                                                (UYTO-) UNIV TORINO.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-226610/23.
N-PSDB; AAS00021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases)
                                                                                                                        Human Plexin-B3
                                                                                                                                                                                                                                                                                                                        WO200114420-A2
                                                                                                                                                                                                                                                                                                                                                            25-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                             25-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                           r, s
                                                                                                                                                                                         Homo sapiens
                                                                                                      09-MAY-2001
                                                                                                                                                                                                                                                                                                                                           01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                           Artigiani
Tamagnone
 1843
                                                                                                                                                                                                           Key
Peptide
                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                           Domain
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The sequence represents Human Plexin-B3. Plexins are large transmembrane proteins whose extracellular domain shares homology with Scatter factor receptors and contain an approximately 500 amino acid Semaphorin domain. The plexin polymucleotides and polypeptides, and plexin-specific binding agents are useful in diagnosis, therapy and in the biopharmaceutical industry. In particular, the plexin polymucleotides and polypeptides are useful for generating compounds (e.g. plexin-specific binding agents on antibodies) for treating or diagnosing a disease or disorder involving aberrant cell growth (e.g. hyperplasia, neoplasia, cancer or neurodegenerative disease), or diseases or disorders involving aberrant immune regulation (e.g. autoimmune diseases such as lupus, inflammatory bowel disease or Diabetes Type 1), or immunosuppressive diseases such as multiple sclerosis or rheumatoid arthritis.

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|                      | QY 959 LKPSRGPM9GGTQVTITGTNLNAGSNVVNMFGKQPC<br> | QY 1014 VLEMKVSVQVĎRAKIHQDLVFQYVEDPTIVRI                          | CY 1059 AVWGTHLDLIQNPQIRAKHGGKEHINICEVLNATEMTC : | Qy 1119 GFILDNVQSLLILNKTNFTYYDNPVFEAFGPSG | QY 1174 GGNVKLNYTVLVGEKPCTV-TVSDVQLLCESP Db 1027 KEEVRVHIGRGECLVKTLTRTHLYCEPPAHAPOP | Qy 1226 VYIAPDSPLSLPAIVSIAVAGGLLIIFIVAVLIAY   :     : :     : :       Db 1083 VQYEAEPPLSAFPVEAQAGVGMGAAVLIAAVLLITMY | QY 1283 SRVALECKEAFAELQTDIHELTSDLDGAGIPFLDVRTY :   :  :         | Qy 1343 YRQERVEKGIKLFAQLINNKVFLILSFIRTLESGRSF  | CY 1401 ATDVLKQLLADLIDKNLESKNH-PKILL-RRTESVAEK | Qy 1459 FSLFCAIKQQMEKGPIDAITGEARYSLSEDKLIRQQID :      :   :   :   :   :   :   :   : | Qy 1512 SPEVPVKILNCDTITQVKEKILDAIFKNVPCSHRPKAA           | Qy 1572 TKIENDWRRLNTLAHYQVPDGSVVALVSKQVTAYNAVN<br>               | Qy 1632 D-SLRSRTPMITPDLESGYKAWHLVKANHEHGD<br>Db 1412 QLCLTMNIPTLEDGEEGGYCLWHLVKATEEPEGAKVRC | Oy 1681 LL   | Qy 1692 VDDLFETIFSTAHRGSALPLAIKYMFDFLDEQADKHGI<br>                            | Qy 1752 IKNPQFVEDIHKNSITDACLSVVAQTFMDSCSTSEHRL:  | CY 1792  | Qy 1817 DIGKMPAISDQDMNAYLAEQSRMHMNEFNTMSALSEIF<br> |
|----------------------|---|---|--|---|---|---|---|--|--|---|--|--|---|--|---|--|--|--|
| SO Semience 1788 bb. | Query Match<br>Best Local Sim                   | 25 LLTRQPAPLSQKQRSFVTFRGEPAEGFNHLVVDERTGHIYLGAVNRIYKLSSDLKVLVTH 8 |  | -   | 199 ISSRKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFTIIPDFDIXYVYGFSSGNFVYF  185 I               | RLCKEDTAFNSYVEVPIGCERSGVEYRLLQAAYLS 31  | 317 KAGAVLGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCY | 376EGTLDLAWLKVKDIPCSSALLTIDDNF-CGLDWNAPLGVSDWV | 318<br>420<br>374                              | 479 GPVLR-DWAFSKDHBQLXIMSERQLTRVPVESCGQYQSCGBCLGSGDPHCGWCVLHNTCT                    | 538 RKERCERSKEPRRFASEMKQCVRLTVHPNNISVSQXNVLLVLETXNVPELSA | 590 GVNCTFEDLSEMDGLVVGNQIQCYSPAAKEVPRIITENGDHHVVQLQLKSKETGMTFAST | 650 SFVFYNGSVHNSCLSCVESPYRCHWCKYRHVCTHDPKTCSFQEGRVKLPEDCPQLLRVDK 697 NRSFVPNGS              | 710 ILVPVEVIKPITLKAKNLPQPQSGQRGYECILNIQGSEQRVPALRFNSSSVQCQNT | 766 SYSYEGMEINNLPVELITVVMNGHFNIDNPAQNKVHLYKCGAMRESCGLCTPAQNKVHLYKCGAMRESCGLCT | 816KADPDPACGEPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | 939 PAQESQWLELSGAKSKCTNPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAG |  |

PMGGRLIRVRGTGLDVVQRPLLSV 876 -IEPEWSIVSGN-----TPI 1058 TCQAPALALGPDHQSDLTERPEEF 1118 |::||: || || CLRSPAV---PDR----AHPQRV 966 EKMLTNWFTFLLYKFLKECAGEPL 1458 SPSNKILYAKDIPSYKNWVERYYS 1816 ----LFHRRSPSYIVCNTTSSDE 1013 SGILELKPGTPIILKGKNLIPPVA 1173 : | | | | : :: | : | : | : | : | ARPYRLKPGHVLDVEGEGLNLGIS 1026 ---NLIGRHKVMARVGGMEYSPGM 1225 | | : ::| :: | QPANGSGLPQFVVQMGNVQLALGP 1082 AYKRKSRESDLTLKRLQMQMDNLE 1282 |: ||::: ::::|| MYRHKSKQALRDYQKVLVQLESLE 1142 INTMRVLFPGIEDHPVLRDLEVPG 1342 SFSMRDRGNVASLIMTVLQSKLEY 1400 IDYKTLVLSCV-----SPDNAN 1511 \*::: | | :: VEFQPLTLMVLVGPGAGGAAGSSE 1346 AADMDLEWRQGSGARMILQDEDIT 1571 HALDLGERASP----- 1394 VNNSTVSRTSASKYENMIRYTGSP 1631 -----QKEGDRGSKMVSEIYLTR 1680 |::|||||| VDGPHTLPSTQPLSPASQGTLQKF 1530 RLGK----- 1791 ::|: KVGRVRAVPAAAGRGLRRKGLWG 1647 ------ATKGTLOKF 1691 SIHDPHVRHTWKSNCLPLRFWVNM 1751 PMGGRLIRVRGTGLDVVQRPLLSV 876 

cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), colliferative retinopathy, atherosclerosis, coronary heart disease, coronary heart disease, carterial ischemmia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and crepair (or nucleic acids encoding them) may be used to promote wound coronary expensively and inclusions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, contoinmune disease or accidental damage. The polypeptides and nucleotides cutoimmune disease or accidental damage. The polypeptides and in drug screening techniques. The present sequence represents a novel human compared to invention.

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Human; cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haematopoiesis regulation, tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; Jumphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; osronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiatthmatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NOV/plexin-Al homologue, SEQ ID NO:2123
                                                                                                                                                                                                                                   ABB11753 standard, peptide, 362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C, Drmanac RT;
1877 OKLAYKLEQVITLM 1890
                                   : | | : | : | : | : | 1768 LQLACRLQQVAALV 1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2001; 2001WO-US03800.
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27-APR-2000; 2000US-0560875
                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-457740/49.
N-PSDB; ABA08997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                      ABB11753;
                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                          ABB11753
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comptibiling a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence polypeptides of the invention activities, explications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities, stem cell growth factor activity; haematopoiesis regulatory activity; tissue growth activities; hemokancoulatory activity; activity or inhibin-related activities; chemotactic or chemokinetic activities; haemostatio, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogeneals, cancer cell proliferation or metastasis.

The permittion are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -Claim 20; Page 239; 1963pp; English.

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1480 BARYSLSEDKLIRQIDYKTLVLSCVSPDNANSPEVPVKILNCDTITQVKEKILDAIFKN 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1540 VPCSHRPKAADMDLEWRQGSGARMILQDEDITTKIENDWKRLNTLAHYQVPDGSVVALVS 1599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGDQKEGDRGSKMYSEIYLTRLLATKGTLQKFVDDLFETIFSTAHRGSALPLAIKYMFDF 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1420 KNHPKLLLERRTESVAEKMLTNWFTFLLYKFLKECAGEPLFSLFCAIKQQMEKGPIDAITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 KNHPKLLIRRTESVAEKMLTNWFTFLLYKFLKESAGEPLFMLYCAIKHQMEKGPIDAITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 HLDQREGDRGSKMVSEIYLTRLLATKGTLQKFVDDLFETIFSTAHRGSALPLAIKYMFDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1720 IDEQADKHGIHDPHVRHTWKSNCLPLRFWVNMIKNPQFVFDIHKNSITDACLSVV 1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.8%; Score 1573.5; DB 22
84.5%; Pred. No. 5.5e-128;
tive 22; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide, SEQ ID NO: 3042.
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA essiby without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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   1810 WVERYYSDIGKMPAISDQDMNAYLAEQSRMHMNEFNTMSALSEIFSYVGKYSEEILGPLD
                                                                                                                                  629 WVEDYYKGIRQMVQVSDQDMNTHLAEISRAHTDSLNTLVALHQLYQYTQKYYDEIINALE
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T, Koga
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S, Otsuki
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55.3%; Pred. No. 1.6e-110;
iive 70; Mismatches 106;
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K, Kojima S,
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ı T, Nagai
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11-JAN-2000; 2000JP-0118774.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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                                                            Ishii S, Kawai Y;
S, Otsuki T, Koga
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                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 3042; 1380pp + sequence listing; English.
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                                                            ai T, Hayashi K, Is
Nagai K, Kojima S,
                                                         Isogai T,
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                                                                                      Wakamatsu A, Sugiyama T,
(HELI -) HELIX RES INST
                                                         Nishikawa T,
                                                                                                                                                  WPI; 2001-524255/58.
N-PSDB; AAK94342.
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                                                                                                                                                     244 PSDTLALVSHFDIFYIYGFASGGFVYFLTVQPE--TPEGVAINSAGDLFYTSRIVRLCKD
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                                                                                      FGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVASMIKI
                                                                                                    Zollinger-Ellison syndrome; gastrointestinal ulceration;
congenital microvillus atrophy; skin disease; cell growth;
abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
anti-thrombotic; wound healing; tissue repair.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of protein PRO235.
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97US-0063128.
97US-0063128.
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97US-0063327.
97US-0063541.
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Length 552;

13.5%; Score 1351.5; DB 20;

552 AA;

Query Match

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                                                                             DTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRK 346
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                                                                                                                                    103 TFNHLIVHQGTGAVYVGAINRVYKLTGNLIIQVAHKTGPEEDNKSRYPPLIVQPCSEVLT
                                                                                                                                                                           110 TTNNVNKWILLIDYKENRLIACGSLYQGICKLLRLEDLFKLGEPYHKKEHYLSGVNESGSV
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                             Gaps
                             55;
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51.6%; Fr. 81; }
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AAB33420 standard; Protein; 552 AA AAB33420

AAB33420;

29-JAN-2001 (first entry)

Human PRO235 protein UNQ209 SEQ ID NO:31.

dermacological; antiarthritic; antitheumatic; immunosuppressive; haemostatic; antithyroid; antidabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; systemic sclerosis; sarcoidosis; systemic vacultis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; Human; immune related disease; diagnosis; antiinflammatory; cardiant; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease.

Homo sapiens

WO200053758-A2

14-SEP-2000

02-MAR-2000; 2000WO-US05841.

28849 99WO-US28313 99WO-US28301 99WO-US28634 99WO-US28564 99WO-US31274 -Sn66 0M66 33-JUN-1999 -VON-6 

(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W; Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V; Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M; Lu Y, Pe Tumas D, Stewart TA,

WPI; 2000:572271/53. N-PSDB; AAC58585. Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 33; Fig 14; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic solerosis, idiopathic inflammatory myopathies, Sjogren's systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demopelinary diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, untoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease.

ARCS837 to AACS8278 represent PCR primers and hybridisation probes used in the isolation of human PRO polynucleotide and protein

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170 FGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVASMIKI 229
129 YGVIVRSEGEDGKLFIGTAVDGKQDYFPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKI 282
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                                                                                                                                                          -----SFVTFRGEPAE-
                                                                         Query Match 13.5%; Score 1351.5; DB 21; Length 552; Best Local Similarity 51.6%; Pred. No. 2.7e-108; Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps
sequences given in the exemplification of the present invention.
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                                       552 AA;
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Search completed: June 24, 2003, 18:56:54 Job time : 102 secs

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TOPOLOGY: linear

MOLECULE TYPE: protein

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5: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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| 1.9 650 1 | 650 2 US-09-060-692-60<br>650 3 US-08-833-391-60 | 1.9 650 4 US-09-060-610-60 Sequence<br>1.9 650 5 PCT-US94-10151A-60 Sequence | 1.5 666 4 US-09-240-410-2 Sequence<br>1.5 606 4 US-09-041-236-4 Sequence | 1.5 634 4<br>1.4 775 4 | 1.3 1453 1 US-08-308-872B-6 Sequence 1.3 768 1 US-08-454-455-4 Sequence | 771 4 US-09-188-930-183 Sequence 1<br>1525 3 US-09-191-647-2 Sequence 2 |             | 1416 4 US-09-071-035-404 Sequence 1448 4 US-09-071-035-402 Sequence |
|-----------|--|--|--|------------------------|---|---|-------------|---|
| 185       | 185  | 185<br>185   | 147<br>146.5   | 146<br>140             | 131<br>130  | 129<br>128  | 128.<br>128 | 126.5   |
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## ALIGNMENTS

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US-09-181-706-2

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Sequence 2, Application US/09181706

Sequence 1. Sequence 2. Application US/09181706

Sequence 1. Sequence 2. Application US/09181706

Sequence 2. Application US/09181706

Sequence 3. Application US-09181706

APPLICANT: Robert F. DuBose Richard S. Johnson

TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN

CORNERS OF SEQUENCES: 1. Heary

STREET: MA

COUNTRY: Seattle

STREET: MA

COUNTRY: Jains C. Henry

STREET: MA

COMPUTER RADABLE FORM:

MEDILOATION WHERE: PLODS/MS-DOS

SOFTWARE: PROME OF COMPATABLE PROME

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COMPUTER: OCCODER 28, 1997

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| 74;  | 123<br>113  | 172<br>165  | 208<br>224  | 267  | 326<br>302   | 38 <u>4</u><br>344   | 443<br>387  | 490<br>435   | 550<br>487   | 610  | 699  | 542<br>729  | 551   | 787<br>585   | 847<br>615   | 907  | 625 | 961  | 1014<br>728  |
| <pre>ch 13.5%; Score 1349; DB 4; Length 1568; 1 Similarity; 24.8%; Pred. No. 5.8e-112; 480; Conservative 291; Mismatches 591; Indels 576; Gaps</pre> | YKLSSDLKVLYTHETGPDEDNPKCYPPRIVQTCNBPLTTNNVNKMLLIDYK | ENRLIACGSLYQGICKLLRLEDLFKLGEPYHKKEHYLSGVNESGSVFGV | IVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNS : :::::: :: :: :: :: :: :: :: :: :: :: | BADGMFAYVFHDEFV-ASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPP | GSTTKEQVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVE-YRLLQAAYLSKAGAVLGRTL | GVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLA | W-LKVKDI PCSSALLTI DDNFCGLDMNAPLGVSDMVRGI PVFTEDRDRMTSVI AYVKNH<br> | SLAFVGTKSGKLKKIRVDGPRGNALQYETVQVVDPGPVLRDMAFSKD :: | HEQLYIMSERQLTRVPVESCGQYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPRR : | FASEMKQCVRLTVHPNNISVSQXNVLLVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQI | QCYSPAAKEVPRITTENGDHHVVQLQLKSKETGMTFASTSFVFYNCSVHNSCL-SCVESP | ÀKKCPKİQIIRSŠKĒKTIVTMYGŠFSPRHSKCMYKNVDŠS YRCHWCKYRHVCTHDPKTCSFQEGRVKLPEDCPQLLRVDKILVPVEVIKPITLKAKNLPQ | QNKSQ | PQSGQRGYECILNIQGSEQRVPALRFNSSSVQCQNTSYSYSGMEINNLPVELTVVWNG | HPNIDNPAQNKVHLYKCGAMRESCGLCLKADPDFACGWCGGPGQCTLRQHCPAQESQWLE | LSGAKSKCINPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDG |     | YIPAEQIVCEMGEAKPSQHAGFVEICVAVCRPEFMARSSQLYYFMTLTLSDLKP | SRGPMSCGTQVTITGTNLNAGSNV-VVMPGKQPCLFHPRSPSYIVCNTTSSDEV : |
| Ti ti  | 72  | 124   | 173   | 209  | 268  | 327  | 385   | 444  | 491  | 551  | 611  | 503   | 543   | 730  | 788  | 848  | 616 | 908  | 962  |
| Query Ma<br>Best Loc<br>Matches  | <u>ک</u> ۾  | è a   | 2<br>2<br>3   | දුරු අ   | 상 음  | & <del>8</del>   | \text{\delta} \frac{1}{2}   | 송 원  | \$ A   | Š t  | B &  | 음 &   | ΟP    | 중 음  | දු ද   | 3 8  | qq  | දු දු  | Yo qa  |

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1015 LEMK-VSVQVDRAKIHQDLVFQYVEDPTIVRIEPEWSIVSGNTPIAVWGTHLDLIQNPQI 1073
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                                                                                                                             1134 T----NFTYYPNPVFEAFGPSGILELKPGTPIILKGKNLIPPVAGGNVKLNYTVLVGEK
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US-09-458-791-2
iS-09-458-791-2
sequence 2, Application US/09458791
serient No. 6174689
general information:
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
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1514 ---EVPVKILNCDTITQVKEKILDAIFKNVPCSHRPKAADMDLEWRQGSGARMILQDEDI 1570
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                                                                                                                                                                                                                                                                                                                  PQSGQRGYECILNIQGSEQRVPALRFNSSSVQCQNTSYSYEGMEINNLPVELTVVWN--G 787
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                                                                                                                                                611 QCYSPAAKEVPRIITENGDHHVVQLQLKSKETGMTFASTSFVFYNCSVHNSCL-SCVESP
                                                                                                                                                                                       -----AKKCPKI------QIIRSSKEKTTVTMVGSF----SPRHSKCMVKNVDSS
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                                                               FASEMKQCVRLTVHPINI SVSQYNVLLVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQI
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586 RFNFTN-----CSSLKE-CPACVET----GCAWCKSARRC-
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166 VYR-AGRNNRWYLAVAATYVLPEPETASRCNPAASDHDTAIALKDTEGRSLATQELGRLK 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 ENR-----LIACGSLYQGICKLLRLEDLFKLGEPYHKKEHYLSGV-----NESGSVFGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 13.5%; Score 1349; DB 4; Length 1568; Local Similarity 24.8%; Pred. No. 5.8e-112; nes 480; Conservative 291; Mismatches 591; Indels 576
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLAFVGTKSGKLKKIRVDGPRGNALQYETVQVV--
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/458,791
FLING DATE: 10-Dec-1999
CLASSIFICATION: «Unknown»
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/958,598
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
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NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: (206)470-4189
(206)233-0644
                                                                                                                                            ZIP: 98101
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                CITY: Seattle
STATE: WA
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53 HLVVDERTGHIYLGAVNRIYKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTTTN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.3%; Score 227; DB 1; Length 724; Best Local Similarity 20.4%; Pred. No. 4.4e-11; Matches 147; Conservative 118; Mismatches 260; Indels 196;
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713D
FILING DATE: 13-SEP-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
                                     E: SCIENCE & TECHNOLOGY LAW GROUP
268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 62: SEQUENCE CHARACTERISTICS: LENGTH: 724 amino acids TYPE: amino.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                          San Francisco
                                     ADDRESSEE:
STREET: 268
CITY: San 1
STATE: CA
                                                                                                                                                                                                                94104
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1074 RAKHGGKEHINICEVLNATEMTCQAPALALGPDHQSDLTERPEEFGFILDNVQSLLILNK 1133
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                                                                           --KSSKVRTNVTVKLRVQD
                                                                                                                                            1134 T----NFTYYPNPVFEAFGPSGILELKPGTPIILKGKNLIPPVAGGNVKLNYTVLVGEK
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Sequence 62, Application US/08121713D

Patent No. 5639856

GENERAL INPORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Matthes, David
APPLICANT: Bentley, David
APPLICANT: Bentley, David
APPLICANT: APPLICANT: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
                                                                                                                                                                                          786 IISHELKGNINVSEYCVATYCGFLAPSL------
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1540 ERERGLEEAQKQLLHVKV 1557
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Gaps

379

470 485 529

320 332 376

us-09-964-956-13.rai

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: O'CONDOL, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
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Patent No. 5935865
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Kolodkin, Alex L.
Matthes, David
Bentley, David R.
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K 677
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APPLICANT:
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                                                989
                                                                                                                                                 -----CSYNITVDAHRCTPPNKSNDYQ 676
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                                                LVLETYNVPELSAGVNCTPEDLSEMDGLVVGNQIQCYSPAAKEVPRIITENGDHHVVQLQ
                                                                               ----VKIPEVLKNEQVTWYHHSKDKGRY---EIR-YSPTK-----YIETTERGLVVVS
                                                                                                                   637 LKSKETGMTFASTSFVFYNCSVHNSCLSCVESPYRCHWCKYR----HVCTHDPKTCSFQ
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Sequence 62, Application US/08835268
Patent No. 5807826
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Bentley, David
APPLICANT: Bentley, David
APPLICANT: Gonnor Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: SCIENCE & TECHNOLOGY LAW GROUP
268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 20.4%; Pred. No. 4.4e
Matches 147; Conservative 118; Mismatches
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       -----YDCHLGGSLL
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COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62:
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amino acid
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APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
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SOFTWARE: Patent T
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                                                                                                                                                     637 VNEADGGR-
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--- DRLYVCGTNAHNPKDYVIYANLTHLPRSE 171
                                                                                                                                                                                                                                                                                                                                        ---FNSYVEVPIGCERSG---VEYRLLQAAYLSKAGA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 VLGRTLGVHPDDDLLFTVFSKGOKRKMKSLDESALCIFILKOI----NDRIKERLQSCYR 376
                                                                                                                           172 YVIGVGLGIAKCPYDPLDN----STAIYVENGNPGGLPGLYSGTNAEFTKAD---TVIFR 224
                                                                                                                                                                                                  220 DEFVASMIKIPSDTFT1IPDFDI-----YYVYGFSSGNFVYFLTLQP--EMVSPPGSTT 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---CERSKEPRRFASEMKOCVRLTVHPNNISVSOYNVL
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                                                                      168 SVFGVIVS----YSNLDDKLFIATAV---DGKPEYFPTISSRKLTKNSEADGMFAYVFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 GEGTLDLAWLKVKD--IPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIP------
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                                                                                                                                                                                                                                                              225 TDLYNTSAKRLEYKFKRTLKYDSKWLDKPNFVGSFDIGEYVYFFFRETAVEYIN--
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53 HLVVDERTGHIYLGAVNRIYKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTTTN 112
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Best Local Similarity 20.4%; Pred. No. 4.4e-11;
Matches 147; Conservative 118; Mismatches 260; Indels 196; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,391
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matches, David R.
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 268 Bush Street, Suite 3200 CITY: San Francisco COUNTE: CAN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFRAX: (415)343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/121,713
FILING DATE: 13-SRP-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                         Sequence 62, Application US/08833391
Patent No. 6013781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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; MOLECULE TYPE: protein
US-08-833-391-62
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677 K 677
                692 E 692
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2.3%; Score 441;
Best Local Similarity 20.4%; Pred. No. 4.4e-11;
Matches 147; Conservative 118; Mismatches 260; Indels 196;
FILING DATE:
CLASELFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELECHORE: (415) 343-4341
TELEFRONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
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(415) 343-4342
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                                                                                                                                                                                                                                                                                                                                                                                                                                 637 LKSKETGMTFASTSFVFYNCSVHNSCLSCVESPYRCHWCKYR-----HVCTHDPKTCSFQ 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YDCHLGGSLL-----CSYNITVDAHRCTPPNKSNDYQ 676
                                                                                                                                        ----NSAMLPVINSRVPEPRPGTCVNDT----SNLPDTVLNFIRSHPLMDKAVNHEHN 429
                                                                                                                                                                                              430 NPVYYKRDLVFTKLVVDKIR----IDILNQEYIVYYVGTNLGRIYKIVQYYRNGESLSKL 485
                                                                                                                                                                                                                                                                                                       ----CERSKEPRRFASEMKQCVRLTVHPNNISVSQYNVL 576
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                                                                                                                                                                                                                                                                                                                                                                      577 LVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQIQCYSPAAKEVPRIITENGDHHVVQLQ 636
                                                                                                                                                                                                                                                           : | | :: | |: | |: || 486 LDIFEVAPNEALQVMEISQTRKSLYIGTDHRIKQIDLAMCNRRYDNCFRCV--RDPYCGW
                                                  321 VLGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQI----NDRIKERLQSCYR
                                                                                                               377 GEGTLDLAWLKVKD--IPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIP-----
                                                                                                                                                                           -----VFTE---DRDRMTSVIAYVYKNHSLAFVGTKSGKLKKIRVDGPRGNAL-QY
                                                                              -----QLPSDKSRFFATFT----TSTNGLIGSAVCSFHINEIQAAFNGKFKEQSSS-
280 GKAVY-SRIARVCKKDVGKNILAHNWATYLKARINCSISGEFPFYFNEIQSVY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David R.
APPLICANT: Bentley, David R.
APPLICANT: O'Comnor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCIENCE & TECHNOLOGY LAW GROUP 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 62, Application US/09060610 Patent No. 6344544 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            530 CVLHNTCTRKER------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Osman, Richard A. REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS: ADDRESSE: SCIENCE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           San Francisco
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     637 VNEADGGR--'-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 724;
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GENERAL INFORMATION:
APPLICANT: The Regents of the University of Callfornia
TITLE OF INVERTION: The Semaphorin Gene Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
2.3%; Score 227; DB 4; L
Best Local Similarity 20.4%; Pred. No. 4.4e-11;
Matches 147; Conservative 118; Mismatches 260;
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                                                                                                                 LENGTH: 724 amino acids TYPE: amino acid
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-09-060-610-62
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530 CVLHNTCTRKER-------CERSKEPRRFASEMKQCVRLTVHPNNISVSQYNVL 576
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713D
FILING DATE: 13-5EP-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jenny Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%; Score 207; DB 1; L
Best Local Similarity 18.9%; Pred. No. 2.9e-09;
Matches 111; Conservative 107; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: SCIENCE & TECHNOLOGY LAW GROUP
I: 268 Bush Street, Suite 3200
San Francisco
                                                                                                                                                                                                                -----YDCHLGGSLL
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX:
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                637 VNEADGGR---
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5639856
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 VLGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQI----NDRIKERLQSCYR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::| | | | : :| | | 380 ----NSAWLPVLNSRVPEPRPGTCVNDT----SNLPDTVLNFIRSHPLMDKAVNHEHN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VFTE---DRDRMISVIAYVYKWHSLAFVGTKSGKLKKIRVDGPRGNAL-QY 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 SVFGVIVS----YSNLDDKLFIATAV---DGKPEYFPTISSRKLTKNSEADGMFAYVFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 NPVYYKRDLVFTKLVVDKIR----IDILNQEYIVYYVGTNLGRIYKIVQYYRNGESLSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 GEGTLDLAWLKVKD--IPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.3%; Score 227; DB 5; Length 724;
Best Local Similarity 20.4%; Pred. No. 4.4e-11;
Matches 147; Conservative 118; Mismatches 260; Indels 196; Gaps
                                              & HERBERT
                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: PCT/US94/10151A
FILING DATE: PCT/US94/10151A
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:

NAME: Osman, Richard A.

REGISTATION NUMBER: 36,627

REPERENCE/DOCKET NUMBER: FP-58750-PC/RAO
TELECOMMUNICATION INFORMATION:
TELERAX: (415) 781-1989
TELERX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: 1nnear
                 CORRESPONDENCE ADDRESS:
ADDRESSER: FLEHR HOHBACH TEST ALBRITTON
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                              ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein PCT-US94-10151A-62
NUMBER OF SEQUENCES:
                                                                                                                            USA
                                                                                                        STATE: CA
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591 636 691 ------CSYNITVDAHRCTPPNKSNDYQ 676 97 -PPRIVQTCNEPLTTTNNVNKMLLIDYKENRLIACG-SLYQGICKLLRLEDLFKLGEPYH 154 43 FRGEPAEGFNHLVVDERTGHIYLGAVNRIYKLS-SDL----KVLVTHETGPDEDNPKCY 96 592 ----VKIPEVLKNEQVTWYHHSKDKGRY---EIR-YSPTK-----YIETTERGLVVVS 577 LVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQIQCYSPAAKEVPRIITENGDHHVVQLQ 637 LKSKETGMTFASTSFVFYNCSVHNSCLSCVESPYRCHWCKYR----HVCTHDPKTCSFQ Indels 150; Gaps 544 DKEANTCRPYBLDLLQDVANETSDICDSSVLKKKIVVTYGQSVHLGCF---

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27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461
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                                                                                                                                                                                                                                                                                                                                                                                KKE------HYLSGVNESGSVFGVIVS-YSNLDDKLFIATAVDGKPEYFPTISS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 RKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQP 261
                                                                                                                                                                                                                                                         98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 BMVSPPGSTTKEQVYTSKLVRLCKEDTA-----FNSYVEVPIGCERSGVEYRLLQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              462 GPRGNALQYETVQVVDPGPVLRDM---AFSKDHEQLYIMSERQLTRVPVESCG--QYQSC
                                                                                                                                                                                                                    43 FRGEPAEGFNHLVVDERTGHIYLGAVNRIYKLS-SDL----KVLVTHETGPDEDNPKCY
                                                                                                                                                                                                                                             | | | : ::|: : | : | : | 197 RSDLKQLNAPNFVNTMEYNDFI-------FFFFRETAVEXI---NCGKAIX
                                                                                                                                                                                 Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           558
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                                                                                                                                         Length 730;
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                                                                                                                                                              Best Local Similarity 18.9%; Pred. No. 2.9e-09; Matches 111; Conservative 107; Mismatches 219;
                                                                                                                                         2.1%; Score 207; DB 1; 18.9%; Pred. No. 2.9e-09;
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APPLICANT: Matthes, David
APPLICANT: Bentley, David
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Far
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUI
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 58, Application US/09060692
Patent No. 5935865
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Kolodkin, Alex L.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: line-
      SEQUENCE CHARACTERISTICS
                                                                          MOLECULE TYPE: protein US-08-835-268-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: CA
COUNTRY: USA
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US-09-060-692-58
                                                                                                                                             Query Match
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Sequence 58, Application US/08833391

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 EMVSPPGSTTKEQVYTSKLVRLCKEDTA-----PNSYVEVPIGCERSGVEYRLLQAA 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.1%; Score 207; DB 2; Length 730;
Best Local Similarity 18.9%; Pred. No. 2.9e-09;
Matches 111; Conservative 107; Mismatches 219; Indels 150; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 RSDLKQLNAPNFVNTMEYNDFI------PFFFRETAVEYI---NCGKAIY----
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
APLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATORNEY/AGENT IMPORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECHONE: (415)343-4341
                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,692
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-060-692-58
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RESULT 13 US-08-833-391-58

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238 ....-SRVARVCKHDKGGPHQGGDRWTSFLKSRLNCSVPG-DYPFYFNE 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 -PPRIVQTCNEPLTTTNNVNKMLLIDYKENRLIACG-SLYQGICKLLRLEDLFKLGEPYH 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 RKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQP 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
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197 RSDLKQLNAPNFVNTMEYNDFI------FFFFRETAVEYI---NCGKAIY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 207; DB 3; Length 730;
Best Local Similarity 18.9%; Pred. No. 2.9e-09;
Matches 111; Conservative 107; Mismatches 219; Indels 150; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,391
APPLICANT: Goodman, Corey S.
APPLICANT: Rolodkin, Alex L.
APPLICANT: Matches, David
APPLICANT: Bentley, David
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                           .....RESSEE: CYCENOLOGY LAW GROUP STREET: 268 Bush Street, Suite 3200 CITY: San Francisco STATE: CA COUNTRY: USA ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,713
FILING DATE: 13-58P-1993
ATTORNEY/AGENT INFORMATION:
NAME: OSMMAN, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                           ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
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447 ----SVVIEELQVLPPGVPVKNLYVVRMDGDDSKLVVVSDDEILAIKLHRCGSDKITNC 501
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                                                                                                                                                                                                                                                                                                                                            281 IQSTSDIIEGNYGG--QVEKLIXGVFT----TPVNSIGGSAVCAFSMKS----ILESFDG 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KNHSLAFVGTKSGKLKKI------RVD
                                                                                                                                                                                                                                                        -HYLSGVNESGSVFGVIVS-YSNLDDKLFIATAVDGKPEYFPTISS
                                                                                                                                               202 RKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQP
                                                                                                                                                                                                                                262 EMVSPPGSTTKEQVYTSKLVRLCKEDTA-----FNSYVEVPIGCERSGVEYRLLQAA
                                                                                                                                                                                                                                                                                                                  314 YLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQS
                                                                                                                                                                                      ---FFFFRETAVEYI---NCGKAIY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 58 Application PC/TUS9410151A
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
APPLICANT: The Semaphorin Gene Family
NUMBER OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                     147 EKBYEGRGLCPFDPDHNSTAIYSEGQLYSATVADFSGTDPLIYRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/10151A FILING DATE: 13-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE JOCKET NUMBER: FP-58750-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                               197 RSDLKQLNAPNFVNTMEYNDFI----
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TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 56
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 730 amino acids
amino acid
3Y: linear
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ZIF: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
COMPUTER
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CLASSIFICATION:
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PCT-US94-10151A-58
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                                                                                                     461
               374 CYRGEGTLDLAWLKVKDI------PCSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVF 425
                                            43 FRGEPAEGFNHLVVDERIGHIYLGAVNRIYKLS-SDL-----KVLVTHETGPDEDNPKCY
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                                                                                                                             Indels 150; Gaps
                                                                                                                                                                                                                                                                                                         502 RECVSLQDPYCAWDNVELKCHAVGSPDWSAGKRRFIQNISLGEHKAC 548
                                                                                                                                                                                                                                                                        517 GECLGSGDPHCGWCVLHNTCTRKERCERSKEPRRF-----ASEMKQC 558
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                                                                                                       ----KNHSLAFVGTKSGKLKKI---
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 58, Application US/09060610

Patent No. 6344544

GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Matches, David R.
APPLICANT: Matches, David R.
APPLICANT: Matches, David R.
APPLICANT: Pentley, David R.
APPLICANT: Portley, David R.
APPLICANT: Portley, David R.
APPLICANT: Portley, David R.
APPLICANT: Portley, David R.
APPLICANT: Portley, David R.
APPLICANT: Portley, David R.
APPLICANT: ACCURATION: The Semaphorin Gene Family NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.1%; Score 207; 'DB 4; Lu Best Local Similarity 18.9%; Pred. No. 2.9e-09; Matches 111; Conservative 107; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: SCIENCE & TECHNOLOGY LAW GROUP
268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B94-002-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET'NUMBER: B9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEPRX: (415)343-4342
                                                                                                           426 TEDRDRMTSVIAYVY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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STREET: 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94104
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PCT-US94-10151A-58

27; 155 KKE------HYLSGVNESGSVFGVIVS-YSNLDDKLFIATAVDGKPEYFPTISS 201 :|| 147 EKEYEGRGLCPFDPDHNSTAIYSEGQLYSATVADFSGTDPLIYRG------PLRTE 196 97 -PPRIVQTCNEPLTTINNVNKWLLIDYKENRLIACG-SLYQGICKLLRLEDLFKLGEPYH 154 202 RKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQP 261 197 RSDLKQLNAPNFVNTMEYNDFI------ 237 262 EMVSPPGSTTKEQVYTSKLVRLCKEDTA------PNSYVEVPIGCERSGVEYRLLQAA 313 314 YLSKAGAVLGRILGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQS 373 281 IQSTSDIIEGNYGG--QVEKLIYGVFT----TPVNSIGGSAVCAFSMKS----ILESFDG 330 374 CYRGEGILDLAWLKVKDI------PCSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVF 425 426 TEDRIDRMTSVIAYVY-----RVNHSLAFVGTKSGKLKKI------RVD 461 462 GPRGNALQYETVQVVDPGPVLRDM---AFSKDHEQLYIMSERQLTRVPVESCG--QYQSC 516 86 Query Match 2.1%; Score 207; DB 5; Length 730; Best Local Similarity 18.9%; Pred. No. 2.9e-09; Matches 111; Conservative 107; Mismatches 219; Indels 150; Gaps 41 FLGNESHKDHFKLLEKDHNSLLVGARNIVYNISLRDLTEFTEQRIEWHSSGAHRE--LCY 43 FRGEPAEGFNHLVVDERTGHIYLGAVNRIYKLS-SDL----KVLVTHETGPDEDNPKCY 517 GECLGSGDPHCGWCVLHNTCTRKERCERSKEPRRF----ASEMKQC 558 238 셤 g g ઠે g ð ઠે 8

Search completed: June 24, 2003, 19:01:28 Job time : 38 secs



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APPLICANT:
APPLICANT:
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                                                                                                                                               (without alignments)
2889.579 Million cell updates/sec
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Sequence 170,
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/ cgn2_6/ptodate/2/pubpaa/NCT NEW_PUB.pep:*
/ cgn2_6/ptodate/2/pubpaa/NCT NEW_PUB.pep:*
/ cgn2_6/ptodate/2/pubpaa/USO6_UNEGONB.pep:*
/ cgn2_6/ptodate/2/pubpaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodate/2/pubpaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodate/2/pubpaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodate/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodate/2/pubpaa/USO9_NEW_PUB.pep:*
/ cgn2_6/ptodate/2/pubpaa/USO9_PUBCOMB.pep:*
                                                                                                                         June 24, 2003, 19:00:01 ; Search time 71 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-907-853-170
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US-10-208-072-332
US-10-121-049-332
US-10-121-904-332
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US-09-907-942-170
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Gapop 10.0 , Gapext 0.5
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| Ap        | Ap       | Ap       | Ap       | Ap       | Ap       | Ap       | Ap        | Ap       | AD       | AD       | Ap         | Ap        | Ap       | Ap         | Ap       | Ap       | Ap       | Ap       |  |
|-----------|----------|----------|----------|----------|----------|----------|-----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|------------|-----------|----------|------------|----------|----------|----------|----------|--|
| 170.      | 170,     | 332,     | 332,     | 170,     | 170,     | 170,     | 33        | 17       | 17       | 170,     | 332,     | 170,     | 170,     | 170,     | 170,     | 332,     | 332,     | 170,       | 170,      |          | 170,       |          | 170,     | 332,     | 332,     |  |
| Segmence  | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence  | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence   | Sequence  | Sequence | Sequence   | Sequence | Sequence | Sequence | Sequence |  |
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| 4-859-170 | -204-    | 2-431-33 | 3-114-33 | 4-786-17 | 6-646-17 | 6-700-17 | 0-002-332 | 2-903-17 | 3-749A-1 | -786-17  | 2-419-   | 2-736-17 | -119-17  | -956-17  | 7-794-1  | 3-262-3  | 2-42     | 02-692-17( | 3-520-170 | -943-1   | 04-462-170 | 5-0      | 7-925-17 | 1-050-33 | 1-755-33 |  |
| US-09-904 | -60-     | 4        | 7        | 6        | 06-60-SD | 6-60-    | 7         | 06-60-SD | US-09-90 | 6        | US-10-14 | 9        | 6-60-    | 6-60-    | 06-60-SD | US-10-12 | US-10-14 | 6-60-      | 06-60-SD  | 6        | 06-60-SD   | 06-60-SD | 06-60-SD | US-10-12 | US-10-14 |  |
| σ         | σ        | σ        | σ        | σ        | σ        | Φ        | σ         | 0        | 9        | Φ        | σ        | Q        | σ        | σ        | σ        | 9        | σ        | σ          | σ         | 6        | σ          | σ        | σ        | ο        | σ        |  |
| ິດ        | 552      | 5        | S        | ß        | S        | S        | S         | S        | S        | S        | S        | ß        | S        | S        | S        | S        | S        | ß          | S         | S        | S          | S        | S        | S        | S        |  |
|           | 13.5     | ۳.       | m.       | m.       | m.       | έ.       | ω.        | ë.       | 'n.      | •        | ë.       | ۳.       | ë.       | ۳.       | ω.       | ω.       | ë.       | ë.         | ë.        | ë.       | ۳.         | •        | •        | •        | •        |  |
| 1351.5    | ä        | 51.      | 51.      | 51.      | 51.      | 51.      | 51.       | 51.      | 51.      | 1351.5   | 51.      | 51.      | 51.      | 51.      | 51.      | 351.     |          | 51.        |           | 51.      | 1351.5     | 51.      | 51.      | 51.      |          |  |
|           | 21       |          |          |          |          |          |           |          |          |          |          |          |          |          |          |          |          |            |           |          |            |          | 43       |          |          |  |

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## ALIGNMENTS

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-114 CURRENT APPLICATION VMBER: US/09/905,291A CURRENT FILING DATE: 2001-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PAPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
                Sequence 170, Application US/09905291A Patent No. US20020160374A1 GENERAL INFORMATION: APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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                                                                                                                                                                                                   Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                 Kenneth, J
                                                                                                                                                                                                                                                                                        Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                            Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                            Goddard, A.
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US-09-905-291A-170
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283 PSDTLALVSHPDIFYIYGFASGGFVYFLTVQPE--TPEGVAINSAGDLFYTSRIVRLCKD 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 LTNNVNKLLIIDYSENRLLACGSLYQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTM 222
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLIING DATE: 1999-09-08
PRIOR PLIING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PLIING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PLIING DATE: 1999-09-15
PRIOR PLIING DATE: 1999-09-15
PRIOR PLIING DATE: 1999-10-05
PRIOR PLIING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PLIING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/2813
PRIOR PLIING DATE: 1999-11-29
PRIOR PLIING DATE: 1999-12-02
PRIOR PLIING DATE: 1999-12-02
PRIOR PLIING DATE: 1999-12-02
PRIOR PLIING DATE: 1999-12-16
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51.6%;
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Best Local Similarity 51.6°
Matches 269; Conservative
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GOGANISM: Homo sapiens
US-09-905-291A-170
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TLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TLE OF INVENTION: Acids Encoding the Same
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PLICATION NUMBER: PCT/US99/21547
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FILING DATE: 2000-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLICATION NUMBER: PCT/US99/20594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLICATION NUMBER: PCT/US99/23089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLICATION NUMBER: PCT/US99/28564
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PLICATION NUMBER: US_60/145,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/143,048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLICATION NUMBER: US 60/146,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Irt, Timothy A.
                                                                                                                                                        errara, Napoleone
ilvaroff, Ellen
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US20020192659A1
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ather, Jennie P
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 170
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81;
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Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Hom
US-09-907-824-170
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                                                                                                                                                                                                              163 LTNNVNKLLIDYSENRLLAGGSLYQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTM 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                          DTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRK 346
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                                                                                                                                    --SFVTFRGEPAE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 MKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIPCSSALLTIDDNFCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVASMIKI
                                                                                                       Gaps
                                                                                                       55;
                                                                          Length 552;
                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 ALOYE ---- TVQVVDPGPVLRDMAFSK-DHEQLYIMSERQ 501
                                                                          DB 9;
                                                                                      ; Pred. No. 1.2e-97; 81; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 170, Application US/09907824
Publication No. US20020197671A1
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Grimaldi, Christopher J.
                                                                      13.5%;
51.6%;
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Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Roy, Margaret Ann
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Gao, Wei-Qiang
Gerber, Hanspeter
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                     Query Match
Best Local Similarity 51.6
Matches 269; Conservative
                                                                                                                                    STLLTROPAPLSOKOR
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APPLICANT: Ashkenazi, Avi
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              ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-170
LENGTH: 552
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APPLICANT:
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APPLICANT: WIlliams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, Becreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPRENCE: 10466-14
CURRENT PLILING DATE: 2000-09-18
RIOR PILING DATE: 2000-09-18
RIOR PILING DATE: 2000-09-18
RIOR PILING DATE: 2000-09-18
RIOR PILING DATE: 1099-07-07
RIOR APPLICATION NUMBER: DC/1059-09-08
RIOR PILING DATE: 1999-09-03
RIOR PILING DATE: 1999-09-13
RIOR PILING DATE: 1999-09-13
RIOR PILING DATE: 1999-09-13
RIOR PILING DATE: 1999-09-13
RIOR PILING DATE: 1999-09-15
RIOR PILING DATE: 1999-09-15
RIOR PILING DATE: 1999-09-15
RIOR PILING DATE: 1999-09-15
RIOR APPLICATION NUMBER: PC/1059/2094
RRIOR PILING DATE: 1999-09-15
RRIOR PILING DATE: 1999-09-15
RRIOR PILING DATE: 1999-09-15
RRIOR RILING DATE: 1999-10-05
RRIOR RAPLICATION NUMBER: PC/1059/2094
RRIOR RAPLICATION NUMBER: PC/1059/2099
RRIOR RAPLICATION NUMBER: PC/1059/2099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 SRLLT--AAPLSMEQRQPWPRALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDW 102
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1; Mismatches 11
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us-09-964-956-13.rapb

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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 423
SEQ ID NO 170
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
PRIOR FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard, A.
                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                            US-09-907-841-170
                                                              LENGTH: 552
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                DTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGOKRK 346
 PSDTLALVSHFDIFYIYGFASGGFVYFLTVQPE--TPEGVAINSAGDLFYTSRIVRLCKD 340
                                                   CANT: Williams, P. Mickey
CANT: Wood, William, I.
OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
OF INVENTION: Acids Encoding the Same
                                                                                                347 MKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIPCSSALLTIDDNFCG
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CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/04414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1999-07-28
PPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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FILING DATE: 1999-09-15
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FILING DATE: 1999-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/28214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-02-22
APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
                                                                                                                                                                                                                                                                                                                                                Sequence 170, Application US/09907841 Publication No. US20020198366A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul J.
Grimaldi, Christopher
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dan L.
APPLICANT: Baton, Dan L.
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                                                                          --SFVTFRGEPAE-
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                                      Gaps
                                        55;
Length 552;
  Score 1351.5; DB 9; Length
Pred. No. 1.2e-97;
81; Mismatches 116; Indels
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Publication No. US20030003530A1
GENERAL INFORMATION:
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  Query Match
Best Local Similarity 51.6%;
Matches 269; Conservative 81
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Filvaroff, Ellen
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                                                                                23 STLLTROPAPLSOKOR-
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Gao, Wei-Qiang
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Eaton, Dan L.
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407 LDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAYVYKNHSLAFVGTKSGKLKKIRVDGPRGN 466
223 YGVIVRSEGEDGKLFIGTAVDGKQDYFPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKI 282
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CURRENT FILING DATE: 2001-12-19
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PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-28
PRIOR PLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059122
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PAPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059363
PRIOR PILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-09-19
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Filvaroff, Ellen
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FITLE OF INVENTION:
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Pred. No. 1.2e-97;
1; Mismatches 116; Indels
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                                                                                                                                            Williams, P. Mickey Wood, William, I.
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51.6%;
                                                    Roy, Margaret Ann
Stewart, Timothy A
                            Nicholas F
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Best Local Similarity 51.64
Matches 269; Conservative
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; ORGANISM: Homo Sapien
US-09-904-011-170
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GENERAL INFORMATION:
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Grimaldi, Christopher J.
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PRIOR FILING DATE: 1998-07-01
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Mather, Jennie P.
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Botstein, David
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Eaton, Dan L.
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Paoni, Nicholas F

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACRES OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF ACROSS OF A
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Watanabe, Colin K
Wood, William
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APPLICANT: Beresini, Maureen
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Filvaroff, Ellen
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Smith, Victoria
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Best Local Similarity 51.6
Matches 269; Conservative
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Publication No. US20
GENERAL INFORMATION:
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; ORGANISM: Homo
US-10-123-904-332
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                                                    283 PSDTLALVSHFDIFYIYGFASGGFVYFLTVQPE--TPEGVAINSAGDLFYTSRIVRLCKD 340
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                  PSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPPG---STTKEQVYTSKLVRLCKE 286
                                                                                                                                        DTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRK 346
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330/HIL17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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1.2e-97;
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Publication No. US20030022239A1
GENERAL INFORMATION:
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Goddard, Audrey
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APPLICANT: Beresini, Maureen
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Filvaroff, Ellen
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ORGANISM: Homo Sapien
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APPLICANT: ROY, MARGATER Ann APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Unmas, Daniel .
APPLICANT: Tumas, Daniel .
APPLICANT: Williams, P. Mickey .
APPLICANT: Williams, I. TITLE OF INVENTIONS Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTIONS. Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTIONS ACCORDED TO 809,0906,838
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR FILING DATE: 2000-09-18
PRIOR PLING DATE: 2000-02-22
PRIOR PLING DATE: 2000-02-22
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: US 60/143,048
PRIOR PLING DATE: US 60/145,698
PRIOR PLING DATE: US 60/145,698
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                      110 TTNNVNKMLLIDYKENRLIACGSLYQGICKLLRLEDLFKLGEPYHKKEHYLSGVNESGSV 169
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                                           163 LTWNVNKLLIIDYSENRLLACGSLYQGVCKTLRLDDLPILVEPSHKKEHYLSSVNKTGTM
                                                                                                                        170 FGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVASMIKI
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Publication No. US20030027143A1
GENERAL INFORMATION:
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
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Gerritsen, Mary E.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleor
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163 LTNNVNKLLIIDYSENRLLACGSLYQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTM 222
                                                            347 MKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIPCSSALLTIDDNFCG
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R10160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
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                                                                                                                    PSDTFT11PDFD1YYVYGFSSGNFVYFLTLQPEMVSPPG---STTKEQVYTSKLVRLCKE
                                     FGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVASMIKI
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; Pred. No. 1.2e-97;
81; Mismatches 116; Indels
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51.6%;
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Wood, William
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Gurney, Austin L.
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Best Local Similarity 51.64
Matches 269; Conservative
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CORGANISM: Homo Sapien
US-10-140-470-332
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23 STLLTROPAPLSQKQR-----
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51.6%;
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Best Local Similarity 51.6
Matches 269; Conservative
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; ORGANISM: Homo Sapien
US-09-906-838-170
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: Secreted and Transmembrane Polypeptides and Nucleic Pacids Encoding the Same
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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FILING DATE: 2000-01-05
N OF SEQ ID NOS: 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLICATION NUMBER: PCT/US99/20944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US00/04414
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FILING DATE: 1999-07-26
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                                                                                                                                           Gerritsen, Mary E
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                                                     llvaroff, Ellen
                                                                                                                                                                                                                                                              javin, Ivar J
                                                                                                  Wei-Qiang
Desnoyers
                                                                                                                                                            Goddard,
                   aton,
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23 STLLTROPAPLSOKOR------
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Best Local Similarity 51.6
Matches 269; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                        163 LTNNVNKLLIDYSENRLAGGSLYQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTM
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                                                                                          DB 9; Length 552
                                                                                                                      81; Mismatches 116; Indels
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                                                                                       13.5%; Score 1351.5; DB 51.6%; Pred. No. 1.2e-97
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Publication No. US20030027146A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botherazi, Avi
APPLICANT: Bottein, David
APPLICANT: Betsein, David
APPLICANT: Faton, Dan L.
APPLICANT: Faton, Dan L.
APPLICANT: Forg, Sherman
APPLICANT: Forg, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
                                                                                                                                                    23 STLLTROPAPLSOKOR-
                                                                                                     Best Local Similarity 51.6%
Matches 269; Conservative
; SEQ ID NO 170
; LENGTH: 552
; TYPE: PRT
; CRGANISM: Homo sapiens
US-09-907-613-170
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Paoni, Nicl
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APPLICANT:
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APPLICANT: NUMBER: 0.1.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT APPLICATION NUMBER: US/09/07/942
PRIOR APPLICATION NUMBER: US/09/07/14
PRIOR APPLICATION NUMBER: US/09/07/14
PRIOR APPLICATION NUMBER: US/09/07/08
PRIOR PELLIAN DATE: 1999-07-02
PRIOR PELLIAN DATE: 1999-09-13
PRIOR PELLIAN DATE: 1999-09-13
PRIOR PELLIAN DATE: 1999-09-13
PRIOR PELLIAN NUMBER: PCT/US99/21090
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51.6%; Pred. No. 1.2e-97;
ive 81; Mismatches 116; Indels 55;
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230 PSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPPG---STTKEQVYTSKLVRLCKE
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Pred. No. 1.2e-97;
81; Mismatches 116;
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5. US20030027275A1
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Gerritsen, Mary E.
Goddard, Audrey
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Filvaroff, Ellen
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Best Local Similarity
Matches 269; Conserv
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                                                                                                                        347 MKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIPCSSALLTIDDNFCG 406
                                                                                                                                                                       LDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAYVYKNHSLAFVGTKSGKLKKIRVDGPRGN 466
                         DTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRK 346
                                                                                                                                                                                               APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT PILING DATE: 2002-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 TFNHLIVHQGTGAVYVGAINRVYKLIGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLT
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                                                                                                                                                                                                                                                                       467 ALQYE----TVQVVDPGPVLRDMAFSK-DHEQLYIMSERQ 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 1351.5; DB 9; Pred. No. 1.2e-97; 81; Mismatches 116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                              Sequence 332, Application US/10175746 Publication No. US20030027270A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.6%;
Matches 269; Conservative 81
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Wood, William
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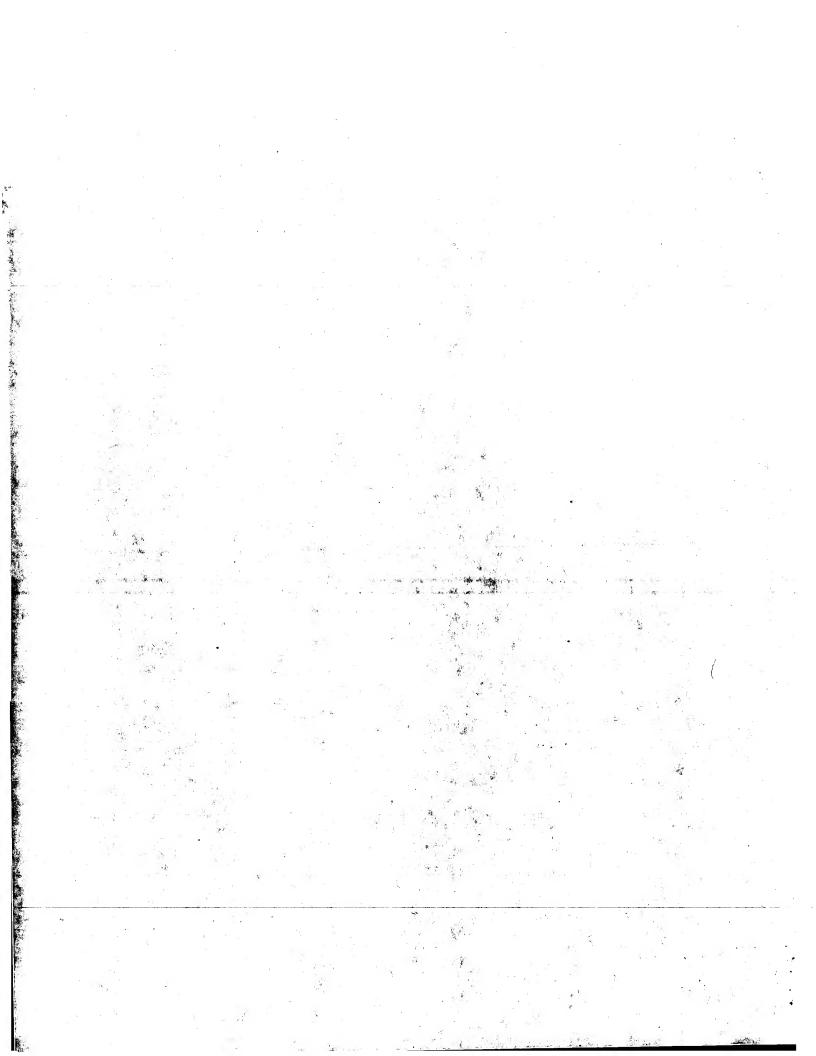
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACTUBE SECRETED SAME
FILE REFERENCE: P3330R1C382
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 332
LENGTH: 552
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                                                                                                     283 PSDILALVSHPDIFYIYGFASGGFVYFLIVQPE--TPEGVAINSAGDLFYTSRIVRLCKD
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                                        230 PSDTFTIIPDFDIYYVYGFSSGNPVYFLTLQPEMVSPPG---STTKEQVYTSKLVRLCKE 286
                                                         283 PSDTLALVSHFDIFYIYGFASGGFVYFLTVQPE--TPEGVAINSAGDLFYTSRIVRLCKD 340
                                                                                              287 DTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRILGVHPDDDLLFTVFSKGQKRK 346
                                                                                                              347 MKSLDESALCIFILKQINDRIKERLOSCYRGEGTLDLAWLKVKDIPCSSALLTIDDNFCG 406
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Search completed: June 24, 2003, 19:10:54 Job time: 73 secs



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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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| protein UNC-89 - C ataxia-telangiecta hypothetical prote semaphorin homolog hypothetical prote hemicentin precurs |            | RESULT 1 UC4975  Dlexin 2 precursor - mouse  Dlexin 2 precursor - mouse  Dlexin 2 precursor - mouse  Dlexin 31-Dec-1996 #text_change 05-Nov-1999  C; Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 05-Nov-1999  C; Accession: UC4975  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F.  R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Murakami, olecule type: mRNA A;Molecule type: mRNA A;Residues: 1-1884 <kam> A;Cross-references: DDBJ:D86949; NID:g1655431; PIDN:BAA13189.1; PID:d1013878; PID:g16554: C;Comment: TDBJ:Daprotein is a membrane protein C;Keywords: duplication; transmembrane protein F;1-21/Domain: signal sequence #status predicted <sig> F;501-549/Region: cysteine-rich duplication F;704-845/Region: cysteine-rich duplication F;7123-1250/Domain: transmembrane #status predicted <twm></twm></sig></kam> | DB 2; Length 1884;<br>; 356; Indels 14; Gaps 8;      | LLTRQPAPLSQKQRSFVTFRGEPAE-GFNHLVVDERTGHIYLGAVNRIYKLSSDLKVLVT 83<br> | HETGPDEDNPKCYPPRIVQTCNEPLTTINNVNKMLLIDVKENRLIACGSLYQGICKLIRL 143<br> -   -   -   -   -  - | EDLFKLGEPYHKKEHYLSGYNESGSVFGVIVSYSNLDDKLFIATAVDGKDEYFPTISSRK 203<br> | LTKNSEADGWFAYVFHDEFVASMIKIPSDTFTIIPDFDIYYVVGFSSGNFVYFLTLQPEM 263<br>  ::  : | VSPPGSTTKEQVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGA 320<br>      | VLGRTLGVHPDDDLLFTVFSKGOKRKMKSLDESALCIFILKQINDRIKERLQSCYRGEGT 380<br> |
| 42 2 T29757<br>56 2 T51174<br>53 2 T03102<br>53 2 T03902<br>75 2 T43290   | ALIGNMENTS | RESULT 1  JC4975  plexin 2 precursor - mouse  plexin 2 precursor - mouse  C;bpcies Mus musculus (house mouse)  C;bate: 31-B0-1996 #sequence_revision 31-Dec-1996 #text_cl  C;Accession: JC4975  R;Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takas  Biochem. Biophys. Res. Commun. 25c, 396-402, 1996  A;Title: Identification of plexin family molecules in mice  A;Reference number: JC4975, MUID:96400270; PMID:8806646  A;Accession: JC4975   | A. Molecule type: mRNA<br>A. Residues: 1-1884 «KAM»<br>A. Residues: 1-1884 «KAM»<br>A. Kross-references: DDBJ. DB6949; NID:g1655431; PIDN<br>C. Comment: This protein is a membrane protein with c<br>C. Keywords: duplication; transmembrane protein with<br>F. 1-21/Domain: signal sequence #status predicted «SI<br>F. 501-549/Region: cysteine-rich duplication<br>F. 544-691/Region: cysteine-rich duplication<br>F. 794-845/Region: cysteine-rich duplication<br>F. 794-845/Region: cysteine-rich duplication<br>F. 794-8123-1250/Domain: transmembrane #status predicted  | %; Score 6764;<br>%; Pred. No. 0;<br>239; Mismatches | QRSFVTFRGEPAE-GFNHLVVDI<br>:  | YPPRIVQTCNEPLTTTNNVNKMLLII<br>  | KEHYLSGVNESGSVFGVIVSYS)<br>  | YVFHDEFVASMIKIPSDTFTII)<br>   | BQVYTSKLVRLCKBDTAFNSYVI<br>:     ::        <br>DLFYTSRIVRLCKDDPKFHSYVV | DLLFTVFSKGOKROMKSLDESAI<br> :   :       <br>DVLFAIFSKGOKOYHHPPDDSAI  |
| 1.6 6642<br>1.5 3856<br>1.5 4307<br>1.5 653<br>1.4 5175   |            | RESULT 1 JO4975 plexin 2 precursor - mouse C;Species: Whe museulus (house mouse) C;Date: 31-Dec-1996 #sequence_revisio C;Accession: JC4975 R;Kameyama, T.; Murakami, Y.; Suto, F Biochem. Biophys. Res. Commun. 226, 3 A;Title: Identification of plexin fam A;Reference number: JC4975; MUID:9640 A;Accession: JC4975;  | A. Molecule type: mRNA<br>A. Molecule type: mRNA<br>A. Residues: 1-1884 «KAM»<br>A. Kross-references: DDBJ:DB<br>C. Comment: This protein is<br>C. Keywords: duplication; tr<br>F. 1-21/Domain: signal seque<br>F. 501-549/Region: cysteine-<br>F. 546-691/Region: cysteine-<br>F. 794-845/Region: cysteine-<br>F. 794-845/Region: cysteine-<br>F. 794-845/Region: cysteine-<br>F. 794-845/Region: cysteine-   | ilarity<br>Conservat                                 | JLTROPAPLSOK(<br>   | IETGPDEDNPKC)<br> -   -   <br> KTGPEEDNKAC)   | DLFKLGEPYHKI<br>            <br> DLFILVEPSHKI                        | TKNSEADGMFA)<br>::  :  <br>.PRDPESSAMLD)                                    | /SPPGSTTKG<br>   | /LGRTL/GVHPDDI<br>  : :  :<br>\LAQAFNISSDEI                          |
| 162<br>154<br>147.5<br>146.5<br>144.5   |            | RESULT 1 UC4975 plexin 2 precursor Cipecies Mus musc C; Date: 31-Dec-1996 C; Accession: UC4975 R; Kameyama, T.; Mur. Barichen: Identificat A; Reference number: A; Accession: UC4975   | 11e type<br>11e type<br>12e type<br>12e type<br>11: Thie<br>16: dup<br>19/Regio<br>11/Regio<br>15/Regio  | Query Match<br>Best Local Simi<br>Matches 1267;      | 25 I<br>17 I  | 84 F  | 144 E  | 204 I   | 264 \  | 321 7  |
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Cispecies: Xenopus laevis (African clawed frog)
Cispecies: Xenopus laevis (African clawed frog)
Cispecies: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
Cispeciesion: 151553
Riohta, Kr. Mizutani, A.; Kawakami, A.; Murakami, Y.; Kasuya, Y.; Takagi, S.
Riohta, Kr. Mizutani, A.; Kawakami, A.; Murakami, Y.; Kasuya, Y.; Takagi, S.
A;Title: Plexin: a novel neuronal cell surface molecule that mediates cell ax
A;Accession: 151553
A;Accession: 151553
A;Accession: Is1553
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1905 <OHT>
A;Residues: 1-1905 <OHT>
A;Cross-references: GB:D38175; NID:g961514; PIDN:BAA07374.1; PID:g961515
C;Keywords: duplication
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|                              | 481 VLRDMAFSKDHEQLYIMSERQLTRVPVESCGGYQSCGECLGSGDPHCGWCVLHNTCTRKE 540 :   :  : : : : | 601<br>597<br>661<br>657 | 721<br>717<br>781          | 841<br>837<br>901<br>897   | 960 KPSRGPMSGGTQVTITGTMLNAGSNVVMFGKQPCLFHRRSPSYIVCNTTSSDEVLEMKV 1019   | 1079<br>1077<br>1136   |  | 1256 VLIAYKRKSRESDLTLKKLOMOMDNLESRVALECKEAFAELQTDIHELTSDLDGAGIPFL 1315 | 1316 DYRTYTMRVLFPGIEDHPVLRDLEVPGYRQERVEKGLKLFAQLINNKVFLLSFIRTLESQ 137 : | 1376 RSFSMRDRGNVASLIMTVLOSKLEYATDVLKQLLADLIDKNLESKNHPKLLIRRTESVAE 1435 |
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Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, F. mun. 226, 524-529, 1996
a neuronal cell surface molecule, plexin, in mice.
MUID:96400291; PMID:8806667
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S.; Hirata, T.; Fujisawa, F PID:d1013879; PID:g16554: Cispecies: Mus musculus (house mouse)
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Cispecies: Musculus (house mouse)
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Cipate: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 05-Nov-1999
Cipate: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 05-Nov-1999
Cipate: Biochem. Biophys: Res. Commun. 226, 396-402, 1996
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Length 1872;

DB 2; 441;

Query Match 59.9%; Score 5984.5; Best Local Similarity 59.7%; Pred. No. 0; Matches 1130; Conservative 290; Mismatches

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pleazin A - fruit fly (Drosophila melanogaster)
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C;Species: Drosophila melanogaster
C;Date: 20-69p-1999 #sequence\_revision 20-Sep-1999 #text\_change 17-Nov-2000
C;Accession: Ti3397
R;Winberg, M.L; Noordermeer, J.N; Tamagnone, L.; Comoglio, P.M.; Spriggs, M.K.; Tessier
Cell 95, 903-916, 1998
A;Title: Plexin A is a neuronal semaphorin receptor that controls axon guidance.
A;Reference number: Z17621; MUID:99091049; PMID:9875845
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary;
A;Retus: preliminary;
A;Retus: preliminary;
A;Retus: preliminary;
A;Retus: preferences: EMBL:AF106932; NID:94056673; PID:94056674; PIDN:AAD09425.1
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 4
C;Function:

1708 1836 1888 1180 1202 1354 1409 1430 1469 1490 1529 1539 1589 1716 1036 1088 1254 1312 1370 1656 g g ò g ò 셤 a g ò g à g δ ద Š 8 ò g ò g ઠે ò 셤 ò g ò ద ઠે qq ò 셤 à 977 887 947 GVSDMVRGIPVFTEDRDRMTSVIAYVYKNHSLAFVGTKSGKLKKIRVDGPRGNALQYETV 473 NTCTRKERC-ERSKEPRRFAS-EMKQCVRLT-VHPNNISVSQYNVL-LVLETYNVPELSA 589 643 745 774 SEQRVPAL -- RFNSSSVQCQNTSYSYEGMEINNLPVELTVVWNGHFNIDNPAQNKVHLYK 803 ---RVTSLNAQLLGDTIYCDSMEFQYTSRS-PNLTATFAVIWGGSKPLDNPHNIHVVIYR 830 VECISDAQGGTKFNLVQAGFLGKPSSNLAQSLGISIQNDVLFAVFSKGEGN--TPTNNSA\_369 413 PDLVSTDFTFFDCSTHSSCTRCVSSEFPCDWCVEAHRCTHDTAENCRNDILVTGVSRIGP 719 237 255 354 107 163 83 HTPQPKTGPWEGGTNITIRGINLGKNYNDIYSGVRIAGINCMPFPQFYIDTKQIVCŢVDS -GEAKPSQHAGFVEICVAVCRPEFMARSSQLYYFWTLTLSDLKPSRGPMSGGTQVTITGT 206 YVGVTYTNNSPYRSEIPAVASRSLEKTK----MF-----QIASSAVTYGTRTFINSYAR SFQEGRVKLPEDCPQLLRV---DKILVPVEVIKPITLKAKNLPQPQSGQRGYECILNIQG CGAMRESCGICLKADPDFACGWCQGPGQCTLRQHCPAQ---ESQWLELSGAKSKCTNPRI TEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGYIPAEQIVCEM--IGC---ERSGVEYRLLOAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESA GGETPIISVPV-AMFNIKLISVAAISTSGYTVVFVGTSDGFLKKVVIES-SSIANEYASF 487 AVDLGSEINRDMQFDNQNLYIYVMSKTKVSKVKVFDCSDYKTCGDCLGARDPYCGMCSLE GVNCTFEDLSEMDGLVVG-----NQIQCYSPAAKEVPRIITENGDHH-VVQLQLKSKETG CREMADSCGICLALSEKYNCGWCSSTNTCEVEEQCNKNKEGKTDWLNRS---BICPNPEI RLEDLFKLGEPYHKKEHYLSGVNESGSVFGVIVSYSNLDDKLFIATAVDGKPEY--------PPTISSRKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFT---II PDFDIYYVYGFSSGNFVYFLTLQPEMVSPPGSTTKFQVYTSKLVRLCKEDTAFNSYVEVP LCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIPC-SSALLTIDDNFCGLDMWAPL QVVDPGPVLRDMAFSKDHEQLYIMSERQLTRVPVESCGQYQSCGECLGSGDPHCGWCVLH HETGPDEDNPKCYPPRIVQTC - NEPLTTINNVNKMLLIDYKENRLIACGSLYQGICKLL LTROPAPLSQKQRSFVTFRGEPA--EGFNHLVVDERTGHIYLGAVNRIYKLSSDLKVLVT Gaps Indels 190; 861 746 775 804 831

1468 1489 1655 1707 MPDFLDEQADKHGIHDPHVRHTWKSNCLPLRFWVNMIKNPQFVFDIHKNSITDACLSVVA 1775 1179 NINAGSNVVVMFGKQ-PCLFHRRSPSYIVCNTTSSDEVLEMKVSVQVDRA-KIHQDLVFQ 1035 1776 QTFMDSCSTSEHRLGKDSPSNKLLYAKDIPSYKNWVERYYSDIGKMPAISDQDMNAYLAE 948 PGEQMYRNGKIVVQI-----GDYRGESKEDYEFVDPKILDFNPKFGPTSGGTEIHITGK ESPN-----LIGRHKVMARVG-GMEYSPGMV-YIAPDSPLSLPAIVSIAVAGGLLIIFI --VAVLIAYKRKSRESDLTLKRLQMQMDNLESRVALECKEAFAELQTDIHELTSDLDGAG RTLESQRSFSMRDRGNVASLIMTVLQSKLEYATDVLKQLLADLIDKNLESKNHPKLLLRR TESVAEKMLTNWFTFLLYKFLKECAGEPLFSLFCAIKQQMEKGPIDAITGEARYSLSEDK LIRQQIDYKTL-----VLSCVSPD--NANSPEVPVKILNCDTITQVKEKILDAIFK SKOVTAYNAVNNSTVSRTSASKYE - - NMIRYT - GSPDSLRSRTPMITPDLESGVKMWHLV YVEDPTIV-----RIEPEWSIVSGNTPIAVWGTHLDLIONPOIRAKHGGKEHINICE VINATEMICQAPALALGPDHQSDLTERP -- EEFGFILDN --- VQSLLILNKTNFTYYPNP 1143 VFEAFGPSGILELKPGTPIILKGKNLIPPVAGGNVKLNYTVLVGEKPCTVT-VSDVQLLC IPFLDYRTYTMRVLFPGIEDHPVLRDLEVPGYRQE--RVEKGLKLFAQLINNKVFLLSFI OSRMHMNEFNTMSALSEIFSYVGKYSEEILGPLDHDDQCGKQKLAYKLEQVITLMS 

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plexin B - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000 C;Accession: T13164

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| nberg, M.L.; Noordermeer, J.N.; Tamagnone, L.; Comoglio, P.M.; Spriggs, M.K.; Tessie 95, 903-916, 1998 tle: Plexin A is a neuronal semaphorin receptor that controls axon guidance.                          |   |
|--|---|
| 17621; MUID:99091049; PMID:9875845<br>; translated from GB/EMBL/DDBJ   | Qy 847 ELSGAKSKCTNPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECS 902   |
| sidues: 1-2051 «WIN» sidues: 1-2051 «WIN» oss-references: EMBL:AF106933; NID:g4056675; PID:g4056676; PIDN:AAD09426.1 netics:   | QY 903 PLVDGYIPAEQIVCEMGEA  |
| :  | Qy 955 TLSDLKPSRGPMSGGTQVTITGTNLNAGSNVVVMFGKQPCLFHRRSPSYIVCNTT 1009   |
| ecription: plays a role in neuronal cell contact, axon guidance and fasciculation erry Match 29.4%; Score 2932.5; DB 2; Length 2051; Stated. No. 5.2e-181; February 34.4%; Pred. No. 5.2e-181; February 106. | OY 1010SSDEVLEMKVSVOVDRAKIHQDLVFQYVEDP 1040 :     :   :   :   :   :     :   |
| FURLYVDERTGHIYLGAVNRIXKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTT 1   | Qy 1041 TIVRIBPEWSIVSGNTPIAVWGTHLDLIQNPQIRAKHGGKEHINICEVLNATEMTCQA 1098   |
| . დ •  | Qy 1099 PALALGPD  |
| GVNESGSVFGVIVSYS-NLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFA : :  : : : : :  :  :   ANDENASTYAFVGPARYAWKEBDILKYGTTFTNVGDYRHDVPALSSRLDDLANYAE  | OY 1120TILDNVQSLLILAKTINFTYYPNPVFEA 1146  DS 1217 ANYFVANNMDVTTFVKVHETQLALQLSFVMDNVQLVRALAKYFHDIRSTIVYLADPKYLP 1276                           |
| YVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPGSTTKEQV  | OY 1147 FGPSGILELKPGTPIILKGKNLIPPVAGGNVKLAYTVLVGEKPCTVT-VSDVQLLCESPN 1205  1277 FPNDGV-KLYKGDTLVIEGELLNLAADEYDVNVTIGTSQCNITSLALNQLLCIPPE 1331 |
| YTSKLVRLCKEDTAFNSYVEVPIGCERSGYEYRLLQAAYLSKAGAVLGRTLGVHPDDD   | QY 1206LIGRHKWARVGGMEYSPGMVYIAPDSPLSLPAIVSIA 1243   |
| LLFTVFSKGQKRKWKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIPC   | Qy 1244 VAGGLLIFIVAVLIAYKRKSRESDLTLKRLQMQMDNLESRVALECKEAFAELQTDIHEL 1303  |
| SSALLTIDDNPCGLDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAY  | Qy 1304 TSDLDGAGIPPLDYRTYTMRVLPPGIEDHPVLRDLEVPGYRQRVEKGLKLFAQLI 1359  |
| ∑2   | QY 1360 NNKVPLLSFIRTLESQR-SFSMRDRGNVASLIMTVLQSKLEYATDVLKQLLADLIDKNLE 1418   |
| SEROLTRVPVESCGOYOSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPRRFASEM   | OY 1419 SKNHPKILLRRTBSVAEKMLTNWFTFILVKFIKECAGEPLFSLFCAIKQOMEKGPIDAIT 1478   |
| KQCVRL_TVHPNNISVSQYNVL_LVLETYNVPE_LSAGVNCTFEDLSEMDGLVVGNQIQC:  : :     : :     : :     : :     : :     : :     : :       : :       : :       :   | Qy 1479 GEARYSLSEDKLIRQQIDYKTLVLSCVSPDNANSPEVPVKILNCDTITQVKEKILDAIFK 1538   |
| XSPAAKEVPRIITENGDHHVVOLQLKSKETGMTFASTSFVFYNCSVHNSCLSCVESPYRC   | QY 1539 NVPCSHRPKAADMDLEWRQGSGARMILQDEDITTKIENDWKRLNTLAHYQVPDGSVVALV 1598   |
| HWCKYRHVCTHDPKTCSFQEGRVKLPEDCPQLLR-VDKILVPVEVIKPITLKAKNLPÒPQ   | QY 1599 SKQVTAXNAVNNSTVSRTSASKXENMIRYTGSPDSLRSRTPMITPDLESGVKAWHLV 1655   :-   |
| SQORGYBCILNIOGSEORVPALRFNSSVOCONTSYSYSGMEINNLPVBLITVVWNGHFNI   | Qy 1656 KNHEHGDQXEGDRGSXMVSEIYLTRLLATKGTLQKFVDD 1694  |
| DNPAQNKVHLYKCGAMRESCGLCLKADPDFACGWCQGPQCTLRQHCPAQESQML   | Qy 1695 LFETIFSTAHRGSALPLAIKYMFDFLDEQADKHGIHDPHVRHTWKSNCLPLRFWVNMIKN 1754   |

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| CMVK   | PAAKEVPRI  |   | 589 FİSPNTFEILLİTSIŚNNPISRHNFTVŸDĆŚGYGTĆSŚCMSSEYNCAWCSGLHKCSN 645<br>684 DPKTCSFOEGRVKLPEDCPQLLRVDKILVPVEVIKPITLKAKNLPQPQSGQRGYEÇ 739 |              | 740 ILNIQGSEQRVPALRENSSSVQCQNTSYSYEGMEINNLPVELTVVW-NGHFNIDNPAQNK 798 .  .:  | 799 VHLYKCGAMRESCGLCLKADPDFACGWCQGPGCTLRQHCPAQESQWLELSGAKSKCTNP 858                     |  |   | 849 DKGVSSGPIRISVGRATVA-VAESSELYSFVRTSIFSAYPLYGPISGGTRITLYGQN 904 |  | 1037 VEDPTIVRIEPEWSIVSGNTPIAVWGTHLDLIQNPQIRAKHGGKEHINICEVLN 1090 | 1091 ATEMTCQAPALALGPDHQSDLTERPEEFGFILDNVQSLLILNKTNFTYYDNPVFEAFGPS 1150                                   | GILELKPGTPIILKGKNLIPPVAGGNVKLNYTVLVGEKPCTVTVSDV-QLLCESPNL | 1063 GVRYHQGEQSLİLEĞHNÜNLAAEPNDFKIFIGNERCYVTLVDVRQLVCSGP 1113<br>1207 IGEHKVMARVGGMEXSPGMVYIAPDŞPLSLPAIVŞIAVAĞGLLII 1251 | .:   | 1252 FIVAVLIAYKRKSRESDLTLKRLOMOMDNLESRVALEKKERFALLOTDIHELTS 1305 |   |   | 1363 VELLERITUES PER PREDETENT VEGETAL | 1423 PKILIRRIESVAEKMLINWFTFILYKFIKECAGEPIRSLFCAIKOOWEKGPIDAITGEAR 1482 | o 6 |  |
|--|--|---|---|--------------|---|---|--|---|---|--|--|--|---|--|--|--|---|---|--|--|-----|--|
| qa V   | q &  | g &   | g &   | 7 A          | δ d   | yo q  | ò  | a ò   | do ,  | à g  | oy<br>d  | y g  | 8 8   | 음 · 승  | 7 A  | y d  | ò | qa .  | <u>8</u>   | δ f  | 8 8 | q<br>q   |
|  |  | <del></del>   |   | •            |   | -   |  |   | 1414/3;   |  |  |  | ***   |  |  | _  |   |   |  | <del></del> .  |     |  |
| 1851 FFSIILTVNEBLPPAVKMLFDLLDEAARRHXIADTDIVHAWXSNCLPLRFWVNFIKN 1907 1755 PQFVFDIHKNSTTDACLSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIPSYKNWVERY 1814 | 1908 PDFIFDVNKTYSVDSCLSVXAQTFMDACSTSEHRLGKDSPSNKLLFAKDIPNYRIMVKEF 1967  1915 YSDIGKMPALIAEQSRWHNNEFNTWSALSEIFSYVGKYSEEILGPLDHDDQC 1874 | 1968 YRDVSRLPQISDQEMSTAMQQLSVRQNREPDTISALKELYIVITKYKDQIMESLETDINC 2027<br>1875 GKQKLAYKLEQVITLMSLD 1893 | 2028 RKWHLSRKLGNVAATLDGD 2046   | JLT 7<br>298 | hypothetical protein K04B12.1 - Caenorhabditis elegans<br>C.Species: Caenorhabditis elegans<br>C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999<br>C.Accession: T23298 | teward, C.<br>mitted to the EMBL Data Library, December 1996<br>eference number: Z19723 | Accession: 123298<br>Status: preliminary; translated from GB/EMBL/DDBJ<br>Aolecule type: DNA<br>Desidnes: 1-1806 cWIL> | irossareferences: EMBL:283232; PIDN:CAB05755.1; GSPDB:GN00020; CESP:K04B12.1<br>Sxperimental source: clone K04B12 | 9/3;  | Query Match<br>16.1%; Score 1609.5; DB 2; Length 1806;<br>Best Local Similarity, 26.4%; Pred, No. 2.6e-95; | WGSSTLLTRQPAPLSQKQRSFVTFRGEPAEGFNHLVVDERTGHIYLGAVNR 7            | 37 LISHFLRAVTQPPFETEGVKQKLFHFSGHIDDFIVSRDQCTIXVASLNR 85 71 IYKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTTN 112 |   | 113 NVRMALIDYKENKLIAGSLYGGICKLEKLEDERKAGSETIKKARIAGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG                                   | 173 IVSYSNLDDKLFIATAVDGKPEYFPTISSRKLT-KNSEADGMFA 215 |  |   | OY 276 YISKLVRLCKEDTAFNSYVEVPIGCE-RSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDL 334 | LPTVPSKGOKRKWKSLDESALCIFILKOINDRIKERLOSCYRGEGTLDLAWLKVKDIPCS   | STSPKŚSIĆVFSMQKVKLTFWYNVDRCR<br>SLDMNAPLGYSDMVRGIPVFTED-RDRMTS         |     | 454 KLKKIRVDGPRGNAL-QYETVQVVDPGPVLRDMAPSKDHEQLYIMSERQLTRVPVBSC 510 |

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|   | 129 - EMKDVCIQFDGGNCSSVGSLSYIALPHCSLIFPATTMISGGQNITMMGRNFDVIDNL.  1074 RAKGGKEHINICEVLNATEMTCQAPALALGPDHQSDLTERPEEFGFILDNVQSLJILNK   |
|---|--|
| 8   | 8 6 8 6 8 6 8 6 8 6 8  |
| 1543 SHPRYADMOLEWRGOSGARNILQDEDITTKIENDWKRLAWILAHYOVPGSVV 1595 1456 SQRPRITQPELKYKCPKRGDVKLTDVLPIETLIGGKKLPWILAHYOVPGSSVV 1595 1516 SALVEKQVTAXNAVNSTVSTRASKYRMIRYCG-SPDSLRSRTPMITPDLEGGYWGHH 1653 1511 BMSPAVT | St. Local Similarity 24.8%; Pred. No. 1.6e-78; tches 480; Conservative 291; Mismatches 591; Indels 576; Gaps 74;   Conservative 291; Mismatches 591; Indels 576; Gaps 74;   Conservative 291; Mismatches 591; Indels 576; Gaps 74;   Conservative 291; Mismatches 591; Indels 576; Gaps 74;   Conservative 291; Mismatches 291; Indels 576; Gaps 74;   Conservative 291;   C |

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            1689 QKEVDDLFETIFSTAHRGSALPLAIKYMFDFLDEQADKHGIHDPHVRHTWKSNCLPLRFW 1748
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                                                                                                                                                               ---EVPVKILNCDTITQVKEKILDAIFKNVPCSHRPKAADMDLEWRQGSGARMILQDEDI 1570
                                                                                                                                                                                                                                                                                   TTKIENDWKRLNTLAHYQVPDGSVVALVSKQVTAYNAVNNSTVSRTSASKYENMIRYTGS 1630
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                    PLFSLFCAIKQQMEKGPIDAITGEARYSLSEDKLIRQQIDYKTLVLSCV---SPDNANSP 1513
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C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Dates: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46426
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Recerence number: Z23028
A;Recerence number: Z33028
A;Accession: T46426
A;Accession: T46426
A;Accession: T46426
A;Residues: J317 <AAAA
A;Cross-references: BMBL:AL137352
A;Experimental source: adult testis; clone DKFZp434G0625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 PPGSTTKEQVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNSEADGMFAYVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVS
                                                                                                                                                                                                                                      1216 VCRNISVNVLDCDTIGQAKEKIFQAFLSKNGSPYGLQLNEIGLELQMGTRQKELLDIDSS
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                                                                                                                                                                                                                                                                                                                                                       1631 PDSLRSRTPMITPDLESGVKMWHLVKNHEHGDQKEGDRGSK--MVSEIYLTRLLATKGTL
                                                                    KLEYATDVIKQLLADLIDKNLESKNHPKLLLRRTESVAEKMLTNWFTFLLYKFLKECAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein DKFZp434G0625.1 - human (fragment)
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Best Local Similarity, 97.0
Matches 256; Conservative
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C; Accession: JC5148
N; Aoki, S.; Takahashi, K.; Matsumoto, K.; Nakamura, T.
N; Biochem: 120, 961-968, 1996
N; Title: Molecular cloning of the Xenopus c-met/hepatocyte growth factor receptor and its A; Reference number: JC5148; MUID:97137526; PMID:9982863
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C;Comment: This protein is involved in early multiple organogenesis in Xenopus embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1718 DFLDEQADKHGIHDPHVRHTWKSNCLPLRFWVNMIKNPQFVFDIHKNSITDACLSVVAQT 1777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1778 FMDSCSTSEHRLGKDSPSNKLLYAKDIPSYKNWVERYYSDIGKMPAISDQDMNAYLAEQS 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecession: T47133
Cispecession: T47133
Submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24374
A;Accession: T47133
A;Status: preliminary
A;Accession: T47133
A;Residues: 1-177 <AAAA
A;Coss-references: EMBL:AL162013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hepatocyte growth factor receptor precursor - African clawed frog N;Contains: protein-tyrosine kinase (EC 2.7.1.112) c-Met C;Species: Xenopus laevis (African clawed frog) (C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
121 LGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 LKVKDIPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAYVYKNHSL
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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Pred. No. 2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Experimental source: adult amygdala; clone DKFZp761P19121
                                                                                                                                                                                                                                                                                                                            hypothetical protein DKFZp761P19121.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 766; DB 2;
79.1%; Pred. No. 2.3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Mismatches
                                                                                                                                                       446 AFVGTKSGKLKKIRVDGPRGNALO 469
                                                                                                                                                                                                   241 AFVGTKSGKLKKSFGTGPQGGITQ 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.7%
Best Local Similarity 79.1%
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-1375 <AOK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: DKFZp761P19121.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Accession: JC5148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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6.5%;

| ; Conservative 194; Mismatches 394; Indels 416; GHIYLGAVNRIYKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTTIN-  |
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|  |
| KMLLI-DYKENRLIACGSLYQQICKLIRLEDLFKLGEPYHKKEHYLSG   |
| VNESGSVFGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFDD   :   :     :     :     :     :     :     :     :     :     :     :   :     :   :     :   :     :   :   :     : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   : |
| BFVASMIKIPSDTFTIIPDF-DIYYVYGFSSGNFVYFLTLQPEMVSPPGSTTKEQVY :::                  SYIDVLPHLRDIYPIRYIYTFESNNFVYFLTVQRESLDSQAY  |
| TSKLVRLCKEDTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLG   ::  :   :  |
| VHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLK   |
| 388 VKDIPCSSALLFIDDNFCGLDMNAPLGVSDMVRGIPVFTEDRDRM-TSVIAYVKNHSLA<br>  |
| 447 FVGTKSGKLKKIRVDGPRGNALQYETVQVVDPGPVLRDMAFSKDHEQLYIMSERQLTRVP<br>   ::::  |
| 507 VESCGQYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPRRFASEMKQCVRLTVHPN<br>   |
| NISVSQY-NVLLVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQIQCYSPAAKEVPRIIT<br>   |
| ENGDHHVVQLQLKSKETGMTFASTSFVFYNCSVHNSCLSCVESPYRCHWCKYRHVCTHDP<br>   |
| KTCSFQEGRVKLPEDCPQLLRVDKILVPVEVIKPITLKAKNLPQPQSGQRGYECILNIQG<br>   |
| SEQRVPALRENSSSVQCQNTSYSYEGMEINNLPVELTVVWNGHFNIDNPAQNKVHLYKCG<br>   |
| AMRESCGLCLKADPDFACGWCQGPGQCTLRQHCPAQESQWLELSGAKSKCTNPRITEIIP   |
| VTGPREGGIKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGYIPAEQIVCEMGEAK :             :  |
| PSQHAGFVEICVAVCRPEFMARSSQLYYFMTLTLSDLKPSRGPMSGGTQVTITGT  |
| NLNAGSNVVVMFGKQPCLFHRRSPSYIVCNTTSSDEVLEMKVSVQVDRAKIHQDLVFQYV<br> ::  :   |
| EDPTIVRIEPEWSIVSGNTPLAVWGTHLDLIQNPQIRAKHGGKEHINICEVLNATEM  |

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liccule type: mRNA
sidues: 1-1390 cGIO>
ooss-references: EMBL:X54559
rkk, M.; Dean, M.; Kaul, K.; Braun, M.J.; Gonda, M.A.; Vande Woude, G.
rk, M.; Dean, M.; Kaul, K.; Braun, M.J.; Gonda, M.A.; Vande Woude, G.
rk, M.; Dean, M.; Kaul, K.; Braun, M.J.; Bonda, M.A.; Vande Woude, G.
rk, M.; Dean, M.; Raul, K.; Braun, M.J.; Gonda, M.A.; Vande Woude, G.
rk, M.; Dean, M.; Raul, K.; Braun, M.J.; Braun, M.J.; Braun, M.A.; Vande Woude, G.
rk, M.; Braun, M.J.; Braun, M.J.; Braun, M.J.; Braun, M.A.; Vande Woude, G.
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seidues: 1-14 cGAM>
seidues: 1-14 cGAM>
stractini, R.; Longati, P.; Naldini, L.; Vigna, E.; Comoglio, P.M.
tiol. Chem. 266, 19558-19564, 1991
tele: Identification of the major autophosphorylation site of the Met/hepatocyte grow:
ference number: A40.197; MID:92011756; PMID:1655790
nntents: annotation; autophosphorylation site
an, M.; Park, M.; Vande Woude, G.F.
cell: Biol. 7, 921-924, 1987
tele: Characterization of the rearranged tpr-met oncogene breakpoint.
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seidues: 1-755, TWWKEPLNIVSFLFCFAS',756-1190,'A',1192-1390 <PAR>
seidues: 1-755, TWWKEPLNIVSFLFCFAS',756-1190,'A',1192-1390 <PAR>
sear. A.M.L.: King, H.W.S.; Tempest, P.R.; Deakin, E.A.; Cooper, C.S.; Brookes, P.
gene 1, 229-233, 1987
Lele: Primary structure of the met protein tyrosine kinase domain.
ference number: A93749; MUID:88143699; PMID:3325883
1095 T-CQAPALALGPDHQSDLTERP---EEFGFILDNVQSLLILNKTNFTYYPNPVFEAFGPS 1150
                                                                                                                                                                                                                                              1151 GILELKPGTPIILKGKNLIPPVAGGNVKLNYTVLVGEKPCTVTVS-DVQLLCESPNLIGR 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1210 HKVMARVGGMEYSP----GMVYIAPDSPLSLPAIVSIAVAGGLLIIFIVAVLIAYKRKSR 1265
                                                                        793 IWCSTPSL-----KELNLEPPITTRVFFILDGV----ISNNFELSYVNNPIFETFGKP 841
                                                                                                                                                                                                                                                                                                                             842 VVPPIGNKNILEIKGDHIDSEAVRGEV----LKVGNKSCEIVQSKSDSVSCSVPTDLFK 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           897 SNSELKIEFVQEVPSIIIGKVMVTQDQ--NFTGIITGVVSCVVLLLLMPGILIMMKKRKQ 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tocyte growth factor receptor precursor - human ntains: protein-tyrosine kinase (EC 2.7.1.112) met ecies: Homo sapiens (man) te: 31-Mar-1991 #sequence revision 30-Sep-1992 #text change 11-Jun-1999 cession: A40175; A28303; A93349; A93369; A53761; IS7632; A30008; B24569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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ference number: A40175
cession: A40175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     955 LKDL 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        session: A53761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ordano, S.
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| 157632  | qa         | 489EVIVEHTLNQ 498  |
|---|------------|--|
| A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA   | δ          | 735 RGYECILNIQGSEQRVPALRFNSSSVQCQNTSYSYEGMEINNLPVELTVVWNGHFN 790   |
| rences: G   | qq         | 499 NGYTLVITNGLGCRHF- 523  |
| is receptor to a unifer or arounded bounded by arbina and the bounded by  | δγ         | 791 IDNPAQNKVHLYKCGAMRESCGLCLKADPDFACGWCQGPGOCTLRQHCPAQESQWLELSG 850   |
| A) General Cos: A) Cone: Cos: | දු<br>ධ    | 524  |
|   | oy<br>G    | 851 AKSKCTNPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSP 903 ::   |
| 7.124/Domain: signal sequence #status predicted <sig.<br>F;1-24/Domain: signal sequence #status predicted <sig.<br>F;25-303/Product: hepatocyte grawth factor receptor alpha chain #status predicted <alp-< td=""><td>70</td><td></td></alp-<></sig.<br></sig.<br>  | 70         |  |
| 308-1390/Product: nepatocyte growth ractor receptor beta chain #statu<br>933-955/Domain: transmembrane #status predicted <twn><br/>1076-1344/Domain: profein kinase homology <kin></kin></twn>  | qa         |  |
| F;1084-1092/Region: procein kinase ATP-binding motif<br>F;45,106,149,202,399,405,635,785,930/Binding site: carbohydrate (Asn) (covalent) #status  | රි සි      | 964 GPMSGGTQVTITGTNLNAGSNVVVMFGKQPCLFHRRSPSYIVCNTISSDEVLEMKVSVQV 1023    -   -   -   -  -  -  - - - - - - -  |
| F;1110/Active site: Lys #status experimental<br>F;1235/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experim  |            | GPMAGGILLILIUNILUNSGNOKRILGILGGALILLING VONGILLECI IFPATIOLIS EN AVAGARA   |
| 6.5%; Score 651; DB 1; Length 1390; illarity 19.9%; Pred. No. 2.4e-33;  | à 4        |  |
| Matches 364; Conservative 266; Mismatches 557; Indels 640; Gaps   | ò          | 1082 HINICEVLNATE-WTCOAPALALGPDHOSDLTERPEEFGFILDNVOSLLILNKTNFTYYP 1140   |
| OY 62 HIYLGAVNRIYKLS-SDLKVLVTHETGPDENNPKCYPPRIJQTCNEPLITI   | Ωp         |  |
| 116 KMLLID-YKENRLIA-GSLYOGICKLIRLEDLFKLGEPYHKKEHYLSGVNES  |            |  |
| ::  ::  ::  :   :   :   :   :   :   :   |            | NPVFKPFEKPVMISMGNENVLEIKGNDIDP   |
| Qy 167 GSVFGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADG 212   | S S        | 1200 LCBSIN-LIGHTNOWHENCOMBISSGNOTINE DSTED - LEGAL OF THE SERVICE OF THE S |
| Db 170 SQCPDCVVSALGAKVLSSVKDRFINFFVGNTINSSYFPDHPLHSISVRRLKETKDG 225   | ò          | 1250 IIFIVAVLIAYKRKSRESDLTLKRLQMQMDNLESRVALECKEAFAELQTDIHELTSDLDG 1309   |
| 213 MFAYVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPPG  | qQ         |  |
| DD 226 -FMFLIDQSIIDVLFEFKDSIFIKIVHAFESNNFIIFLIVUKE 20/  | λŏ         | 1310 AGIPFLDYRTYTMRVLFPGIEDHPVLRDLEVPGYRQERVEKGLKKFAQLINNKVFLLSFI 1369<br>   |
| TIDEQY ISACVARACE TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE T   |            | 999ESVDYRATFPEDOFPNSSQNGSCRQVQYP   |
| CY 320 AVLGRILGVHPDDDLLFTVFSKGQKRKMKSLDBSALCIFILKQINDRIKERLQSCYRGEG 379   | දු අ       | 1370 KTLESQRSFSMKURGNVASLIMIYUQSKLEIAIDVALKULANDIJUNUESSANTFALLIKK 1423<br>1028LITDMSPILTSGDSDISSPLLQNTVHIDLSALN-PELV 1063   |
|   | ٠.         | TESVAEKMLTNWFTFLLYKFLKECAGEPLF-  |
| 380 TLDLAWLKVKDIPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAYV  |            | GCVYHGTLLDNDG  |
| Db 3771V 378 Qy 440 YKNHSLAFVGTKSGKLKKIRVDGPRGNALQYETVQVVDPGPVLRDMAFSKDHEQLYIMSE 499  |            | 1476 AITGEARYSLSEDKLIRQQIDYKTLVLSCVSPDNANSPBVPVKILNCDTITQVKEKIL 1533   |
| Db 379 NKNNV395   | g è        | GARMILODEDITTKIEND   |
| QY 500 RQLTRVPVESCGQYQSCGECLGSGDPHCGWCVLANICTRKER-CERSKEPRRFASEMK 556   |            | RNFIRNETHNPTVKDLIGFGLQVAKGMKYLASKKFVHRDLAARNCMLDEKFTVKVAD-   |
| Db 396  | ò          |  |
| Qy 557 QCVRLTVHPNNISVSQYNVLLVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQIQCYS 614   | qa         | 1223FGLARDMYDKEYYSVHNKTGAKLPV-KMMALESLQTQ 1258   |
| 615 PAAKEVPRIITENGDHHVVQLQLKSKETGMTPASTSFVFYNCSVHNSCLSCVESPYRCHW  |            | TPMITPDLES-GVXGWHLVXXHEHGDQKEGDRGSKAVSEIYLTRLLATKGTLQK   |
| 472   | අ <b>ද</b> | 1259 KETTKSDVMSFGVVLWELMTRGAPPYPDVNIFULIVYLLLQSKKLLQFEI 130/<br>1401 ennntebatbertahPGSalelatkymen-FlübGankHGTHDPHVRHTWKS-N 1741   |
| OY 675 CKYRHVCTHDPKTCSFQEGRVKLPEDCPQLLRVDKILVPVEVIKPITLKAKNLPQPQSGQ 734   | දි දි      | CPDPLYEVMLKCWHPKAEMRPSFSELVSRISAIFSTFIGEHYVHVNATYVNVK  |
| -   |            |  |

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| 1742 CL   | රි සි      | 277 TSKLVRLCKEDTAFNSYVEVPIGCBRSGVEYRLLQAAYLSKAGAVLGRTLG 327   :::  |
|---|------------|--|
| 1361 CVAPYPSLLSSEDNADDEVDTRPASFW 1387   | 3 8        | THATTAR COVED OF THE PROCEED OF THE PART O |
| ULT 13  | qa         | :     :: : ::   :    : :   |
| tocyte growth factor receptor precursor - mouse<br>ntains: protein-tyrosine kinase (EC 2.7.1.112) met<br>ecies: Mus musculus (house mouse)  | & 8<br>8   | 388 VKDIPCSSALLTIDDNFCGLDMAPLGVSDMVRGIPVFTEDRDR 431 ::   |
| ate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999<br>ccession: S01224; JH0115; A45453<br>han, A.M.L.; King, H.W.S.; Deakin, E.A.; Tempest, P.R.; Hilkens, J.; Kroezen, V.; Edw   | රි සි      | AFVGTKSGKLKKIRVDGPRGNALQYETVQVVDPGPVLRDWAF   |
| ler   | G &        |  |
| olecule type: mRNA<br>esidues: 1-1379 <cha></cha>   | qq         | 466 465  |
| ross-references: EMBL:Y00671; NID:g53058; PIDN:CAA68680.1; PID:g53059<br>ilks, AF.; Kurban, R.R.; Hovens, C.M.; Ralph, S.J.<br>e BS, G7-74, 1989  | <b>ራ</b> ස | 548 PRRPASEMKQCVRLITVHPNNISVSQYNVLLVLETYNVPELSAGVNCTFEDLSEMDGLVVG 607 1 :  |
| itle: The application of the polymerase chain reaction to cloning members of the proteference number: JH0112; MUID:90152381; PMID:2482828   | 8 8        | NQIQCYSPAAKEVINITENGDHHVVQLGKSKETGMTFASTSFVFYNCSVHNSCLSCVE 66  |
| .cession: Onoin: MRNA<br>blecule type: mRNA<br>esidues: 'I', 1200-1254,'R',1256-1260,'T',1262-1268 <wil></wil>  | qa         |  |
| Experimental source: hemopoletic cell cote and the authors translated the codon ACG for residue 1261 as Lys eidner, K.M.; Sachs, M.; Blrchmeler, W.   | ඊ සි       | 668 SPYRCHWCKYRHVCTHDPKTCSFQEGRVKLPEDCPQLLRVDKILVPVEVIKPITLKAKNL 727<br>494  |
| Cell Biol. 121, 145-154, 1993<br>Ittle: Tib Met receptor tyrosine kinase transduces motility, proliferation, and morphd   | ò          | 728 POPOSGORGYECILNIQGSEGRVPALRFNSSSVQCQNTSYSYSGMEINNLPVELTVVWNG 787   |
| cocessince named: Arithmy including the company of the content of translation and the company of the content of translation   | Ωp         | 494PSNQNGYTLVVTGKKITKIP-LNGLGCG 520  |
| iolecule type: mRNA<br>esidues: 924-935 <wei></wei>   | ò          | HFNI DNPAQNKVHLYKCGAMRESCGLCLKADPDFACGWCGGPGGCTLRQHCPAQESQWLE  |
| enetics:<br>ene: met  | οg         | NQCVRFDECPSGTWTQ   |
| uperfamily: hepatocyte growth factor receptor; protein kinase homology<br>eywords: APP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;<br>24/Domain: signal sequence #etatus preditted <sig»< td=""><td>ò a</td><td>848 LSGAKSKCTNPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECS 902 558EICLPAVYKVEPTSAPLEGGTVLTICGWDFGFRONKFDLRKTKVLLGNESC 609</td></sig»<> | ò a        | 848 LSGAKSKCTNPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECS 902 558EICLPAVYKVEPTSAPLEGGTVLTICGWDFGFRONKFDLRKTKVLLGNESC 609   |
| s predicted <ac< td=""><td>ò</td><td></td></ac<>  | ò          |  |
| 08-13/9/Product: hepatocyte growth factor receptor beta chain #status predicted <bch><br/>30-954/Domain: transmembrane #status predicted <tmm><br/>56-1379/Domain: intracellular #starus nredicted <tmn.< td=""><td>qq</td><td>610 TLTLSESTINTLKCTVGPAM-SEHFN-VSVIISNSRETTQYSAFSYVDPVITSISPR 664</td></tmn.<></tmm></bch>   | qq         | 610 TLTLSESTINTLKCTVGPAM-SEHFN-VSVIISNSRETTQYSAFSYVDPVITSISPR 664  |
| main:<br>gion:<br>site:   | o 9        | 963 RGPMSGGTQVTITGTNLANAGSNVVVMFGKQPCLFHRRSPSYIVCNTTSSDEVLEMKV 1019  |
| 233/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict uery Match 6.5%; Score 646.5; DB 1; Length 1379; Per Local Similarity 20 7%. Pred No. 4 75.33.  | <u>ک</u> ج | 1020 SVQVDRAKIHQDLVPQYVEDPTIVRIEPEWSIVSGNTPIAVWGTHLDLIQNPQIRAKH 1077 :::   |
| tches 282; Conservative 180 62 HIYLGAVNRIYKLS-SDLK  | λo         | GCKEHINICEVLMATE-MTCQAPAL-ALGPDHQSDLTERPEBFGFILDNVQSLLILMKTN   |
|   | QD ,       | VGVNYTVACQHRSNSEIICCTTPSLKQLGLQLPLKTKAF-FLLDGILSKHFD   |
| 116 XMLLID-YKENRLIACGSLYQGICKLLRLEDLFKLGEPYHKKEHYLSGVNESG 167             ' :::     :             : :   | දු දු      | 1136 FTTYPNPVEAFGPSGILELKFGTPIILKGKNIJPPVAGGNVKLNYTVLVGEKPC 1190   |
| SVFGVIVSYSNLDDKLFIATAVDGKPEY-FPTISSRKLTKNSEADGMFAYVFHD  | y d        | 1191TVTVSDVQLLCESPNLIGRHKVMARVGGMEYSPGMVYIAPDSPLSLPAIVSIAV 1244  |
| 175 VVSALGAKVLLSEKDRFINFFVGNTINSSYPPGYSLHSISVRRLKETQDG-FKFLTDQ 231<br>221 EFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPPGSTTKEQVY 276  | ò          | rvaleckeafaelo<br>   |
|   | g ò        | 941 SVVVLLLSGLFLWMRKRKHKDLGSELVRYDARVHTPHLDRLVSARSV 987 1298 TDIHELTSDLDGAGIPFLDXRTYTWRVLFPGIEDHPVLRDLEVP 1341   |
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C,Accession: T30811
R;Cottage, A.J.; Clark, M.; Hawker, K.; Umrania, Y.; Wheller, D.; Bishop, M.; Elgar, G.
FEBS Lett. 443, 370-374, 1999
A;Title: Three receptor genes for plasminogen related growth factors in the genome of the
A;Reference number: Z20880; MUID:99148833; PMID:10025966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLPAIVSIAVAGGLLIIFIVAVLIAYK-RKSRESDLTLKRLQMQMDNLESRVALECKEAF 1293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           957 SDLKPSRGPMSGGTQVTITGTNLNAGSNVVVMFGKQPCLFHRRS-----PSYIVCNTTSS 1011
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A.Cross-references: EMBL:AJ009961; NID:e1354962; PID:e1354963; PIDN:CAA08917.1
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C,Species: Fugu rubripes
C,Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                              501 FKVPSLGPGCAHF-----RTCSMCLMAPRFMNCGWCS--GVCSROHQC---DMOW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                909 IP----AEQIVCEMGEA-KPSQHAGFVEICVAVCRPEFMARSS-----QLYYFMTLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1012 DEVLEMKVSVQVDRAKIHQDLVFQYVEDPTIVRIEPEWSIVSGNTPIAVWGTHLDLIQNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 EDVGSVPVKVLIDSFPVTATKMFFYKRNPVITLVEPQCSLHSGSR-LVIQGQNLDSAHKT
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                                                                    669 PYRCHWCKYRHVCTHDPKTCSFQEGRVKLPEDCPQLLRVDKILVPVEVIKPITLKAKNLP
                                                                                                                                                                                                         729 QPQSGQRGYECILNIQGSEQRVPALRFNSSSVQCQNTSYSYEGMEINNLPVELTVVWNGH
                                                                                                                                                                                                                                                                                                                                       789 FNIDNPAQNKVHLYKCGAMRESCGLCLKADPDFACGWCQGPGQCTLRQHCPAQESQWLEL
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                                                                                                                                                  -----GHFGTSD-----GRI-
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                 ----TTVMVTTTGNHTL-
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Ipate: 0.2-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
Accession: T30813
Cottage, A.J.; Clark, M.; Hawker, K.; Umrania, Y.; Wheller, D.; Bishop, M.; Blgar, G.
SBS Lett 443, 370-374, 1999
SBS Lett 443, 370-374, 1999
Title: Three receptor genes for plasminogen related growth factors in the genome of the Feterence number: Z20880; MUID:99148833; PMID:10025966
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Ajintrons: 400/3; 459/3; 499/3; 556/3; 611/2; 655/3; 701/2; 761/2; 794/3; 870/3; 919/3;
C;Superfamily: hepatocyte growth factor receptor; protein kinase homology
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Best Local Similarity 21.0%; Pred. No. 2.2e-27;
Matches 306; Conservative 189; Mismatches 442; Indels 522;
SPITEMVSN-----ESVDYRATFPEDQFPNSSQNGACRQVQYP 1025
                                                                                                                                                                                        asminogen related growth factor receptor 2 - Fugu rubripes
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| Db 630 WTBIQCSPWFSGNFTPSGHTQy 968 GGTQVTITGTNLNAGSNVVVMFGKQF  | 1028   | 1085   | 1142 PVFE<br>    :   :<br>  852 PLFQ  | CY 1193TVSDVQLLCESFNLIGHTRY  DD 908 TELQTTTSKELQVEWRQADSI-RHL | 1247  | Qy 1295 ELQTDIHELTSDLDGAGIFPLDYRTY : : :   :    :    :     | Qy 1355 FAQLINNKVFLLSFIRTLESQRE :   :::  Db : 1034 YGGNGELLSPRLVALG | Qy 1412 LIDKNLESKNHPKLLLRRTESVAE<br>                         | Qy 1462 FCAIKQQMEKGPIDAITGEARYSI<br>  :  :        <br> Db 1124 HCAVKSLNRITDLEEVSQFI | 1515  | Qy 1560 -GARMILQDEDITTKIEN  Db 1223 :.AARNCMLDESYTVKVADFGLARDVY      | Qy 1594 VVALVSKQVTAYNAVRNS<br>     -::    -  :<br>  Db 1283 DVMSFGVLLWELMTRGAPPYSDVNSF | Qy 1646 ESGVKMWH 1653<br>:     <br>Db 1336ECWH 1339              | Search completed: June 24, 2003, 19:01:0<br>Job time : 80 secs       |  |  |   |
|---|--|--|---|---|---|--|---|--|---|---|--|--|--|--|--|--|---|
| A;Introns: 407/3; 475/3; 518/3; 576/3; 629/2; 667/3; 713/2; 768/2; 801/3; 871/3; 921/3; C;Superfamily: hepatocyte growth factor receptor; protein kinase homology Query Match Query Match Best Local Similarity 20.6%; Pred: No. 3.6e-27; Matches 372; Conservative 223; Mismatches 565; Indels 648; Gaps 83; | 15 LLAWGMGSSTLLTRQPAPLSQKQRSFVTPRGE-PAEGFNHLVVDERTGHIYLGAV 6 | 69 NRIYKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTTTNNVNKMLLID 121 | 122 -YKENRLIACGSLYQGICKLLRLEDLFKLGEPYHKKEHYLSGVNESGSVFGVIVSYSNL- 179  117 NIYDKGLFSCGSADNGVCRRHVLEDDVSLDEEGRQKSVDELVYCFTDLK 165 | 180 DDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVAS 225        | 226MIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPPG 268 218 MSLRKMKTSQNGFTFFSNRSYMDLIPPLRGSYYLRYVYSFHSGPFTYFLTVQ 269 | 269 STTKE-OVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVEYRLLQAAYLSK 317 | AGAVLGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCY          | RGEGTLDLAWLKVKDIPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFTEDRDRMTSV | IAYVYKNHSLAFVGTKSGKLKKIRVDGPRGNALQYETVQVVDPGPVLRDMAFSKDHEQLY                        | 402 402 401 402 402 403 406 406 407 408 408 408 408 408 408 408 408 408 408 | 556 KQCVRLTVHPNNISVSQXNVLLVLETYNVPELSAGVNCTPEDLSEMDGLVVGNQIQCYSP 615 | AAKEVPRIITENCDHHVVQLQLKSKETGMTFASTSFVFYNCSVHNSCLSCVESPYRCHWC                           | KLPEDCPQLLRVDKILVPVEVIKPITL<br>             <br>NIRLDSRPVSGSVVLP | 736 GYECILNIQSSEQRVPALRENSSSVQCQNTSYSYSGMEINNLPVELTVVWNGHFNIDNPA 795 | 796 QNKVHLYKCGAMRESCGLCLKADPDFACGWCQGPGOCTLRQHCPAQESQWLELSGAKSKC 855 | 856 TNPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGYIPA 911 | 912 -EQIVCEMGBAKPSQHAGFVEICVAVCRPEFMARSSQLYYFMTLTLSDLKPSRGPMS 967 |
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein gearch, using sw model

June 24, 2003, 18:44:26; Search time 32 Seconds Run on:

(without alignments)
2457.472 Million cell updates/sec

US-09-964-956-13 9990 1 MKAMPWNWTCLLSHLLMVGM......QKLAYKLEQVITLMSLDSNK 1896 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES |      |        | Description        |
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| Score Match Level  | 81           |  |           | sgult<br>No.      |     | 7                           | m                            | 4                         | Ŋ                      | 9                            | 7                | 80               | σ              | 10             | 11                        | 12                       | 13                       | 14                       | 15                        | 16           | 11         | 18                    | 19                  | 20                  | 21                  | 22           | 23                  | 24                  | 25                    | 56                | 27           | 28           | 53           | 30                       | 31     | ٠  |

| 014563 homo sapien<br>09ntn9 homo sapien<br>042217 mus musculu<br>042236 gallus gall<br>09w7jl brachydanio<br>035464 mus musculu<br>026872 tribolium c<br>09w686 brachydanio<br>090607 gallus gall<br>09h3t2 homo sapien<br>092854 homo sapien<br>052181 mus musculu |
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| SM3A_HUMAN<br>SM4G_HUMAN<br>SM3B_MOUSE<br>SM3C_CHICK<br>SZ1A_BRARE<br>SMA_MOUSE<br>SM1A_TRICF<br>SZ1B_BRARE<br>SM3A_CHICK<br>SM6C_HUMAN<br>SM4D_HUMAN<br>SM4D_HUMAN  |
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                                                                                                Best Local Similarity 60.0%; Pred. No. 0;
Matches 1133; Conservative 293; Mismatches 437; Indels
                                                                         MW; 28420CEBDB22E9CE CRC64;
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SEQUENCE OF 1267-1390 FROM N.A.
MEDLINE=86065462; PubMed=4069211;
Dean M., Park M., 1e Beau M.M., Robins T.S., Diaz M.O., Rowley J.D.,
Blair D.G., Vande Woude G.F.;
"The human met oncogene is related to the tyrosine kinase oncogenes.";
Nature 318:385-388(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91118019; PubMed=1846706;
Bottaro D.P., Rubin J.S., Faletto D.L., Chan A.M.-L., Kmiecik T.E.,
Vande Woude G.F., Aaronson S.A.;
"Identification of the hepatocyte growth factor receptor as the c-met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1206-1264 FROM N.A.
MEDLINES-940677791, PubMeda-8247543;
Lee S.-T., Strunk K.M., Spritz R.A.;
"A survey of protein tyrospine kinase mRNAs expressed in normal human
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              MET_HUMAN STANDARD; PRT; 1390 AA.

909581; 090PL8; 060366;
01-AUG-1988 (Rel. 08, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Heparocyte growth factor receptor precursor (EC 2.7.1.112) (Met progne tyrosine kinase) (c-met) (HGF receptor) (HGF-SF receptor)
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=87317655; PubMed=2819873;
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Chan A.M.L., King H.W.S., Tempest P.R., Deakin B.A., Cooper C.S.,
                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Primary structure of the met protein tyrosine kinase domain.";
Oncogene 1:229-233(1987).
[5]
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MEDLINE=92011756; PubMed=1655790;

Ferracini R., Longati P., Naldini L., Vigna E., Comoglio P.M.
"Identification of the major autophosphorylation site of the Met/Anepatocyte growth factor receptor tyrosine kinase.";
J. Biol. Chem. 266:19558-19564(1991).
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
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Science 251:802-804(1991)
                                                                                                                                                                                                  sapiens (Human)
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                                                                                                                                                       Lerman M.I., Linehan W.M., Zbar B.;
"Germline and sometic mutations in the tyrosine kinase domain of the
MET protc-oncogene in papillary renal carcinomas.";
Nat. Genet. 16:68-73(1997)
                                                                                        -i- FUNCTION: RECEPTOR FOR HEPATOCYTE GROWTH FACTOR. HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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ProDom; PD000001; Buk_pkinase; 1.
SMART; SM00429; IPT; 4.
SMART; SM00429; IPT; 4.
SMART; SM00219; TYRKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00119; PROTEIN KINASE TYR; 1.
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InterPro; IPR002909; IPT_TIG.
InterPro; IPR003699; Plexin-like.
InterPro; IPR00165; Plexin-repeat.
InterPro; IPR001627; Sema.
InterPro; IPR00145; Tyr_pkinase.
Pfam; PF00069; pkinase; I.
Pfam; PF001403; Sema, I.
Pfam; PF01437; PSI; I.
Pfam; PF01833; TIG; 3.
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EMBL; X54559; CAB56793.1; -.
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| 84;<br>115<br>117<br>116<br>116<br>116<br>122<br>225<br>225<br>267<br>379<br>376<br>439<br>378   |
| 1009 1010 BREAKCOLTE POR FRANSLOCATION TO FORM TER-MINED (GLCANG ) (POTENTIAL). 1045 1245 1245 PHOSPHORALATION (GLCANG ) (POTENTIAL). 105 106 N-LINEED (GLCANG ) (POTENTIAL). 106 106 N-LINEED (GLCANG ) (POTENTIAL). 107 107 N-LINEED (GLCANG ) (POTENTIAL). 108 108 N-LINEED (GLCANG ) (POTENTIAL). 109 109 100 N-LINEED (GLCANG ) (POTENTIAL). 109 100 N-LINEED (GLCANG ) (POTENTIAL). 109 100 N-LINEED (GLCANG ) (POTENTIAL). 109 100 N-LINEED (GLCANG ) (POTENTIAL). 100 N-LINEED (GLCANG ) (POTENTIAL). 100 N-LINEED (GLCANG ) (POTENTIAL). 101 N-LINEED (GLCANG ) (POTENTIAL). 102 N-LINEED (GLCANG ) (POTENTIAL). 103 N-LINEED (GLCANG ) (POTENTIAL). 104 N-LINEED (GLCANG ) (POTENTIAL). 105 N-LINEED (GLCANG ) (POTENTIAL). 106 N-LINEED (GLCANG ) (POTENTIAL). 107 N-LINEED (GLCANG ) (POTENTIAL). 108 N-LINEED (GLCANG ) (POTENTIAL). 109 100 N-LINEED (GLCANG ) (POTENTIAL). 100 N-LINEED (GLCANG ) (POTENTIAL). 100 N-LINEED (GLCANG ) (POTENTIAL). 101 N-LINEED (GLCANG ) (POTENTIAL). 102 N-LINEED (GLCANG ) (POTENTIAL). 103 N-LINEED (GLCANG ) (POTENTIAL). 104 N-LINEED (GLCANG ) (POTENTIAL). 105 N-LINEED (GLCANG ) (POTENTIAL). 106 N-LINEED (GLCANG ) (POTENTIAL). 107 N-LINEED (GLCANG ) (POTENTIAL). 108 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL). 109 N-LINEED (GLCANG ) (POTENTIAL).  |
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                   PIR; S01254; S01254.
HSSP, P11362; 1FGK.
                                                       MGD; MGI: 96969; Met
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Best Local Similarity
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                                                                                                                               1114 RITDIGEVSQFLTEGIIMKDFSHPNVLSLLGICLRSEGSPLV------VLPYMKHGDL 1165
                                                                    1166 RNFIRNE--THNPTVKDLIGFGLQVAKGMKYLASKKFVHRDLAARNCMLDEKFTVKVAD- 1222
                                                                                                                                                                                                                   1259 KFTTKSDVWSFGVVLWELM------TRGAPPYPDVNTFDITVYLLQGRRLLQPEY 1307
                                                                                                                                                                                                                                                      1691 FVDDLFETIFSTAH-----RGSALPLAIKYMFD-FLDEQADKHGIHDPHVRHTWKS-N 1741
                                                                                                                                                                                                                                                                                        1308 CPDPLYEVMLKCWHPKAEMRPSFSELVSRISAIFSTFIGE-----HYVHVNATYVNVK 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MET_MOUSE STANDARD; PRT; 1379 AA.
P16056; Q62125;
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel., 14, Last sequence update)
15-UTM-2002 (Rel. 41, Last annotation update)
Hepatocyte growth factor receptor precursor (EC 2.7.1.112) (Met proto-
oncogene tyrosine kinase) (C-met) (HGF receptor)
                                      --GARMILQDEDITTKIEND
                                                                                                                                                                                 1638 TPMITPDLES-GVKMWHLVKNHEHGDQKEGDRGSKMVSEI----YLTRLLATKGTLQK--
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                                                                                                        1578 WKRLNTLAHYQVPDGSVVALVSKQVTAYNAVNNSTVSRTSASKYENMIRYTGSPDSLRSR
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MEDLINE=90152381; PubMed=2482828;
Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;
"The application of the polymerase chain reaction to cloning members of the protein tyrosine kinase family.";
Gene 85:67-74(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: RECEPTOR FOR HEPATOCYTE GROWTH FACTOR. HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
-!-SUBUNIT: HETERODIMER FORMED OF AN ALPHA CHAIN (50 kDa) AND A CHAIN (145 kDa) WHICH ARE DISULFIDE LINKED.
-!-SUBCELLULAR LOCATION: Type I membrane protein.
-!-DISEASE: ACTIVATION OF MET AFTER REARRANGEMENT WITH THE TPR (TRANSLOCATED PROWOTER) LOCUS OF CHROMOSOME I PRODUCES AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88262253; PubMed=2838789;
Chan A.M.L., King H.W.S., Deakin E.A., Tempest P.R., Hilkens J.,
Kroezen V., Edwards D.R., Wills A.J., Brookes P., Cooper C.S.;
"Characterization of the mouse met proto-oncogene.";
Oncogene 2:593-599(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SIMILARITY: CONTAINS 1 SEMA DOMAIN.
                                  1534 DAIFKNVPCSHRPKAADM---DLEWRQGS-----
                                                                                                                                                                                                                                                                                                                              CL-----PLRFW 1748
                                                                                                                                                                                                                                                                                                                                                                1361 CVAPYPSLLSSEDNADDEVDTRPASFW 1387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                            1742
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MET\_MOUSE

EMBL; Y00671; CAA68680.1; -

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 HIYLGATNYIYVLNDKDLQKVSEFKTGPVLEHPDCLPCR---DCSSKANSSGGVWKDNIN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 HIYLGAVNRIYKLS-SDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTTT-----NNVN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 ..-SVFGVIVSYSNLDD--KLFIATAVDGK--PEY-FPTISSRKLTKNSEADGMFAYVFHD 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 EFVASMIKIPSDTFTIIPDF----DIYYVYGFSSGNFVYFLTLQPEMVSPGSTTKEQVY 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 NMLLID-YKENRLIACGSLYQGICK--LLRLEDLFKLGEPYHKKEHYLSGVNESG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY-SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 483; Gaps
                                                                                                                                                                                                                                                                                                                                                                      Transferase; Tyrosine-protein kinaee; Proto-oncogene; ATP-binding; Receptor; Transmembrane; Glycoprotein; Phosphorylation; Signal. SIGNAL
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(POTENTIAL).
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PHOSPHORYLATION (AUTO-)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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-> R (IN REF. 2)
-> T (IN REF. 2)
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PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
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Interpro: IPR001019; Buk pkinase.
Interpro: IPR002090; IPT TIG.
Interpro: IPR002105; Plexin-1ike.
Interpro: IPR00165; Plexin-repeat.
Interpro: IPR001627; Sema.
Interpro: IPR001627; Sema.
Interpro: IPR001645; Tyr_pkinase.
Pfam; PP00069; pkinase; I.
Pfam; PP01403; Sema; I.
Pfam; PP01437; PSI; I.
Pfam; PP01437; TIG; 3.
                                                                                                                                                                                                    PRINTS; PRO0109; TYRKINASE.
ProDom; P0000001; Euk_pkinase; 1.
SMART; SM0429; IPT; 4.
SMART; SM00429; PSI; 1.
PROSITE; PS00107; PROTEIN KINASE AT
PROSITE; PS00109; PROTEIN_KINASE_TY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGPMSGGTQVTITGTNLNAGSNVVVMFGKQPCLFHRRSPSYIVCNT---TSSDEVLEMKV 1019
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274 HTRIIRFCSVDSGLHSYMEMPLECILTEKRRKRSTREEVFNILQAAYVSKPGANLAKQIG 333
                                                   VHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLK 387
                                                                                                                                                  380 -NNVRCLQHFYGPNHEHC---FNRTLLRNSSGCEARSDEYR--TEFTTALQRVDLFMGRL 433
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-poctore growth factor receptor precursor (BC 2.7.1.112) (Met protonocogene tyrosine kinase) (c-met) (HGF receptor)
                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsujii M., Kawano S., Tsuji S., Ito T., Hayashi N., Horimoto M., Mita E., Nagano K., Masuda E., Hayashi N., Fusamoto H., Kamada T.; "Increased expression of c-met messenger RNA following acute gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Montesano R.;
"Modulation of hepatocyte growth factor and c-met in the rat mammary
gland during pregnancy, lactation, and involution.";
Exp. Cell Res. 219:204-210(1995).
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR HEPATOCYTE GROWTH FACTOR. HAS A TYROSINE-
PROTEIN KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                        Wallenius V.R., Rawet H., Skrtic S., Helou K., Qiu Y., Levan G., Ekberg S., Carlsson B., Isaksson O.G.P., Nakamura T., Jansson J.-O. "Chromosomal localization of rat hepatocyte growth factor (Hgf) and HGF receptor (Met) and characterization of HGF receptor CDNA.";
                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley; TISSUB=Kidney;
MEDLINE=97006137; PubMed=8853431;
Liu Y., Tolbert E.M., Sun A.M., Dworkin L.D.;
"Primary structure of rat HGF receptor and induced expression in glomerular mesangial cells.";
Am. J. Physiol. 271:F679-F688(1996).
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MEDLINE=95354758; PubMed=7628535;
Pepper M.S., Soriano J.V., Menoud P.-A., Sappino A.-P., Orci L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 364-495 FROM N.A.
STRAIN-Sprague-Dawley, TISSUE-Gastric mucosa,
MEDLINE-94220137; PubMed-8166728;
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                                                                                                                                                                                                                             TISSUE=Liver;
                                                                                                                                                                                                                             STRAIN=Sprague-Dawley; TISSUE=Live
MEDLINE=97419268; PubMed=9271668;
MET_RAT STANDARD; PI
P97523; P97579; Q63119; Q63964;
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                                                                                                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI_TaxID=10116;
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Brodocol; Euk pkinase; 1.

SMART; SM00429; IPT; 4.

SMART; SM00429; PST; 1.

SMART; SM00129; TYRC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

Transferase; Tyrosine-procein Kinase; Proto-onçogene; ATP-binding; SIGNAL 1.

POTENTIAL.
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P -> H (IN REF. 2).
P -> G (IN REF. 2).
R -> A (IN REF. 2).
Y -> H (IN REF. 2).
EVIVEH -> CAAGIR (IN REF. 3).
P -> A (IN REF. 2).
V -> F (IN REF. 2).
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Interpro; IPR002809; IPT_TIG.
Interpro; IPR001859; Plexin-like.
Interpro; IPR00185; Plexin_repeat.
Interpro; IPR001827; Sema.
Interpro; IPR001827; Sema.
Pfam; PF00169; pkinase.
Pfam; PF00169; pkinase; I.
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Pfam; PF01833; TIG; 3.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkina
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118 MALLVDTYYDDQLISCGSVNRGTCQRHVLPPDNAADIQSBVHCMFSPLA-EEESGQCPDC
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                                                                                                                                                                                                                                                                                                                             221 EFVASMIKIPSDTFTIIPDF----DIYYVYGFSSGNFVYFLTLQPEMVSPPGSTTKEQVY
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                                                                                                                                                62 HIYLGAVNRIYKLS-SDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTTT-----NNVN
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                                                                                                                      Gaps
                                                                                    Query Match 6.4%; Score 635; DB 1; Length 1382;
Best Local Similarity 19.6%; Pred. No. 9.8e-33;
Matches 334; Conservative 248; Mismatches 522; Indels 604;
L -> P (IN REF. 2).
P -> Q (IN REF. 2).
V -> A (IN REF. 2).
V -> F (IN REF. 2).
MW; 6688F2C88FE34427 CRC64;
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MEDLINE=95025877; PubMed=7939629; Wang M.-H., Ronsin C., Gesnel M.-C., Coupey L., Skeel A., Leonard E.J., Breatnach R.; Identification of the ron gene product as the receptor for the human macrophage stimulating protein."; Science 266:117-119(1994).

SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=96413302; PubMed=8816464;
Collesi C., Santoro M.M., Gaudino G., Comoglio P.M.;
M. splicing variant of the RON transcript induces constitutive tyrosine kinase activity and an invasive phenotype.";
Mol. Cell. Biol. 16:5518-5526(1996).

novel putative receptor protein tyrosine kinase of the met

Oncogene 8:1195-1202(1993)

-! - FUNCTION: RECEPTOR FOR MACROPHAGE STIMULATING PROTEIN (MSP). HAS

TYROSINE-PROTEIN KINASE ACTIVITY.

tyrosine phosphate.
-!- SUBGUNT: HETERODIMER FORMED OF AN ALPHA CHAIN AND A BETA
-:- SUBGUNT: HETERODIMER FORMED LINKED.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; RON (SHOWN HERE) AND DELTA-RON;
-!- ALTERNATIVE SPLICING. DELTA-RON LACKS PART OF THE
EXTRACELLULAR DOMAIN, OLIGOMERIZES AND IS CONSTITUTIVELY

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1356 AQLINNKVFLLSFIRTLESQRSFSMRDRGNVASLIMTVLQSKLEYATDVLKQLLADLIDK 1415
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RGPMSGGTQVTITGTNLNAGSNVVVMFGKQPCLFHRRSPSYIVCNTTSSDEVLEMKVSVQ 1022
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                                                                               S33 DLTYVHDPMFKPFEKPVMISMGNENVVEIKGDDIDPEAVKGEV----LKVGNKSCENLH
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-i-TISSUE SPECIFICITY: KERATINOCYTES, AND LUNG.
-i-PTM: THE TWO SUBUNITS ARE PROTECLYTICALLY DERIVED.
-i-PTM: THE TWO SUBUNITS ARE PROTECLYTICALLY DERIVED.
-i-SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
-i-SIMILARITY: CONTAINS 1 SEMA DOMAIN.
-i-DATABASE: NAME=PROW; NOTE=CD guide CDw136 entry;
-i-MATABASE: NAME=PROW; NOTE=CD guide CDw136 entry;
-i-DATABASE: NAME=RLUS Genet. Cytogenet. Oncol. Haematol.;
-i-DATABASE: NAME=Albas Genet. Cytogenet. Oncol. Haematol.;
-i-DATABASE: NAME=Albas Genet. Cytogenet. Oncol. Haematol.;
-i-DATABASE: NAME=Albas Genet. Cytogenet. Oncol. Haematol.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000001; Euk pkinase; 1.
SMART; SM00429; IPT; 3.
SMART; SM00429; TYRC; 1.
SMART; SM000219; TYRC; 1.
SMART; SM000219; TYRC; 1.
PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE TOM; 1.
Transferase; Tyrosine-profein kinase; Grocoptor; Transmembrane; Glycoptotein; Signal; Phosphorylation; ATP-binding; Polymorphism; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro; IPR002909; IPT_TIG.
InterPro; IPR003659; Plexin-like:
InterPro; IPR002165; Plexin_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR001245; Tyr pkinase. Pfam; PF00069; pkinase; 1. Pfam; PF010103; Sema; 1. Pfam; PF01437; PGI; 1. Pfam; PF01833; TIG; 3.
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Genew; HGNC:7381; MST1R.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

Homo sapiens (Human)

TISSUE=Keratinocytės; MEDLINE=93241719; PubMed=8386824; Ronsin C., Muscatelli F., Mattei M.-G., Breathnach R.;

SEQUENCE FROM N.A. NCBI\_TaxID=9606;

| VLLVUETYNVPELSAGVNCTFEDLSEMDGLVVGNQIQCYSPAAKEVPRIITENGDHHVVQ      ::   :   | 1199 LCGESPILITONOLOGICAL CONTROL CONT |
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- SUBUNIT: HETERODIMER FORMED OF AN ALPHA CHAIN AND A BETA
- SUBUNIT: HETERODIMER FORMED OF SIMILARITY).
- SUBCELLILAR LOCATION: Type I membrane protein.
- PTM: THE TWO SUBUNITS ARE PROTECLYTICALLY DERIVED (BY SIMILARITY).
- PTM: PHOSPHORYLARED IN RESPONSE TO LIGAND BINDING (BY SIMILARITY).
- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene.";
Oncogene 16:27-42(1998).
-!- FUNCTION: RECEPTOR FOR MACROPHAGE STIMULATING PROTEIN (MSP). HAS
- TYROSINE-PROTEIN KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                   Iwama A., Okano A., Sudo T., Matsuda Y., Suda T.;
"Molecular cloning of a novel receptor tyrosine kinase gene, STK,
derived from enriched hematopoietic stem cells.";
                                                                    062190; 06255;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Macrophage-stimulating protein receptor precursor (EC 2.7.1.112)
(MSP receptor) (p185-Ron) (Stem cell-derived tyrosine kinase).
MSTIR OR RON OR Sţr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/SvJ;
MEDLINE=98127434; PubMed=9467940;
Waltz S.E., Tomas C.L.V., McDowell S.A., Clay L.A., Muraoka R.S.,
Air E.L., Sun W.Y. Thomas M.B., Degen S.J.F.;
"Characterization of the mouse Ron/Stk receptor tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodom; PD000001; Buk pkinase; 1.
SWART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TR; 1.
Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
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                                                   PRT; 1378 AA
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InterPro; IPR000719; Buk pkinase.
InterPro; IPR002109; IPT_IG.
InterPro; IPR002165; Plexin_repeat.
InterPro; IPR001290; Sema.
InterPro; IPR001290; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; I.
Pfam; PF001403; Sema; I.
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94250897; PubMed=8193352;
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EMBL; U65949; AAC39953.1; -.
HSSP; P11362; 1FGK.
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                                                   STANDARD;
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Pfam; PF01833; TIG; 3
                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 TINNVNKMLLIDYKENRLIACGSLYQGICKLLRLEDLFKLGEPYHKKEHY-----LSGVN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 PEMVSPPGSTTKEQVYTSKLVRLCKEDTAFNSYVEVPIGC-----ERSGV-----EYRL 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 PISVTSPPSALH----TRLVRLNAVEPEIGDYRELVLDCHFAPKRRRGAPEGTQPYPV
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(POTENTIAL).
(POTENTIAL).
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MACROPHAGE-STIMULATING PROTEIN RECEPTOR,
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1378;
                ALPHA CHAIN (POTENTIAL).
MACROPHAGE-STIMULATING PROTEIN
BETA CHAIN (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                            VG -> IA (IN REF. 1).
V -> A (IN REF. 1).
W; FC5F932377B57009 CRC64;
                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                PHOSPHORYLATION (AUTO-)
PHOSPHORYLATION (AUTO-)
                                                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                        (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

4.0%; Score 378.3; LL.,
Best Local Similarity 19.5%; Pred. No. 2e-17;
Matches 271; Conservative 164; Mismatches 436;
                                                                                                                                           PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                  SIMILARITY
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713 71
719 71
1378 AA;
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differentially expressed during early embryogenesis.

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994 HSL-----SPTTLSDINDTASGAPNHEESSESRDGTSVPLL--RTESIR------ 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                       676 SVQEGFSFVEPVLTSIKPDFGPRAGGTYLTLEGQSLSVGTSRAVLVNGTQCRLEQVNEEQ 735
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                            728 PQPQSGQRGYECILNIQGSEQRVPALRFNSSSVQCQNTSYSYEGMEINNLPVELTVVWNG
                                                                                                              SLGSSGQPVHRDVSRL-GND----LLFAS------GDQVFKVPIQ-----G
                                                                                                                                                        ----HFNIDNPAQNKVHLYKCGAMRESCGLCLKADPDFACGWCQGPGQCTLRQHCPAQES
                                                                                                                                                                                          -----LTCWRCLRAQRFMGCGWC--GDRCDRQKECPG---
                                                                                                                                                                                                                                                        563 ----SWQQDHCP-PEISEFYPHSGPLRGTTRLTLCGSNFYLRPDDVVPEGTHQITVGQS
                                                                                                                                                                                                                                                                                                            900 ECSPL-VDGYIP-----AEQIVCEMGEAKPSQHAGFVEICVAVCR----PEFMARSS
                                                                                                                                                                                                                                                                                                                                               617 PCRLLPKDSSSPRPGSLKEFIQELECEL-EPLVTQAVGTTNISLVITNMPAGKHFRVEGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               880 ---EEHSVKVEYVGLGAVADC-VTVNMTVGGEVCQHELRGDVVICPLPPSLQLGKDGVPL
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Semaphorin 5A precursor (Semaphorin F) (Sema F)
SEMA5A OR SEMAF OR SEMF.
Mus musculus (Mouse).
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Q62217;
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InterPro; IPR00084; TSP1.
Pfam; PF00090; tsp_1; 5.
Pfam; PF01403; Sema; 1.
Pfam; PF01437; PSI; 1.
SMART; SN00423; PSI; 1.
SMART; SN00209; TSP1; 6.
PROSITE, PS50092; TSP1; 6.
Signal; Transmembrane; Repeat; Multigene family; Neurogenesis;
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SEMAPHORIN 5A.
EXTRACELLULAR (POTENTIAL)
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InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
InterPro; IPR001627; Sema.
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STRAIN=NMRI; MEDLINE=96414430; PubMed=8817451; Adams R.H.; Betz H., Pueschel A.W.; "A novel class of murine semaphorins with homology to thrombospondin

SEQUENCE FROM N.A. NCBI\_TaxID=10090;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

STRAIN=NWRI;
MEDLINE=96414430; PubMed=8817451;
Adams R.H., Betz H., Pueschel A.W.;
Anovel class of murine semaphorins with homology to thrombospondin
"A novel class of murine semaphorins with homology in the semaphorins and any open class of murine semaphorins with homology in the semaphorins win

SEQUENCE FROM N.A.

is differentially expressed during early embryogenesis.";

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL\_TaxID=10090;

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                                                                                                                                                         290 FNSYVEVPIGCERSG----VEYRLLOAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRK 346
                                                                                                                                                                                                                     347 MKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIPCSSALLTIDDNF-C 405
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                                                                                                                                                                                                                                                                                                                                             -LAFVGTKSGKLKKIR--VDGPRGNALQYETVQVV----DPGPVLRDMAFSKDHEQLYI 496
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                                                                                                                 ---VRGIPVFTEDRDRMTSVIAYVYKNHS--- 444
135 AFTPVCTIRSLSNLTEIHDQISGMARCPYSPQHNSTALLTASG--------ELY 180
                                185 IATAVD--GK-PEYFPTISS----RKLTKNSEADGMPAYVFHDEFVASMIKIPSDTFTII 237
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                                                                                               238 PDFDIYYVYGFSSGNFVYFLTLQPEMVSPPGSTTKEQVYTSKLVRLCKED-----TA
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Best Local Similarity 19.6%; Pred. No. 3.8e-12;
Matches 235; Conservative 162; Mismatches 390; Indels 413;
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EXTRACELLULAR (POTENTIAL)
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InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
                                                                                                                                                                                                                                                                                           EMBL; X97818; CAA66398.1; -.
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                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001627; Sema.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00090; tsp_1; 5.
Pfam; PF01403; Semā; 1.
Pfam; PF01437; PSI; 1.
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63;

30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Semaphorin 5B precursor (Semaphorin G) (Sema G).
SEMAS OR SEMG OR SEMG.
Mus musculus (Mouse).

OS OB DA

1093 AA

STANDARD;

SM5B MOUSE 060519;

SMSB\_MOUSE RESULT 8

| SGRKVFMCGTNAFSFVCSSRQVGNLSRTIEKINGVARCPYDPRHNSTAVISSQG 187         | 117 MLLIDYKEN<br>: :: :<br>130 VLIVSGR  |   |   | Db<br>RESULT<br>SM4B_M                  | 9<br>DUSE<br>M4B_MOUS   | EMGEAKPSCHAGF : :     :   |
|--|---|---|---|---|---|---|
|  | 227 IKIPSDTFT 227 287 DT 267 DVGGRFLLE  | FTIIPDFDIXYVGFSSGNPVYFLTLQPEMVSPPGSTTKEQVYTSKLVRLCKE 286  |   |   | SEMATA OR, SEMAC OR SEM Mus musculus (Mouse).  Bukaryota; Metazoa; Ch Mammalia: Butheria Ro NCBI_TAXID=10090;  [1] SEQUENCE FROM N.A.   | MAC OR S<br>(Mouse)<br>etazoa;<br>theria;<br>0090;  |
| IXIPSDTFTIIPDFDIYYVGFSSGNFVYFLTLQPEMVSPPGSTTKEQVYTSKLVRLCKE 286 GN | 335 LFTVPSKGQ<br>::   :<br>313 IYGVFT<br>394 SSALLTIDD<br>364                                     | 393   |   | R R R R R R R R R R R R R R R R R R R   | STRAIN=NWRI; MEDLINE=9526' Pueschel A.W "Murine semal and creates of and creates (2) [2] INTERACTION 1  | TISSUE=7431; Pu., Adams phorin D domains 1-948(19   |
|  | 434 SVIAXVYKOV<br>1: '.',<br>415 HLVVDLVQA<br>487 FSKDHEQLY<br>487 FILHSARALF                     | KNHSLAFVGTKSGKLKKIRVDGPRG-NALQYETVQVVDPGPVLRDMA 486 : : : : :     :     :     :     :     :     :     :       : |   | R R R R R S S S S S S S S S S S S S S S | MEDLINE=9925. Wang LH., "A PDZ prote 9 semaphorin, U. Biol. Cher -!- FUNCTION SPECIFY -!- SUBUNIT:  | X973; PU Kalb R.G Lin regul M.SemF." M. 274:1 INTERALTOR  |
|  | 530C<br>535 LWIQNITTC<br>557 QCVRLTVHP<br>  : :  <br>593 -CLGPSIHI                                | -CVLHN  |   | 38888888                                | -:- SUBCELLU -:- DEVELOPM -:- DEVELOPM -:- SIMILARI -: SIMILARI -: SIMILARI   | LAK LOCATI ENTAL STAG OUND BETWE LEVELS FR TY: BELONG TY: CONTAL TY: CONTAL   |
|  | 617 AKEVPRIIT  638 PRHGGRICV  667 ESPYRCHWC  :       685 QSRRRSC                                  | ITENGDHHVVQLQLKSKETGMTFASTSFVFYNCSVHNSCLSCV 666   |   | 88888888                                | This SWISS-Pi<br>between the<br>the European<br>use by non<br>modified and<br>entities req<br>or send an er   | ROT entrans Swiss Swiss Beinfer - profit this stuires a mail to   |
| INTERDIFFTIED  | 719PITL 735 ROEORFRETC 739 794 LNGGWATWGP 780ELTVVWNG 854 AWSCWTAWS- 826 CQGPGQCTLR 895 HTERALGS- | 138   | • | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0   | EMBL; X8592; CAA5984 MGD; MGI:107559; Semad InterPro; IPR003659; P InterPro; IPR001659; P InterPro; IPR001659; P Fam; PF01403; PS1; 1: SMART; SMO443; PS1; 1: SMART; SMO4423; PS1; 1: SMART; SMO4423; PS1; 1: NON TER 1 DOMAIN 663 683 DOMAIN 664 782 DOMAIN 684 782 DOMAIN 548 603 | 7. CAA59984<br>75.9; Sema4<br>78.00365; P<br>78.001627; S<br>79. PSI; 1.<br>77; PSI; 1.<br>77; PSI; 1.<br>77; PSI; 1.<br>77; PSI; 1.<br>77; PSI; 1.<br>78; PSI; 1.<br>865<br>663<br>664<br>665<br>664<br>665<br>664<br>665<br>664<br>665<br>664<br>665<br>664<br>665<br>664<br>665<br>664<br>665<br>664<br>665<br>664<br>665<br>665 |

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                                 BE---TTSCGGFNL-----IHLIVTGVSCF-LVSGLLTLAVYLSC 1001
                                                                                                                                         LVH------PATPNHLHYKGGGTPKNEKYTPMEFKTLNKNNLJP 1050
858 PRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGYIP-AEQIVC 916
                                                                                                          FVEICVAVCRPEFMARSSQLYY-------FMTLTLSDLKP 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO ORIES INACCESSIBLE FOR GROWING AXONS.

CACTS WITH GIPC PDZ DOMAIN.

CATION: Type I membrane protein.

STAGE: EXPRESSED FROM DAY 10 IN THE EMBRYO. LOW BITWEEN DAYS 10-12. EXPRESSION PEAKS ON DAY 13 WITH STRUMEN THEN UNTIL BIRTH.

LIONGS TO THE SEMAPHORIN FAMILY.

NYAMINS I SEMA DOMAIN.

NYAMINS I IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oglobulin domain, Multigene family, Neurogenesis, n; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brain;
bMed=7748561;
R.H., Betz H.;
/collapsin is a member of a diverse gene family
inhibitory for axonal extension.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hordata; Craniata; Vertebrata; Euteleostomi; odentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Strittmatter S.M.; tes the distribution of the transmembrane
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
SEMA.
IG-LIKE C2-TYPE DOMAIN.
PRO-RICH.
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Last sequence update)
Last annotation update)
Loorin C) (Sema C) (Fragment).
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Sema.
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30-MAY-2000 (Rel. 39, Created)

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253 QLLCSRPDGFPFNVLQDVF-----TLNPNPQDWRKTLSIGVFTSQWHR--GTTE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: | | : : | : | : | : | : | 417 GRLHKAVTLSSRVHII--EELQIFPQGPPVQNLLLDSHGGLLYASSHSGVVQVPVANCSL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         553 SEMKQCVRLTVHPNNISVSQYNVLLVLET----YNVPELSAGVNCTFEDLSEMDGLVVGN 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 VYGFSSGNFVYFLTLQPEMVSPPGSTTKEQVYTSKLVRLCKEDTA------FNSYVEV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESALCIFILKQINDRIKERLQSCYRGEGTLDLAW-LKVKDIPCSSALLTIDDNFCGLDMN 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       609 Q----IQCYS-----PAAKEVPRIITENGDHHVVQLQLKSKETGMTFASTSFVFYNC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRK------QQCSFKGKDPKRDCQNYIKILL-PLNSSHLLTCGTAAFSPLCAYIHIAS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 F------PIISSRKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFTIIPDFDIYY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 PIGCER---SGVEYRLLQAAYLSKAGAVLGRTLGVHPDD----DLLFTVFSKGQKRKMKSLD 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----CTRKERCERSKEPRRFA
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                                                                                                                                                                                                                                                                                          EERLIRKFEAENISNYTALLLSQDGKTLYVGAREALFALNSNLSFLPGGEYQELLWSADA
                                                                                                                                                                                                                                                                                                                                     DNPKCYPPRIVQTCN----EPLTTTNNVNKMLLIDYKENRLIACG-SLYQGICKLLRLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 YTGTVSSFQGNDPALSRSQSSRPTKTESSLNWLQDPAFVASATSPESLGSPIGDDDKIYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----MVRGIPVFTEDRDRMTSVIAY----VYKNHSLAFVGTKS
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                                                                                                                                                                                                   Query Match 3.1%; Score 308.5; DB 1; Length 782; Best Local Similarity 20.9%; Pred. No. 5.3e-12; Matches 156; Conservative 121; Mismatches 292; Indels 177;
                      (POTENTIAL)
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                                                                                                                                                                      86823 MW;
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SMSA HUMAN Q13591; O60408;

SMSA HUMAN RESULT 10

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                                                                                                                                                                                                                                                                                                     Simmons A.D., Puschel A.W., McPherson J.D., Overhauser J., Lovett M., "Molecular cloning and mapping of human semaphorin F from the Cri-du-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AC004615; AAC14668.1; -.

R Genew; HGNC:10736; SEMA5A.

R InterPro; IPR00365; Plexin.like.

InterPro; IPR00165; Plexin.repeat.

R InterPro; IPR00165; Plexin.repeat.

R InterPro; IPR00084; TSP1.

R Pfam; PF00090; Psp1; 1.

R Pfam; PF00403; Sema; 1.

R Pfam; PF0043; PSI; 1.

R SMART; SM00209; TSP1; 6.

R PROSITE; PSS0092; TSP1; 6.

R SG0017E; PSS0092; TSP1; 6.

M Signal; Transmembrane; Repeat; Multigene family; Neurogenesis;

M Developmental protein; Glycoprotein.
                                                                                                                                                  Vertebrata; Euteleostomi;
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                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalicki J., Harmon G.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY ACT AS POSITIVE AXONAL GUIDANCE CUES.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
-!- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
-!- SIMILARITY: CONTAINS 7 TSP TYPE-1 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEMAPHORIN 5A.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 242:685-691(1998)
             30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Semaphorin 5A precursor (Semaphorin F) (Sema F)
SEMASA OR SEMAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                          chat candidate interval.
                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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STANDARD;
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Q9YHX4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 TKEQVYTSKLVRLCKED----TAFNSYVEVPIGCERSG---VEYRLLQAAYLSKAG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 V----FSRAARVCKNDIGGRFLLEDTWITFMKARLNCSRPGEVPFYYNELQSTFFL--- 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 AVLGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCYRGEG 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 NSRSAWLPYPNPNPHFQCG----TVDQ---GLYVNLTERNLQDAQKPILVHEVVQPVTTV 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | | : | | : | :: | :: | :: | SFMEDNSRFSHVAVDVVQGREALVHIYLATDYGTIKKVRVRVPLNQTSSSCLLEEIELFP 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510 MKKCT------SLEESLSMTQWEQSISACPTRNLTVDGHFGV--WSPWTP 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTFEDLSEMDGLVVGNQI----QCYSPAAK-----EVPRIITENGDHHVVQLQLKSKET 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RHVCTHDP-----KTCSFQEGRVKLPEDCPQLLRVD 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----EINNLPVELTVVWNGHFNIDNPAQNKVHLYKCGAMRESCG-----LCLK 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   824 LGPSLEYQECNTLPCPVDGVW----SCWSP-----WTKCSA---TCGGGHYMRTRSCSN 870
                                                                                                                                                                                              66
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                                                                                                                                                                                              43 FRGEPAEGFNHLVVDERTGHIYLGAVNRIYKLS-SDLKVLVTHETGPDEDNPK-CYPP-R
                                                                                                                                                                                                                                                                                                             SKEEC-----QNYIRVLLVG--GDRLFTCGTNAFTPVCTNRSLSNLAEIHDQISGMAR
                                                                                                                                                                                                                                                                                                                                                     - PYHKKEHYLSGVNESGSVFGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEA
                                                                                                                                                                                                                                                                                                                                                                            CPY-SPQHNSTALLTAGG------ELYAATAMD-FPGRDPAI-YRSL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVFTEDRDRMTSVIAYVYKNHS----LAFVGTKSGKLKKIRVD-GPRGNALQYETVQVV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----DPGPVLRDMAFSKDHEQLYIMSERQLTRVPVESCGQYQSCGECLGSGDPHCGWCVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 453 ERRREP---IRSLQILHSQSVLFVGLREHVVKIPLKRCQFYRTRSTCIGAQDPYCGWDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 HNTCTRKERCERSKEPRRFASEMKOCVRLTVHPNNISVSQYNVLLVLETYNVPELSAGVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 TLDLAWLKVKD----IPCSSALLTIDDNFCGLDMNAP------LGVSDMVR---GI
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                                                                                                                                                           Gaps
                                                                                                                 Query Match
2.9%; Score 292.5; DB 1; Length 1074;
Best Local Similarity 19.8%; Pred. No. 9.7e-11;
Matches 203; Conservative 142; Mismatches 347; Indels 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMT-FASTSFVFYNCSV----HNSCLS-----CVES----
56 56 A -> V (IN REF. 2).
149 149 A -> T (IN REF. 2).
382 382 V -> M (IN REF. 2).
494 494 S -> R (IN REF. 2).
1074 AA; 120570 MW; EE3DB763CBE29407 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CT----HTDGSAVGSCLCRTRSCDSPAPQCGGWQCEGPGMEIAN-
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                                              871 PAPAYGGDICLGLHTEEALCN-TQPCPESWSEWSDWSECEASGVQVRARQCILLFPMGSQ 929
817 ADPDFACGWCOG----PGOCTLROHCPAQESOWLELSGAKSKCTNPRITEII---PVTGP 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Danio rerio).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopierygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

NCBI_TAXID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99060909; PubMed=9867349;
Halloran M.C., Severance S.M., Yee C.S., Gemza D.L., Kuwada J.Y.;
"Molecular cloning and expression of two novel zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG-LIKE C2-TYPE DOMAIN.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
M, 0ACBC693FE7D830C CRC64;
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SMART; SM0410; IG like; 1.
Signal; Transmembrane; Immunoglobulin domain; Multigene family; Glycoprotein.
1 24 POTENTAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mech. Dev. 76:165-168(1998).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
-!- SIMILARITY: CONTAINS 1 SENA DOWAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.7%; Score 268.5; DB 1; Length 766;
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Semahorin 27 precursor (Semaphorin 7) (Sema-27)
SEMAZ7 OR SEMA7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003600; Ig_like.
InterPro; IPR003659; Plexin-like.
InterPro; IPR001657; Sema.
InterPro; IPR001627; Sema.
Pfam; PP00447; ig; 1.
Pfam; PP01403; Sema, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85617 MW;
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227
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                                                                                                                                                                                                                                                                                                                                                    220 HIPEGGSN--PDGDDDKIYLFFSETAVEY------ESYTKVDV--SRVARVCKGD 264
                                                                                                                                                                                                                                                                                                                                                                                                    ----- 322
                                                                                                                                                                                                                                                                                                                                                                                                                     YSAVCSYKIEDIK-TVFSKGKFKAPFNVETSFVKWVMYSGELPDPRPGACI----DNHAR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRTLGVHPDDDLLFTVFSKGQKRKMKSLDES------ALCIFILKQINDR 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 IKERLQSCYRGEGTLDLAWLKVKDIPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 EKGITKSLELPDKTLOF----VKDKPLMDQAVTAEQ------PL----LVKRGAAFT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDRDRMTSVIAYVYKNHSLAFVGTKSGK-LKKIRVDGPRGNALQYETVQVVDPGPVLRDM 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
                                                                        ||| |: | | | : | | : | | : | | CAREAIFALDLDDITIKKAMLKWEVTRDQQN-----DCSNKGKDATNDCKNYIRI
                                                                                                                                                                                                                                                                                                                            KI PSDTFTI I PDFDI YYVYGFSSGNFVYFLTLQPEMVSPPGSTTKEQVYTSKLVRLCKED
                                                                                                                      LGAVNRIYKLSSD----LKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTTTNNVNKMLLI
                                                                                                                                                                                       DYKEN--RLIACGS-LYQGICKLLRLED----LFKLGE-----PYHKKEHYLSGVNESG
                                                                                                                                                                                                                                                          SVFGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVASMI
                                                                                                                                                                                                                                                                                            ------VDGAYYSATSMNFRGS--EPVMMRSTEESIRTEFTSTWLSEPNFI-HMA
                                                  10 CLL---SHLLMVGMGSSTL--LTRQPAPLSQKQRSFVTFRGEPAEGFNHLVVDERTGHIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 22.6%; Pred. No. 2e-09;
Matches 153; Conservative 106; Mismatches 267; Indels 151; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              546 KEPRRFAS ---EMKQCVRLTV-HPNNISVSQYN-VLLVLETY-NVPELSAGVN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kimura T., Ishida H.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9H3T3; Q9NRK9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Semaphorin 6B precursor (Semaphorin Z) (Sema Z)
SEMAGB OR SEMAZ.
                                                                                                                                                                                                                                                                                                                                                                                                 TA-----FNSYVEVPIGCERSGVEYRLL--
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SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=21248680; PubMed=11350127;
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598 SNTIQILS--DGLMIFN 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Suropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R EMBL, ABC216313; BAR20669.1; -.

R EMBL, ABC216313; BAR80661.1; -.

R Genew, HGNC:10739; SEMA6B.

R InterPro; 1PR0001627; Sema.

DR InterPro; 1PR0001637; Squash.

DR Frain; PF014013; Semi.

DR FRART; SM00423; PSI; 1.

DR SWART; SM00286; PII; 1.

DR SWART; SM00286; PII; 1.

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DR SWART; SM00286; PII; 1.

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SWART; SW00286; PIII; 1.

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N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
LSVFLEBERTYREDSCREPGESTOGREPGILSLELIALS.
MGFORARGPPR.CR. (SOTENTIAL).
AMFRC -> RVCOVGHACRVCVHERRSWWPORPGRMLSRR.
MGFORARGPPR.CRLCV (IN ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                  Genomics 73:343-340(2001).

-I- FUNCTION: MAY PLAY A ROLE IN BOTH PERIPHERAL AND CENTRAL NERVOUS SYSTEM DEVELOPMENT (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- ALTERNATIVE PRODUCTS: At least 2 isoforms; 1 (shown here) and 2/6B.1; are produced by alternative splicing.

-I- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 LTTINNVNKMLLIDYKENRLIACGS-LYQGICKLLRLEDLFKLGE-----PYHKKEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.6%; Score 263; DB 1; Length 888;
Best Local Similarity 22.7%; Pred. No. 5.8e-09;
Matches 144; Conservative 90; Mismatches 208; Indels 192; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LLSHLLMVGMGSSTLLTRQPAPLSQKQRSFVTF-----RGEPAEGFNHLVVD---
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     Katayama M.L.H.,
de Souza S.J.,
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D -> E (IN REF. 2).

6FFB44D6828C70CB CRC64;
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1., Brentani M.M., Sogayar M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
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                       Salim A.C.M., Brentani M
Simpson A.J.G.,
"Human semaphorin 6b.";
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CONFLICT
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| FT CHAIN 33 762 SEMAPHORIN 4A. FT DOMAIN 33 684 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 685 705 POTENTIAL. FT DOMAIN 706 762 CYTOPLASMIC (POTENTIAL). FT DOMAIN 240 518 SEMA. FT DOMAIN 240 518 SEMA. FT DOMAIN 574 632 IG-LIKE C2-TYPE DOMAIN. FT CARBOHYD 120 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 135 135 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 608 608 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 608 608 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 608 608 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 608 608 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 608 608 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 608 608 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 608 608 N-LINKED (GLCNAC) (POTENTIAL). | Query Match 2.6%; Score 260.5; DB 1; Length 762; Best Local Similarity 21.7%; Pred. No. 6.5e-09; Matches 158; Conservative 105; Mismatches 283; Indels 181; Gaps 33; | QY 5 PWNWTCLLSHLLMVGMGSSTLLTRQPAPLSQKQRSFVTFRGEPAEGFNHLVV 56 | QY 57 DERTGHIYLGANNRIYKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTT 110    | QY 111 TNNVNKM-LLIDYKENRLIACGSL-YQGICKLLRLEDLFKLG | 154 #KKEHYL-SGWNESGSVPGVIVSYSNLDDKLPIATAVDGKPEYFPTISSEKLTKNEEADG 182 #KHTAULVDGMLYSGTFUILIPDFDIYTYYGFSGAWYPFTLLQPEMYSPGSTT 213 MFAYAULDDEFVAA'- IPSTQV   | ID SM4B_HUMAN STANDARD; PRT; 673 AA. |
|---|--|--|---|---|--|--------------------------------------|
| Qy 210 ADGMFAYVPHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPPGS 269  Db 221HDSKWFKEPFYFVHAVEWGSHVYFFREIAMEF 252  QY 270 TTKEQVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVEYRLLQAAYLSK 317  Db 253 NYLEKVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAY  QY 318 AGAVLGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCYRG 377  Db 309 TGVVSLGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFRE 354  | QY 378 BGTLDLAWLKVKDIPCSSALLTIDDNPCGLDMRAPLGVSDWVRGIPVFT 426   | QY 427 EDDRMTSVIAXVYKNHSLAFVGTKSGKLKKIRVD 461<br>            | QY 462 GPRGNALQYETVQVVDPGPVLRDMAFSKDHBQLYIMSBRQLTRVPVESC 510      : | OY 511 GOYOSC-GECLGSGDPHCGWCVLHNTCTR 538          | SULT 13  SM4A HUMAN STANDARD; PRT; 762 AA. GM4AA HUMAN SM4A HUMAN STANDARD; PRT; 762 AA. GM4AA HUMAN SM4A HUMAN STANDARD; 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 16-JUN-2002 (Rel. 41, Last sequence update) 16-JUN-2002 (Rel. 41, Last sequence update) 17-JUN-2002 (Rel. 41, Last sequence update) 18-JUN-2002 (Rel. 41, Last sequence update) 10-JUN-2002 (Rel. 41, Last sequence update) 11-JUN-2002 (Rel. 41, Last sequence update) 11-JUN-2002 (Rel. 41, Last sequence update) 11-JUN-2002 (Rel. 41, Last sequence update) 11-JUN-2002 (Rel. 41, Last sequence update) 11-SIMILARITY: CONTAINS 1 IMMUNOCLOBILIN-LITTIS SWISS-PROT entry is copyright. It is proposed update | FT SIGNAL 1 32 POTENTIAL.            |

91

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290 FNSYVEVPIGCER--SGVEYRLLQAAYLSKAGAVLGRTLGVHPD---DDLLFTVFSKGQK 344
                                                                                                                                                                                                                                                                                                                                                                                                                      240 ARERKINSSLQLPDRVIN---FIKDHFLMDGQVRSRMLLLQPQARYQRVAVHRVPGLHHT
                                                                                                          92 DDDKIYFFFSETGQEFEFF------ENTIVSRIARICKGDEGGERVLQQR
                                                                                                                                                                                                        36 WISFLKAQLLCSRPDDGFPFNVLQDVF-----TLSPSPQDWRDTLFYGVFTSQWH
                                                                                                                                                                                                                                                                             345 RKMKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKV-KDIPCSSALLTIDDN
                                                                                                                                                                                                                                                                                                                           186 R--GTTEGSAVCVFTMKD----VORVFSGLYKEVNRETQOWYTVTHPVPTPRPGACITNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 HSLAFVGTKSGKLKKIRVDGPRGNALQYETVQVVDPGPVLRDMAFSKDHEQLYIMSERQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541 RCERSK--EPRRFASEMKQCVRLTVHPNNISVSQYNVLLVLET----YNVPELSAGVNCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 LCSASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNLATRLWLRNGAPVNASASC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEDLSEMDGLVVGNQ----IQCYS-----PAAKEVPRIITENGDHHVVQLQLKSKETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 -HVLPTGDLLLVGTQQLGEFQCWSLEEGFQQLVASYCPEVV-EDG----VADQTDEGGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | : | . . . . . | | SRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLF
34 VDGELYTGT-VSSFQGNDPAISRSQSLRPTKTESSLNWLQDPAFVASAY-IPESLGSLQG
                                                         239 DFD-IYYVYGFSSGNFVYFLTLQPEMVSPPGSTTKEQVYTSKLVRLCKEDTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            644 MIFASISFVFYNCSVHNSCLSCVESPY-----RCHWCKYRHVCI----
                                                                                                                                                                                                                                                                                                                                                                                             404 FCGLDMNAPLGVSDMVRGIPVFTED------RDRMTSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 503 TRVPVESCGQYQSCGECLGSGDPHCGWCVLHNTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99112778; PubMed=9915572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      736 GYECI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMZ2 BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
SMZ2_BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC110730; SEMA4B.
InterPro; IPR003659; Plexin-like.
InterPro; IPR001659; Plexin-repeat.
InterPro; IPR001657; Sema.
Pfam; PF01403; Sema; 1.
Pfam; PF01403; PS1; 1.
SMART; SM0423; PS1; 1.
Transmembrane; Immunoglobulin domain; Multigene family; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNALS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLUIAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
-!- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOSLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOSLOBULIN-LIKE C2-TYPE DOMAIN.
-!- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITION 550
                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto & Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TSPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS (BY
                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO-BLCH.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (POTENTIAL.)

N-LINKED (GLCNAC. . . ) (POTENTIAL.)

N-LINKED (GLCNAC. . . ) (POTENTIAL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
2.6%; Score 258; DB 1; Length 673;
Best Local Similarity 20.6%; Pred. No. 7.7e-09;
Matches 145; Conservative 104; Mismatches 258; Indels 198;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Carim L., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VAR_010758.
97BFC18E39365EAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Polymorphism.
                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL390080; CAB98204.1; -.
EMBL; AL390081; CAB98205.1; -.
EMBL; AL390082; CAB98206.1; -.
EMBL; AK026133; BAB15372.1; ALT_FRAME.
        Q9NPNO; Q9NPM8; Q9H691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 673 AA; 74480 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ONWARD DUE TO A FRAMESHIFT
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 199-673 FROM N.A.
                                                                                                                  Semaphorin 4B (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Developmental protein;
                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMĀIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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594 471

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735
                    572 LLYRHRNSMKVFLKQGECASVHPKTCP-----VVLPPET-RP--LNGLGPPSTPLDHR 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted (By similarity).
----HDPKTCSFQEGRVKL--PEDCPQLLRVDKILVPVEVIKPITLKAKNLPQPQSGQR
                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 41, Last annotation update)
15-UNV-2002 (Rel. 41, Last annotation update)
Semaphorin Z2 precursor (Semaphorin 2) (Sema-Z2).
SEMAZ2 OR SEMA2.
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TAXID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Analysis of a Zebrafish semaphorin reveals potential functions in
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halloran M.C., Severance S.M., Yee C.S., Gemza D.L., Raper J.A., Kuwada J.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dev. Dyn. 214:13-25(1999).
-!- FUNCTION: MAY PLAY A ROLE IN THE GUIDANCE OF SEVERAL AXON
                                                                      757
                                                                                            -----ENIQGSEORV-----PALRFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAYS
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179 LDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFŢIIP 238

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::| | :: | | :: | | :: | | :: | | :: | | :: :| | | :: :| | | :: :| | | :: :| | | :: :| | | :: :| | :: :| | :: :| | :: :| | :: :| | :: :| | :: :| | :: :| | :: :| | :: :| | :: :| | :: :| | :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :| :: :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 -----FGVIVSYSNLDDDKLFIATAVD--GKPEYF-----PTISSRKLTKNSEADGMFA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 PFDPNQPFASVLT----DQYLYAGTASDFLGKDSTFTRSLGPPPHQQYIRTDISED---Y 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 YVFHDEFVASMIKIP-SDTFTIIPDFD-IYYVYGFSSGNFVYFLTLQPEMVSPPGSTTKE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 VNRIYKLSSDLKVLVTHETGPDEDNPKCYPPRI------VQTC----NEPLTTNNVN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 KMLLIDYKENRLIACGS-LYQGICKLIRLEDLFKLGEPYHKKEHYL---SGVNESGSV-- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 QVYTSKLVRLCKEDTA-----FNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 LGVHPDDDLLFTVF---SKGQKRKM------KSLDESALCIFILKQINDRIKERLQS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 -GVDTHFDELQDIFLLPSRDEKNPMVYGVFTTTSSIFKGSAVCVYTM-----EDIRA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 CYRG----EGTLDLAWLKVKD-IP-----CSSALLTIDDNFCGLDMNAPLGVSDMVR- 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GIPVFT--EDRDRMTSVI----AYVYKONHSLAFVGTKSG---KLKKIR 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 VDGPRGNALQYETVQVV-DPGPVLRDMAFSKDHEQLYIMSERQLTRVPVESCGQY-QSCG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 CLLSHILLMVGMGSSTLLTRQPAPLSQKQRSFVTFRGEPAEG--FNHLVVDERTGHLYLGA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.5%; Score 248.5; DB 1; Length 764;
Best Local Similarity 22.6%; Pred. No. 3.9e-08;
Matches 143; Conservative 91; Mismatches 205; Indels 193; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEMA.

IG-LIKE C2-TYPE DOMAIN.

ARG/LYS-RICH (BASIC).

BY SIMILARITY.

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001627; Sema.
Pfam; PF01403; Sema; 1.
SMART; SM00422; PSI; 1.
Signal; Immunoglobulin domain; Multigene family; Neurogenesis; Developmental protein; Glycoprotein.
                          -!- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
-!- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 SV-LSRVARICRNDVGGLRSLTNKWTTFLKARLVCSIPGPD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87859 MW; A3ED95C2C479D7AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEMAPHORIN Z2.
DURING THE PERIOD OF AXON OUTGROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF124485; AAD21310.1; -.
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| Q9uiv7 homo sapien<br>Q9qy40 mus musculu<br>Q9nny1 homo sapien<br>Q9hla4 homo sapien<br>Q9ull4 homo sapien | Oloval nome sapien<br>Q9y4d7 home sapien<br>Q9brll home sapien<br>Q45657 caenorhabdi<br>Q8rll4 mus musculu | mus<br>bos t<br>homo<br>homo<br>homo           | Q991f0 mus musculu<br>Q9bsu7 homo sapien<br>Q8t687 drosophila<br>Q8stg6 drosophila<br>Q9nem6 homo sanien | homo<br>homo<br>homo<br>gal<br>fug<br>fug<br>gal                   |
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Sekin, Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D., Nomira N., Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D., Nomira N., Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D., "Characterization of cDNA clones in size-fractionated cDNA libraries from human brain.";

DNA Res. 4:345-349(1997).

EMBL, AB007932; BAA32308.1;

EMBL, AB007932; BAA32308.1;

EMPL, AB007932; BAA32308.1;

InterPro; IPR002165; Plexin.like.

InterPro; IPR001657; Sema.

Fram; PF01437; PSI; 3.

Fram; PF01403; Sema; 1.

Pfam; PF01403; Sema; 1.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
KIAAA0463 protein (Fragment).
PRT; 1963 AA
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| RC TISSOUS-BRAIN;<br>RX MEDLINE-96400270; PubMed-8806646;  | 1065 LDLIQNPQIRAKHGGKEHINICEVLNATEMTCQAPALALGPDHQSDLTERPBEFGFILDN 1124     |
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| NCBL_TAXID=10090; [1] SEQUENCE FROM N.A.   | 1006 C-NTTSSDEVLEMKVSVQVDRAKIHQDLVFQYVEDPTIVRIEPEWSIVSGNTPIAVWGTH 1064     |
|  | 946 SQLYYEMILILSDLKPSRGPMSGGTQVTITGTNLNAGSNVVWRGKQPCLFHRRSPSYIV 1005<br>   |
| DT 01-FEB-1997 (TrEMBLrel. 02, Created) DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence upda: DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation up DE Pleaxin 2. | 886 EFRDIASHVKVAGVECSPLVDGYIPAEQIVCEMGEAKPSQHAGFVEICVAVCRPEFMARS 945       |
| SULT 2<br>)207<br>P70207 PRELIMINARY; PRT<br>P70207;   | 826 CQGPGQCTLRQHCPAQESQWLELSGAKSKCTNPRITEIIPVTGPREGGTKVTIRGENLGL 885       |
| 1 н  | 766 SYSYEGWEINNI-PVELTVVWNGHFNIDNPAQNKVHLYKCGAMRESCGLCLKADPDFACGW 825      |
|  | 706 RUDKILVPVEVIKPITLKAKNLPQPGSGQRGYECILNIGGSEQRVPALRFNSSSVQCQNT 765 ::  : |
| 1794 D<br>1785 S   | 646 FASTSFVFYNCSVHNSCLSCVESPYRCHWCKYRHVCTHDPKTCSFQEGRVKLPEDCPQLL 705       |
| 1734   | 586 ELSAGVNCTFEDLSEMDGLVVGNQIQCXSPAAKEVPRIITENGDHHVVQLQLKSKETGMT 645       |
| DD 1674 YNIPASASISRTSISRYDSSFRYTGSPDSLRSRAPMI.   | 526 HCGWCVLHNTCTRKERCERSKEPRRFASEMKQCVRLTVHPNNISVSQXNVLLVLETYNVP 585       |
| 1614 RPRAVDMDLEWROGRIARVVLQ  | 467 ALQYETVQVV-DPGPVLRDMAPSKDHEQLYIMSERQLTRVPVESCGQYQSCGECLG\$GDP 525      |
|  | 407 LDWNAPLGVSDMVRGIPVFTEDRDRMTSVIAYVYKNHSLAFVGTKSGKLKKIRVDGPRGN 466       |
| 1494   | 347 MKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIPCSSALLTIDDNFCG 406       |
| 1434   | 287 DTAFNSYVEVPJGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRK 346       |
| 1374   | 230 PSDTFTIIPDPDIYYVYGFSSGNFVYFLTLQPEMVSPPGSTTKEQVYTSKLVRLCKE 286 [        |
| 1245   | 170 FGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVASMIKI 229 11    |
| 1185   | 110 TTNNVNKMLLIDYKENRLIACGSLYQGICKLLRLEDLFKLGEPYHKKEHYLSGVNESGSV 169       |
| n n  | 50 GFNHLVVDERTGHIYLGAVNRIYKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLT 109        |
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FSPGSVSVISDSLLTLPAIVSIAA 1313
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                                                               YSPGMVYIAPDSPLSLPAIVSIAV 1244
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Kameyama T., Murakami Y., Suto F., Kawakami A., Takagi S., Hirata
tlanta H.;
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X Shimizu M., Muredalary, Suto F., Fujisawa H.;

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E MED, 10684; PAA13189.1; -.

MGD, MGI:107684; PAA13189.1; -.

MGD, MGI:107684; PAA13189.1; -.

R InterPro; IPR002509; IPT IIG.

R InterPro; IPR001565; Plexin-like.

R InterPro; IPR001565; Plexin-like.

R InterPro; IPR00157; Sema.

R Pfam; PF01437; PSI; 3.

R Pfam; PF01437; PSI; 3.

R SMART; SM00429; IPI; 4.

SMART; SM00429; IPI; 4.

R SMART; SM00429; PSI; 3.
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                                                                                                                                   TISSUE=BRAIN;
MEDLINE=20191894; PubMed=10725340;
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SEQUENCE FROM N.A.
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480 476 540 536 600

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720 716 780 776 836

896

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VLIAYKRKSRESDLTLKRLOMOMDNLESRVALECKEAFAELQTDIHELTSDLDGAGIPFL 1315
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364 NDRIKERLOSCYRGEGTLDLAWLKVKDIPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIP
                                                    424 VFTEDRDRMTSVIAYVYKNHSLAFVGTKSGKLKKIRVDGPRGNA---LQYETVQVVDPGP
                                                                                                       VLRDMAFSKDHEQLYIMSERQLTRVPVESCGQYQSCGECLGSGDPHCGWCVLHNTCTRKE
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                                                                                                                                                                                                                                                                                                                                    MEDLINE=95329274; PubMed=7605632; Ohta K., Mizutani A., Kawakami A., Murakami Y., Kasuya Y., Takagi S., Tanaka H., Pijisawa H., Pijisawa H., Pijisawa H., Pijisawa H., Pijisawa H., Pipisawa H., Pipisawa H., Pipisawa H., Pipisawa H., Pipisawa H., Pipisawa Malaka Cell adhesion via a homophilic binding mechanism in the presence of calcium
                          GKMPAISDQDMNAYLAEQSRMHMNERITMSALSEIFSYVGKYSEEILGPLDHDDQCGKQK
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                                      ATAVDGKPEYPPTISSRKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFTIIPDFDIYYV
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Best Local Similarity 63.7%; Pred. No. 0;
Matches 1222; Conservative 245; Mismatches 396; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214401 MW; 243C059690B33D64 CRC64;
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InterPro, IPR002909; IPT TIG.
InterPro, IPR002659; Plexin-like.
InterPro, IPR0021659; Plexin repeat.
InterPro; IPR001627; Sema.
Pfam; PF01437; PSI; 3.
Pfam; PF01437; Sema; 1.
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1869 LAYKVEHLINAMSIES 1884
                                                                             LAYKLEQVITLMSLDS 1894
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1905
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SMART; SM00429; IPT; 4
SMART; SM00423; PSI; 3
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1905 AA;
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                                                                                                                                                      NHEHGDQKEGDRGSKMVSEIYLTRLLATKGTLQKFVDDLFETIFSTAHRGSALPLAIKYM 1716
                                                                                                                                                                                                                                      RSFSMRDRGNVASLIMTALQGEMEYATGVLKQLLSDLIEKNLESKNHPKLLLRRTESVAE 1428
                                                                                                                                                                                               FDFLDEQADKHGIHDPHVRHTWKSNCLPLRFWVNMIKNPQFVFDIHKNSITDACLSVVAQ 1776
                                                                                                                                                                                                                                                                     TFMDSCSTSEHRLGKDSPSNKLLYAKDIPSYKNWVERYYSDIGKMPAISDQDMNAYLAEQ 1836
                                                                                                                                                                                                                                                                                                            SRMHMNEFNTMSALSEIFSYVGKYSEELLGPLDHDDQCGKQKLAYKLEQVITLMSLDS 1894
||:|:::||:||| ||:||: ||:||:|| ||:||
SRLHLSQFNSMSALHEIYSYITKYRDEILTALEKDEQARRQRLRSKLEQVIDTWAQSS 1905
                  ------VLSCVSPDNANSPEVPVKILNCDTITQVKEKILDAI
                                                                                                   FKNVPCSHRPKAADMDLEWRQGSGARMILQDEDITTKIENDWKRLNTLAHYQVPDGSVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96400291, PubMed-8806667;
Kameyama T., Murakami Y., Suto F., Kawakami A., Takagi S., Hirata
Fujisawa H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of a neuronal cell surface molecule, plexin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimizu M., Mirakami Y., Suto F., Fujisawa H.;

"Determination of Cell Adhesion Sites of Neuropilin-1.";

"J. Cell Biol. 148:1283-1294 (2000).

"MGD; MGI:107685; Plxnl.

"MGD; MGI:107685; Plxnl.

"InterPro; IPR002909; IPT TIG.

"InterPro; IPR002165; Plexin-like.

"InterPro; IPR001657; Sema.

"Fam, PP01437; PSI, 3.

"Pfam; PP01403; Sema.

"Pfam; PP01403; TIG; 4.
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Biochem. Biophys. Res. Commun. 226:524-529(1996)
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MEDLINE=20191894; PubMed=10725340;
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                                                                                                                                                          1 MKAMPWNWTCLLSHILMVGMGSSTLLTRQPAPLSQKQRSFVTFRGEPAEGFNHLVVDERT
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                                                                            Length 1894;
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211098 MW; A8E6BB29C6B24C94 CRC64;
                                                                              Query Match 63.4%; Score 6337; DB 11;
Best Local Similarity 63.5%; Pred. No. 0;
Matches 1209; Conservative 267; Mismatches 408;
SMART; SM00429; IPT;
SMART; SM00423; PSI;
SEQUENCE 1894 AA;
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                                                                                                                                               1316 GIPFLDYRTYAMRVLFPGIEDHPVLKEMEV----QANVEKSLTLFGQLLTKKHFLLTFIR 1371
                                                                                                                                                                                                                                                                                             1432 ESVAEKMITNWFTFLLYKFLKECAGEPLFMLYCAIKQOMEKGPIDAITGEARYSLSEDKL 1491
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                                                                                                                                      1191 TVTVSDVQLLCESPNLIGRHKVMARVGGMEYSPGMVYIAPDSPLSLPAIVSIAVAGGLLI 1250
DPHVRHTWKSNCLPLRFWVNMIKNPQFVFDIHKNSITDACLSVVAQTFMDSCSTSEHRLG
                                       1311 GIPFLDYRTYTWRVLFPGIEDHPVLRDLEVPGYRQERVEKGLKLFAQLINNKVFLLSFIR
                                                                                                                                                                                                                                                TLESORSFSWRDRGNVASLIMTVLQSKLEYATDVLKQLLADLIDKNLESKNHPKLLLRRT
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                             DEVLEMKVSVQVDRAKI-HQDLVFQYVEDPTIVRIEPEWSIVSGNTPIAVWGTHLDLIQN
                                                                           LNKTNFTYYPNPVFEAFGPSGILELKPGTPIILKGKNLIPPVAGGNVKLNYTVLVGEKPC
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                                                               POIRAKHGGKEHINICEVLNATEMTCQAPALALGPDHQSDLTERPEFFGFILDNVQSLLI
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P70208; 01-FEB-1997 (TrEMBLrel. 0: 01-FEB-1997 (TrEMBLrel. 0: 01-JUN-2002 (TrEMBLrel. 2: Plexin 3.

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PRELIMINARY,

P70208

RESULT 5

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FSKDHEQLYIMSERQLTRVPVESCGGYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSK 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDRDRMTSVIAXVYKNHSLAFVGTKSGKLKKIRVDGPRGNALQYETVQVVDPGPVLRDMA 486
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                                                                                                                                      Kameyama T., Murakami Y., Suto F., Kawakami A., Takagi S., Hirata T.,
Fujisawa H.;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1872;
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MEDLINE=CO191894; PubMed=10725340;

MEDLINE=CO191894; PubMed=10725340;

MEDLINE=CO191894; PubMed=10725340;

MINITAL M., Murakami Y., Suto F., Fujisawa H.;

L. Cell Biol. 148:1283-1294(2000).

E. MEDL. D86950; BAA13190.1; -.

R. MEDL. D86950; BAA13190.1; -.

R. MIDENPO; IPR002509; IPT_TIG.

R. InterPro; IPR002509; IPT_TIG.

R. InterPro; IPR00155; Plexin-like.

R. InterPro; IPR00155; Plexin-like.

R. InterPro; IPR00155; Plexin-repeat.

R. Ffam; PF01437; PSI; 3.

R. Ffam; PF01437; PSI; 3.

R. SMART; SM00429; IPI; 4.

R. SMART; SM00429; PSI; 3.

SEQUENCE 1872 AA; 207941 MW; 39D5789DCCC4830A CRC64;
                                                                                                                                                                                    "Identification of plexin family molecules in Mice.";
Biochem. Biophys. Res. Commun. 226:396-402(1996).
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Best Local Similarity 59.7%; Pred. No. 0;
Matches 1130; Conservative 290; Mismatches
                                                                                                                           MEDLINE=96400270; PubMed=8806646;
                                                                                      SEQUENCE FROM N.A.
TISSUE=BRAIN;
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                                             NCBI_TaxID=10090
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1601 SLLRAASSPDSLRSRAPMLTPDQEAGTKLWHLVRNHDHTDHREGDRGSKMVSEIYLTRLL 1660
                                                                                  1661 ATKGTLOKEVDDLFETVFSTAHRGSALPLAIKYMFDFLDEQADORQISDPDVRHTWKSNC 1720
                                                                                                                                                   LPLRFWVNMIKNPQFVFDIHKNSITDACLSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAK
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TISSUE-SKELETAL MUSCLE;
MEDLINE-96149362; Pubmed=8570614;
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                                                                                      PSGELRCPSPSLQELQTLTRGHGATHTVRLQLLSMETGVRFAGVDFVFYNCSALQSCMSC 648
                                                                                                                                             VESPYRCHWCKYRHVCTHDPKTCSFQEGRVKLPEDCPQLLRVDKILVPVEVIKPITLKAK 725
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TISSUB—SKELETAL MUSCLE;

MEDLINE=99449305; PubMed=10520995;

MEDLINE=99449305; PubMed=10520995;

Tamagnone L., Artigiani S., Chen H., He Z., Ming G.L., Song H.L.,

Chedotal A., Winberg M.L., Goodman C.S., Poo M.M., Tessier-Lavigne M.,

Comoglio P.M.;

Tamagnone are a large family of receptors for transmembrane, secreted

and GPI-anchored semaphorins in vertebrates.";

Cell 99:71-80(1999).

MEMBL, X879812; CABST724.1; -.

REMIL: X870812; PR00125; Plexin-like.

InterPro; IPR00165; Plexin-like.

InterPro; IPR001627; Sema.

Pfam; PF01437; PSI; 3.

Remi: PF01403; Sema; 1.

REMIL: SM00423; TG; 4.

REMART; SM00423; PSI; 3.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
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INSSUB-SKELETAL MUSCLE;

MEDLINE=56149362; PubMed=8570614;

MEDLINE=561493362; PubMed=8570614;

Maestrini E., Tamagnone L., Longati P., Cremona O., Gulisano M.,

Bione S., Tamanini F., Neel B.G., Toniolo D., Comoglio P.M.;

Bione S., Tamanini F., Neel B.G., Toniolo D., Comoglio P.M.;

A family of transmembrane proteins with homolgy to the MET-hepatocyte growth factor receptor.";
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                                                                                                                                                    1347 RVEKGLKLFAQLINNKYFLLSFIRTLESQRSFSMRDRGNVASLIMTVLQSKLEYATDVLK
                                                                                                                                                                                                                                                                                 QLLADLI DKWLESKWHPKLLLRRTESVAEKMLTWWFTFLLYKFLKECAGEPLFSLFCAIK
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                                                        YIAPDSPLSLPAIVSIAVAGGLLIIFIVAVLIAYKRKSRESDLTLKRLQMQMDNLESRVA
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TISSUE=SKELETAL MUSCLE;
MEDLINE=99449305; PubMed=10520995;
Tamagnone L., Artigiani S., Chen H., He Z., Ming G.L., Song H.L.,
Chedotal A., Winberg M.L., Goodman C.S., Poo M.M., Tessier-Lavigne !
Comoglio P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
0CT/plexin-A2 protein (Fragment)
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MEDINIBE-20196066; PubMed=10731132;

MEDINIBE-20196066; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

A sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Nan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier P.,

Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tacheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sec
01-JUN-2002 (TrEMBLrel. 21, Last and
PLEXA OR CG11081.

Drosophila melanogaster (Fruit fly)
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1319 SITDACLSVV 1328
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       receptors for transmembrane, secreted
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Matches 935; Conservative 152; Mismatches 239;
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"Plexins are a large family of receptors for t and GPI-anchored semaphorins in vertebrates."; Cell 99:71-80(1999).
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                                                               EMBL, X87831; CAB57275.1; -.
InterPro; IPR003569; IPT_TIG.
InterPro; IPR003569; Plexin-like.
InterPro; IPR00165; Plexin-repeat.
InterPro; IPR001627; Sema.
Pfam; PF01477; PST; 3.
Pfam; PF014037; SST; 3.
Pfam; PF014031; TIG; 4.
SMART; SM00429; IPT; 4.
                                                                                                                                                                                                                                                                                                                                     1328
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Best Local 8
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1225 MVYIAPDSPLSLPAIVSIAVAGGLLIIFIVAVLIAYKRKSRESDLTLKRLQMQMDNLESR 1284
                                                                                                                                                                                                                                                                     959 LKQLLSDLIDKNLENKNHPKLLLRRTESVAEKMLTNWPAFLLHKFLKECAGEPLFMLYCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1079 ITQVKEKILDAVYKOVPYSQRPRAVDMDLEWRQGRIARVVLQDEDITTKIEGDWKRLNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1139 MHYQVSDRSVVALVPKQTSSYNIPASASISRTSISRYDSSFRYTGSPDSLRSRAPMITPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1199 LESGVKVWHLVRONDHGDQKEGDRGSKAVSEIYLTRLLATKGTLQKFVDDLFETLFSTVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1705 RGSALPLAIKYMFDFLDEQADKHGIHDPHVRHTWKSNCLPLRFWVNMIKNPQFVFDIHKN
                                                                                                                                                1345 QERVEKGLKLFAQLINNKVFLLSFIRTLESQRSFSMRDRGNVASLIMTVLQSKLEYATDV
                                                                                                                                                                                                                                                                                                                                                     1405 LKQLLADLIDKNLESKNHPKLLLRRTESVAEKMLTNWFTFLLYKFLKECAGEPLFSLFCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1465 IKQQMEKGPIDAITGEARYSLSEDKLIRQQIDYKTLVLSCVSPDNANSPEVPVKILNCDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     779 SVSVISDSLLTLPAIVSIAAGGSLLLIIVIIVLIAYKRKSRENDLTLKRLQMQMDNLESR
                                                                                                                 1285 VALECKEAPABLQTDIHELTSDLDGAGIPFLDYRTYTWRVLFPGIEDHPVLRDLEVPGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITOVKEKILDAIFKNVPCSHRPKAADMDLEWRQGSGARMILQDEDITTKIENDWKRLNTL
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Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Ra Fosler C., Gabriellan A.B., Garg N.S., Gelbart W.M., Glasser K., Gloder C., Gabriellan A.B., Guz N.S., Gelbart W.M., Glasser K., Gloder C., Gabriellan J.J., Harrandez J.R., Houck J., Ra Taris N., Harrey, D., Heinand T.J., Hernandez J.R., Houck J., Ra J. alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D. Lai Z., Ling Y., Lin X., Rasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattel B.E., McIntosh T.C., McLeod M.P., Moshrefi A., Mattlov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Nount S.M., My M., Murphy B., Murphy D., Nusskern D.R., Pallson D.L., Ra Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shen E., Spranington K., Saunders R.D.C., Scheeler F., Shen H., Shen E., Spranington K., Saunders R.D.C., Scheeler F., Shen H., Shen E., Spranington K., Saunders R., Weissenbach J., Massarman D.A., Weissenbach J., Ra Syirskas R., Tector C., Turner R., Venter E., Wang X., Yao Q.A., RA Shen S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Shen S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Zheng X.H., Zhong F.N., Roliber K.S., Zhong W., Zhon W., Zhang G., Zhao Q., Zheng L., Ra Jennes Sequence of Drosophila melanogaster.";

K. Zhong K.A., Myers E.W., Rubin G.M., Venter J.C.;

K. Schence 287:2185-2195(2000)

K. Rhell, AEO03846; AAF59394.1;

K. Schence 287:2185-2196(2000)

K. InterPro; IPRO03659; IPT TIG.

K. Rherpo; IPRO03659; IPT TIG.

K. Rherpo; IPRO03659; IPT TIG.

K. Rherpo; IPRO03659; IPT TIG.

K. Rherpo; IPRO03659; IPT TIG.

K. Rherpo; IPRO03659; IPT TIG.

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K. Rherpo; IPRO03659; IPT TIG.

K. Rherpo; IPRO03659; IPT TIG.

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K. Rherpo; IPRO03659; IPT TIG.

K. Rherpo; IPRO03659; IPT TIG.

K. Rherpo; IPRO03659; IPT TIG.

K. Rherpo; IPRO03659; IPT TIG.

K. Rherpo; IPRO03659; IPT TIG.

K. Rherpo; IPRO03659; IPT TIG.

K. Rherpo; IPRO03659; IP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 VKTGPQNDSVEC----SILDCPLANAVRSPTDNYNKVLLIDRATSRLIACGSLFQGTCTVR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 NLQNVSII-----EHEVPD-----AVVANDANSSTVAFIA---PGPPQHPVTNVM 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLEDLFKLGEPYHKKEHYLSGVNESGSVFGVIVSYSNLDDKLFIATAVDGKPEY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 LIRQPAPLSQKQRSFVIFRGEPA - - EGFNHLVVDERTGHIYLGAVNRIYKLSSDLKVLVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1945 AA; 218356 MW; 4C032CA07C83A745 CRC64;
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SEQUENCE 1945 AA; 218356 MW; 4C
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SMART; SM00423; PSI;
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1354 IPFLDYRSYAMKILFPNHEDHIVLQ----WERPELLRKEKGLRIFGQLIMNKTFLLLFI 1408 1429 TESVAEKMLINWFTFLLYKFLKECAGEPLFSLFCAIKQOMEKGPIDAITGEARYSLSEDK 1489 1469 TESVAEKALSAWFTFILYKFLKECAGEPLYMLFRAVKGQVDKGPVDACTHEARYSLSEEK 1528 978 NINAGSNVVVMFGKQ-PCLFHRRSPSYIVCNTTSSDEVLEMKVSVQVDRA-KIHQDLVFQ 1035 1036 YVEDPTIV -----RIEPEWSIVSGNTPIAVWGTHLDLIQNPQIRAKHGGKEHINICE 1087 1143 VFEAFGPSGILELKPGTPIILKGKNLIPPVAGGNVKLNYTVLVGEKPCTVT-VSDVQLLC 1201 ESPN-----LIGRHKVMARVG-GMEYSPGMV-YIAPDSPLSLPAIVSIAVAGGLLIIFI 1253 948 PGEQMYRNGKIVVQI-----GDYRGESKEDYEFVDPKILDFNPKFGPTSGGTEIHITGK 1001 977 746 SEQRVPAL--RENSSSVQCQNTSYSYEGMEINNLPVELTVVWNGHFNIDNPAQNKVHLYK 803 ---RVTSLNAQLLGDTIYCDSMEFQYTSRS-PNLTATFAVIWGGSKPLDNPHNIHVVIYR 830 604 774 1088 VLNATEMTCQAPALALGPDHQSDLTERP--EEFGFILDN---VQSLLILNKTNFTYYPNP RTLESQRSFSMRDRGNVASLIMTVLQSKLEYATDVLKQLLADLIDKNLESKNHPKLLLRR HTFQPKTGPWEGGTNITIRGINLGKNYNDIYSGVRIAGINCMPFPQFYIDTKQIVCTVDS 919 -GEAKPSQHAGFVEICVAVCRPEFMARSSQLYYFMTLTLSDLKPSRGPMSGGTQVTITGT --VAVLIAYKRKSRESDLTLKRLQMQMDNLESRVALECKEAFAELQTDIHELTSDLDGAG 1312 IPFLDYRTYTMRVLFPGIEDHPVLRDLEVPGYRQE--RVEKGLKLFAQLINNKVFLLSFI TEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGYIPAEQIVCEM--429 GGETPITSVPV-AMFNTKLTSVAATSTSGYTVVFVGTSDGFLKKVVIES-SSIANEYASF 487 AVDLGSEINRDMQFDNQNLY1YVMSKTKVSKVKVFDCSDYKTCGDCLGARDPYCGWCSLB NTCTRKERC-ERSKEPRRFAS-EMKQCVRLT-VHPNNISVSQYNVL-LVLETYNVPELSA 660 PDLVSTDFTFFDCSTHSSCTRCVSSEFPCDMCVEAHRCTHDTAENCRNDILVTGVSRIGP CGAMRESCGLCLKADPDFACGWCQGPGQCTLRQHCPAQ---ESQWLELSGAKSKCTNPRI 590 GVNCTFEDLSEMDGLVVG----NQIQCYSPAAKEVPRIITENGDHH-VVQLQLKSKETG SPOEGRVKLPEDCPOLLRV---DKILVPVEVIKPITLKAKNLPOPOSGORGYECILNIOG 474 QVVDPGPVLRDMAFSKDHEQLYIMSERQLTRVPVESCGOYQSCGECLGSGDPHCGWCVLH 644 MIFASISFVFYNCSVHNSCLSCVESPYRCHWCKYRHVCTHD-PKTC-1409 1430 1370 689 775 804 861 g 유 8 ò 셤 ð 셤 ò ò 셤 엄 d à g ò g ò 셤 Ś 셤 a 셤 ઠ g ò 셤 ò g δ 8 ò 유 à ò ò

195

237 255 297 311 354 369 413 428 533

589

604

643

688 719 745 774 803 830 860 887 918 977

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948 PGEQMYRNGKIVVQI-----GDYRGESKEDYEFVDPKILDFNPKFGPTSGGTEIHITGK 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVSDMVRGIPVFTEDRDRMTSVIAYVXKNHSLAFVGTKSGKLKKIRVDGPRGNALQYETV 473
48 LTNANAPIKNAKNLNSTITNVAAFDTKLNHLLVDTITGRVFVGGVNRLYQLSPDLELSET 107
                                                                                                                  605 NLICAF--TTEDKALFTNATKKRNGVNCTTPRTDMLPQI--EQGKHHFTAKLSVRTR-NG
                                                                                                                                                                                  206 YVGVTYTNNSPYRSEIPAVASRSLEKTK----MF-----QIASSAVTTGTRTFINSYAR
                                                                                                                                                                                                                            238 PDPDIYYVYGFSSGNFVYFLTLQPEMVSPPGSTTKEQVYTSKLVRLCKEDTAFNSYVEVP
                                                                                                                                                                                                                                                 298 IGC---ERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESA
                                                                                                                                                                                                                                                                                                                                                                                QVVDPGPVLRDMAFSKDHEQLYIMSERQLTRVPVESCGQYQSCGECLGSGDPHCGWCVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534 NTCTRKERC-ERSKEPRRFAS-EMKQCVRLT-VHPNNISVSQYNVL-LVLETYNVPELSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              590 3VNCTFEDLSEMDGLVVG-----NQIQCYSPAAKEVPRIITENGDHH-VVQLQLKSKETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               644 MTFASTSFVFYNCSVHNSCLSCVESPYRCHWCKYRHVCTHD-PKTC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              660 PDLVSTDFTFFDCSTHSSCTRCVSSEFPCDWCVEAHRCTHDTAENCRNDILVTGVSRIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   746 SEQRVPAL--RFNSSSVQCQNTSYSYEGMEINNLPVELTVVWNGHFNIDNPAQNKVHLYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              775 ---RVTSLNAQLLGDTIYCDSMEPQYTSRS-PNLTATFAVIWGGSKPLDNPHNIHVVIYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              861 TEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGYIPAEQIVCEM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 888 HTFQPKTGPWEGGTNITIRGINLGKNYNDIYSGVRIAGINCMPFPQFYIDTKQIVCTVDS
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                                               108 VKTGPONDSVBC----SILDCPLNAVRSPTDNYNKVLLIDRATSRIACGSLFOGTCTVR
                                                                                                                                                                                                                                                                                                                LCIFILKOINDRIKERLOSCYRGEGTLDLAWLKVKDIPC-SSALLTIDDNFCGLDMNAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487 AVDLGSEINRDMQFDNQNLYIYVMSKTKVSKVKVFDCSDYKTCGDCLGARDPYCGWCSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                689 SPQEGRVKLPEDCPQLLRV---DKILVPVEVIKPITLKARNLPQPQSGQRGYECILNIQG
                              84 HETGPDEDNPKCYPPRIVQTC - NEPLTTINNVNKMLLIDYKENRLIACGSLYQGICKLL
                                                                                            RLEDLFKLGEPYHKKEHYLSGVNESGSVFGVIVSYSNLDDKLFIATAVDGKPEY----
                                                                                                                                                             -------PPTISSRKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFT---II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             804 CGAMRESCGLCLKADPDFACGWCQGPGQCTLRQHCPAQ---ESQWLELSGAKSKCTNPRI
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                                |:|:
KEHDSDMQKEGERVNKLVSEIYLTRLLATKGTLQKFVDDLFETIFSTAHRGSALPLAIKY
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                                                                                                                                                                                                                                                                                                                                                               -----VLSCVSPD--NANSPEVPVKILNCDTITQVKEKILDAIFK
                                                                             NVPCSHRPKAADMDLEWRQGSGARMILQDEDITTKIENDWKRLNTLAHYQVPDGSVVALV
                                                                                                                                          SKQVTAYNAVNNSTVSRTSASKYB - - NMIRYT - GSPDSLRSRTPMITPDLESGVKMWHLV
                                                                                                                                                                                                             KNHEHGDQKEGDRGSKMVSEIYLTRLLATKGTLQKFVDDLFETIFSTAHRGSALPLAIKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Archropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 36.3%; Score 3631; DB 5; Length 1945; al Similarity 41.9%; Pred. No. 5.4e-252; 828; Conservative 320; Mismatches 638; Indels 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99091049; PubMed=9875845; Winberg M.L., Noordermeer J.N., Tanagnone L., Comoglio P.M., Spriggs M.K., Tessier-Lavigne M., Goodman C.S.; "Plexin A is a neuronal semaphorin receptor that controls ax
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SEQUENCE 1945 AA; 218278 MW; 09D3565598BDEFI CRC64;
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Last sequence update)
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Cell 95:903-916(1998).
EMBL, 9100332; AAD09425.1;
FlyBase; FBGN0025741; plexA.
InterPro; IPR002509; IPT TIG.
InterPro; IPR002165; PlexIn-like.
InterPro; IPR001657; Sema:
InterPro; IPR001627; Sema:
InterPro; IPR001627; Sema:
InterPro; IPR001627; Sema:
InterPro; IPR001627; Sema:
InterPro; IPR001627; Sema:
InterPro; IPR001627; Sema:
InterPro; IPR00429; Sema:
Pfam; PF01403; Sema:
IPFam; PF01403; Sema:
SMART; SM00429; IPT; 3.
SMART; SM00429; IPT; 3.
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01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2002 (TrEMBLrel. 21,
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PLEXA OR CG11081
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813 AA; 91889 MW; A310511C81E2A237 CRC64;

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1469 TESVAEKMLSAWFTFLLIYKFLKECAGEPLYMLFRAVKGQVDKGPVDACTHEARYSLSEEK 1528
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KHHDSDMQKEGERVNKLVSEIYLTRLLATKGTLQKFVDDLFETIFSTAHRGSALPLAIKY 1767
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                                                           ESPN-----LIGRHKVMARVG-GMEYSPGMV-YIAPDSPLSLPAIVSIAVAGGLLIIFI
                                                                                             1409 RILESNRYFSMRERUNVASLIMVTLQSKLEYCTDILKTLLGDLIEKCIEGKSHPKLLLRR
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                        1254 --VAVLIAYKRKSRESDLTLKRLQMQMDNLESRVALECKEAFAELQTDIHELTSDLDGAG
               VLNATEMTCQAPALALGPDHQSDLTERP - - EFFGFILDN - - - VQSLLILNKTNFTYYPNP
                                                 1143 VFEAFGPSGILELKPGTPIILKGKNLIPPVAGGNVKLNYTVLVGEKPCTVT-VSDVQLLC
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                                          1085 ICEVLNATEMTCQAPALALGPDHQSDLTERPEEFGFILDNVQSLLILNKTNFTYYPNPVF
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                       Indels
33.9%; Score 3386.5; DB 4; 79.1%; Pred. No. 5.2e-235; tive 76; Mismatches 92;
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Q96GN9;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (Protein for IMAGE:4130636) (Fragment).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RESULT 10
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[1] SEQUENCE FROM N.A TISSUE=BRAIN;

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584 QQCIEFESIIPEKIPISELSHLHLIIRT -- LPEPFNAKYRCVFGNSTPIDAEILENGLGC
                                                                                                                                                                                                                                                                                   DNPAQNKVHLYKC---GAMRE--SCGLCLKADPDFACGWCQGPGQCTLRQHCPAQESQWL
                                                                                                                                                                                                                                                                                                          DTAI ---VTLYKCDVLGSHREHPDCSLCVTRDPKYKCAWCS--NSCVYNETCIADKNS--
                                                                                                                                                                                                                                                                                                                                                                  847 ELSGAKS----KCTNPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECS
                                                                                                                                                                                                                                                                                                                                                                                       TLSDLKPSRGPMSGGTQVTITGTNLNAGSNVVVWFGKQPCLFH--RRSPSYIVCNTT---
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                                                                               642 ATPPLDERP-LIPTNTDHILVPLSVRSSETNKDFVSRNFAFFDCSHHGNCQECLQSSWGC
                                                                                                                       HWCKYRHVCTHDPKTCSFQEGRVKLPEDCPQLLR-VDKILVPVEVIKPITLKAKNLPQPQ
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE=99091049; PubMed=9875845;
Winberg M.L., Noordermeer J.N., Tamagnone L., Comoglio P.M
Spriggs M.K., Tessier-Lavigne M., Goodman C.S.;
"Plexin A is a neuronal semaphorin receptor that controls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01833; TIG; 3.
SWART; SM00429; IPT; 3.
SWART; SM00423; PSI; 3.
SEQUENCE 2051 AA; 231585 MW; DEF27F9CA8FFF7EA CRC64;
                     Last sequence update)
Last annotation update)
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29.4%; Score 2932.5; DB 5;
Best Local Similarity 34.4%; Pred. No. 1.3e-201;
Matches 708; Conservative 354; Mismatches 682;
                                                                                                                                                                                                                                                                                                                    guidance..;
Coll 95,903-916 (1998).
EMBL, AR106933; AAD009426.1; -.
FlyBase, FBgn0025740; plexB.
InterPro; IPR002909; IPT_TIG.
InterPro; IPR003659; Plexin-like.
InterPro; IPR00165; Plexin-like.
InterPro; IPR001657; Sema.
Pfam; PF01437; PS1; 3.
  Created)
                     01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2002 (TrEMBLrel. 21,
01-MAY-1999 (TrEMBLrel.
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                                          NVPCSHRPKAADMDLEWRQGSGARMILQDEDITTKIENDWKRLNTLAHYQVPDGSVVALV
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Development 0:0-0(2002).
EMBL, AB080022; BAB85224.1; -
SEQUENCE 1951 AA; 217739 MW; D65FA3C8E7E72CD3 CRC64;
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Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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Fujii T., Nakao F., Shibata Y., Shioi G., Kodama E., Fujisawa
Takagi S.,
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC024825; AAF60788.1; -
InterPro; IPR002909; IPT TIG.
InterPro; IPR003659; Plexin-like.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UT-2002 (TrEMBLrel. 21, Last annotation update)
YSSF3AL.1 protein.
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STRAIN-BRISTOL N2;
MEDLINE-99069613; Pubmed-9851916;
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InterPro; IPR002165; Plexin_repeat.
InterPro; IPR001627; Sema.
InterPro; IPR001627; Sema.
InterPro; IPR001627; Sema.
Pfam; PP01403; Sema; 1.
Pfam; PP01403; Sema; 1.
Pfam; PP01833; TIG; 4.
SMART; SM00429; IPP; 3.
SMART; SM00424; SEPFIN; UNKNOWN 1.
SEQUENCE 1944 AA; 216978 MW; DGCSEP7DEA2BDBA8 CRC64;
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                                                                                                                                       LVFQYVEDPTIVRIEPEWSIVSGNTPIAVWGTHLDLIQNPQIRAKHGG--KEHINICEVL 1089
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                                                            CEMGEA -- KPSQHAGFVEICVAVCRPEFMARSSQLYYFMTLTLSDLKPSRGPMSGGTQVT
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                                      TNPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGYIPAEQIV
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Topicions are a large family of receptors for transmembrane, secrete and GPI anchored semaphorins in vertebrates.";

Local 99:14-80(1999).

Coll 99:14-80(1999).

Romer and GPI anchored semaphorins in vertebrates.";

Coll 99:14-80(1999).

Romer anchored in vertebrates.";

Romer anchored semaphorins in vertebrates.";

Romer anchored semaphorins in vertebrates.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LGPALLQALWAGWVLTLQPLP----PTAFTPNGTY-----LQHLARDPTSGTLYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 NRIYKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTTINNVNKMLLIDYKENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 ACGSLYQGICKLIRLEDLFKL-----GEPYHKKEHYLSGVNESGSVFGVIVSYSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 KLFIATAVDGKPEYF-------PTISSRKLTKNSEADGMFAYVFHDEFVAS
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99449305; PubMed=10520995;
Tamaganee L., Artigiani S., Chen H., He Z., Ming G.L., Song H.L.,
Chedotal A., Winberg M.L., Goodman C.S., Poo M.M., Tessier-Lavigne
Comoglio P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFS----
                                                                                                                                                                    Euteleostomi;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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52 PLEXIN-B1/SEP RECEPTOR.
214410 MW; FCAD0630E128EE9C CRC64;
                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Plexin-BJ/SEP receptor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.0%; Score 2792.5; DB 4; ilarity 33.2%; Pred. No. 1.5e-191; Conservative 353; Mismatches 704;
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PROSITE; PS00213; LIPOCALIN; UNKNOWN 1
                                   PRELIMINARY;
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1952
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1952 AA;
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Matches 687; Conserv
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EMBL, AB007867; BAA33703.1; -.

InterPro; IPR003006; Ig MHC.

InterPro; IPR002909; IPT TIG.

InterPro; IPR003659; LipGeln cytFABP.

InterPro; IPR003659; Plexin-Tike.

InterPro; IPR001659; Plexin-repeat.

InterPro; IPR001659; Plexin repeat.

InterPro; IPR001936; RasGAP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1111 LQPSQGLGRRRRVVPETACSLGPSCSSQQFEEPCHVNSSQLITCRTPAL---PGLPEDPW 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1113 ERPEEFGFILDN-VQSLLILNKTNFTYYPNPVFEAFGPSG---ILELKPGTPIILKGKNL 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1169 IPPVAGGNVKLNYTVLVGEKPCTV-TVSDVQLLCESP--NLIGRHKVM------A 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: :: || || :: | : || DLAMS----KEEVVAMIGDGPCVVKTLTRHHLYCEPPVEQPLPRHHALREAPDSLPEFTV 1280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMGEAKPSQHAGFVEICV----AVCRPEFMARSSQLYYFMTLTLSDLKPSRGPMSGGTQ 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       946 ITG-ASGEEVAGATAVEVPGRGRGVSEHDFAYQDPKVH-----SIFPARGPRAGGTR 996
                                    424 SQGQLHRVYL-GPGSDGHPYSTQSIQQGSAVSRDLTFDGTFEHLYVMTQSTLLKVPVASC
                                                                                                                 GQYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPRR----FASEMKQCVRL-TVHP
                                                                                                                                566. NNI SVSQYAVVLLVLETYNVPEL----SAGVNCTFEDLSEMDGLVVGNQIQCYSPAAKEV
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                                                                                                                                                                                                            PRITTENGDHHVVQLQLKSKETGMTFASTSFVFYNCSV-----HNSCLSCVESPYRCHW
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                       SALL ---TIDDNFCGLDMN-APLGVSDMVRGIPVFTEDRDRMTSVIAYVYKNHSLAFVGT
                                                                    451 KSGKLKKIRVDGPRGNALQYETVQVVDPGPVLRDMAFSKDHEQLYIMSERQLTRVPVESC
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1333 PVLRDLEVPGYRQERVEKGLKLFAQLINNKVFLLSFIRTLESQRSFSMRDRGNVASLIMT 1392
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                                                                                                                                                                                                                                    1510 ANSPEVPVKILNCDTITQVKEKILDAIFKNVPCSHRPKAADMDLEWRQGSGARMILQDED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-BRAIN;
MEDLINE=98116655; PubMed=9455477;
IShikawa K., Nagase T., Nakajima D., Seki N., Ohira M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VIII. 78 new cDNA clones from brain which code for large proteins in
                                                                                                    1393 VLQSKLEYATDVLKQLLADLIDKNLESKNHPKLLLRRTESVAEKMLTNWFTFLLYKFLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1627 YTGSPDSLRSRTPMITPDLESGVKWWHLVKNHEHGDQKEGDRGS------KMVSEIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1682 VPG-----BRTPMLEDVDEGGIRPWHLVKPSDEPEPPRPRRGSLRGGERERAKAIPEIY
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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| δŏ             | 694 RVK  | 669        |
|----------------|--|------------|
| q              |  | SLDY 893   |
| ò              | 700 DCPQLLRVDKILVPVEVIKPITLKAKNLPQPQSGQRGY                         | ECI 740    |
| <del>Q</del>   | PVHVEREIRLLG   | ECV 953    |
| ò              | 1-4  | DNP 794    |
| ф              | 954 MELEGLEVVVEÁRVECEPPPDTOCHVTCÓQHOLSYÉALO-PELRÝGÍFLRRAGRLRVÖSA   | 0SA 1012   |
| λõ             | AQESQWI  | 853        |
| qq             | 1013 EGLHVVLYDCSVGHGDCSRCOTAMPQYGCVWCEGERPRCVTREACGEAEAVAT         | VAT 1065   |
| ò              | 854 KCTNPRITBIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGYIPAE :  | Q 913      |
| ф              | 1066 QCPAPLIHSVEPLTGPVDGGTRVTIRGSNLGQHVQDVLGMVTVAGVPCAVDAQEYE      | SSS 1125   |
| ò              | 914 IVCEMGEAKPSQHAGFVEICVAVCRPEFMARSSQLYYFWTLTLSDLKPSRGPMSG :      | 968        |
| q<br>q         | 1126 LVCITG-ASGEEVAGATAVEVPGRGRGVSEHDFAYQDPKVHSIFPARG              | RAG 1176   |
| ò              | 969 GTQVTITGTNLNAGSNVVVMFGKQPC-LFHRRSPSYIVCNTTSSDEVLEMKVSV-        | 1021       |
| qq             | 1177 GTRLTLNGSKLLTGRLEDIRVVVGDQPCHLLPEQQSEQLRCETSPRPTPATLPVAVWFGA  | FGA 1236   |
| ò              | 1022 QVDRAKIHQDLVFQYVEDPTIVRIEPEWSIVSGNTPIAVWGTHLDLIQNPQIRA        | 1075       |
| q <sub>G</sub> | 1237 TERRLQRGQFKYILDPNITSAGPTKSFLSGGREICVRGQNLDVVQTPRIRVTVV        | TVV 1290   |
| ζ              | ICEVLN   | HQS 1109   |
| qa             | 1291 SRMLQPSQGLGRRRRVVPETACSLGPSCSSQQFEEPCHVNSSQLITCRTPALP         | PGLPE 1347 |
| ٥y             | 1110 DLIERPEEFGFILDN-VQSLLILMKTNFTYYPNPVFEAFGPSGILELKPGTPI:        | ILKG 1165  |
| q              | LVFDFATLNPTPFSYEADPTLQPLNPEDPTN                                    | VEG 1404   |
| ò              | 1166 KNLIPPVAGGNVKLNYTVLVGEKPCTV-TVSDVQLLCESPNLIGRHKVM             | 1213       |
| qa             | 1405 ENLDLAMSKEEVVAMIGDGPCVVKTLTRHHLYCEPPVEQPLPRHHALREAPDSL        | LPE 1460   |
| ò              | 1214ARVGGMEYSPGMYIAPDSPLSLPAIVSIAVAGGLLIFIVAVLIAYKRKSRESDL         | SDL 1269   |
| qa             | 1461 FTVQMGNLRFSLGHVQYDGESPGAFPVAAQVGLGVGTSLLALGVIIIVLMYRRKSKQALR  | ALR 1520   |
| ò              | 1270 TLKRLQMQMDNLESRVALECKEAFAELQTDIHELTSDLDGAGIPFLDYRTYTMRVLFPGI  | PGI 1329   |
| qa ,           | 1521 DYKKVQIQLENLESSVRDRCKKEFTDLMTEMTDLTSDLLGSGIPFLDYKVYAERIF      | PGH 1580   |
| ò              | 1330 EDHPVLRDLEVPGYRQERVEKGLKLFAQLINNKVFLLSFIRTLESQRSFSMRDRGNVASL  | ASL 1389   |
| qa             | 1581 RESPLHYDLGVPESRRPTVEQGLGQLSNLINSKLFLTKFIHTLESQRTFSAKDRAY      | ASL 1640   |
| ò              | 1390 IMTVLQSKLEYATDVLKQLLADLIDKNLESKNHPKLLLRRTESVAEKMLTNWFTFLLYKF  | YKF 1449   |
| QO             | 1641 LTVALHGKLEYFTDILKTLLSDLVAQYV-AKN-PKLMLKRTETVVEKLLTNWMSIC      | YTF 1698   |
| δλ             | 1450 LKECAGEPLFSLFCAIKQQMEKGPIDAITGEARYSLSEDKLIRQQIDYKTLVLSCVS     | CVS 1506   |
| QΩ             | 1699 VRDSVGEPLYMLFRGIKHQVDKGPVDSVTGKAKYTLNDNRLLREDVEYRPLTLNAL      | AVG 1758   |
| <i>₹</i> 0     | 1507 PDNANSPEVPVKILNCDITIQVKEKILDAIFKONVPCSHRPKAADMDLEWRQGSGARMILQ | ILQ 1566   |
| qq             | 1759 PGAGEAQGVPVKVLDCDTISQAKEKMLDQLYKGVPLTQRPDPRTLDVEWRSGVAGH      | irs 1818   |
| λö             | 1567 DEDITIKIENDWKRLNTLAHYQVPDGSVVALVSKQVTAYNAVNNSTVSRTSASKYEN     | YEN 1623   |
| qq             | 1819 DEDVISEVQGLWRRINILQHYKVPDGATVALVPCLIKHVLR                     | -EN 1861   |

| ò  | 1624 MIRYTGSPDSLKSRTPMITPDLESGVKWWHLVKNHEHGDQKEGDRGSKMVS 1674          |
|----|--|
| qa | 1862 QDYVPGERTPMLEDVDEGGIRPWHLVKPSDEPEPPRPRGSLRGGERERAKAIP 1915        |
| δ  | 1675 BIYLTRILATKGTLQKFVDDLFBT!FSTAHRGSALPLAIKYMFDFLDEQADKHGIHDPHV 1734 |
| qa | 1916 BIYLTRILISMKGTLQKFVDDLFQVILSTSRPVPLAVKYFFDLLDEQAQQHGISDQDT 1972   |
| ģ  | 1735 RHTWKSNCLPLRFWVNMIKNPQFVPDIHKNSITDACLSVVAQTFMDSCSTSEHRLGKDSP 1794 |
| qq | 1973 IHIWKTNSLPLREWINIKAPQFVFDVQTSDNMDAVLLVIAQTFMDACTLADHKLGRDSP 2032  |
| δ  | 1795 SUKLLYAKDIPSYKNWVERYXSDIGKMPAISDQDMNAYLAEQSRMHMNEFNTMSALSEIF 1854 |
| qq | 2033 INKLLYARDIPRYKRMVERYYADIRQTVPASDQEMNSVLAELSWNYSGDLGARVALHELY 2092 |
| ģ  | 1855 SYVGKYSEEILGPLDHDDQCGKQKLAYKLEQV 1886                             |
| qq | 2093 KYINKYYDQIITALEEDGTAQKAQLGYRLQQI 2124                             |

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LECKEGTBRHAGGHVCYPYCICVQHICVCCICFIYKQAGWAAVGSAGGWRCVCLC
ECVCWHYCVCTYVSYTEKQAGQO,"
                                                                                                                                                                                                                                                                                            2 (bases 1 to 5986)
Ohara, O., Magase, T. and Kikuno, R.
Ohara, O., Magase, T. and Kikuno, R.
Diract Submission
Submitted (03-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research, 1532-3, Tana, Kisarazu, Chiba
292-0812, Japan (E-mall:conalnfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
Fax:81-438-22-3914,
On May 9, 2002 this sequence version replaced gi:10047164.
             PRI 10-MAY-2002
                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                        mRNA, clone_lib:pBluescriptII SK plus
                                                                                                                                          Nagase, T.I., Kikuno, R., Nakayama, M., Hirosawa, M. and Ohara, O. Prediction of the coding sequences of unidentified human genes.

XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro

DNA Res. 7 (4), 273-281 (2000)
                protein, partial cds
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Conservative:
Mismatches:
Indels:
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           Homo sapiens mRNA for KIAA1550 p
AB046770
                                                                                           Ç
                                                                                         Homo sapiens brain cDNA
                                                          GI:20521937
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                                                            AB046770.2
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FEATURES
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|  | 1.50/ Seraspieurinzbeluysargueudinmetdinmetaspaspieeudilberargyalata.1286<br> | 1287 LeuGluCysLysGlu 1291<br>                            | BC028744 2020 1<br>Homo sapiens, similar to plex.       | IMAGE:4828816,<br>BC028744<br>BC028744.1 GI<br>MGC.                      | -   | 1 (bases 1 to 2020) Strausberg, R. Direct Submission Submitted (29-APR-2002) National Institutes of Health, M | <pre>Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA INTH-MGC Project URL: http://mgc.nci.nih.gov</pre> | Contact: MGC help desk<br>Email: Gagabs-rémail.nih.gov<br>Tissue procurement: Miklos Palkovits, M.D., Ph.D.<br>cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki | Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org | contact: amadan@systemsblology.org<br>Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha<br>Madan, Stephanie Rodriques, Amy Sanchez and Michelle Whiting | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLLL at: http://image.llnl.gov Series: IRMK Plate: 47 Row: b Column: 11 This clone was selected for full length sequencing because it |  | /organism="Homo sapiens"<br>/db_xref="texon:9606"<br>/clone="MGC:34033 IMAGE:4828816"<br>/tissue_type="Testis" | /clone_llb="%lH_MGC_9/"<br>/lab_host="DH10B"<br>/note="Vector: pBluescript"<br>383, .1951 | /codon_start=1<br>/product="similar to plexin protein"<br>/protein_id="AAH28144.1"<br>/db_xref="GI:22382105" | /translation="MKAMPWNWTCLLSHLLMYGMGSSTLLTROPAPLSGYGREFYTFR GEPAEGFNHLVYDERTGHIYLGAVNRIYLTKSSDLKVLVYHETGPDEDNPKCYPPRIVQ TCNEPLTTNNVNKMALLIDYKENRLIAGGSLYGGICKLLREDEFKLGEPFRKEHYL SGVNESGSYFGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVF | HOEFVASMILIPOFDITIVOEDSGNEYTELDEMYSPGSSTREGYY TSKLEKEDTANSYVENTEGERSGVEYRLLGAAYLSKAGVUGRTLGVHPDDDL LFTVFSKOGKRKKSLDESALCIFLLKQINORIKERLQSGYRGEGTLDLAMLKVKDIP CSSALLTIDDNFCGLDMNAPLGVSDMYRGIPYFTEDRDRMTSVIAYVKNHSLAFVGT | NSUKLKASTGTGFQUGGITGEWIGVAGDFPGANIASQEQMLCVYLQUSSHKAISDQKVQ<br>PLLCCFLNVPGNSS"<br>T 490 a 544 c 536 g 450 t |
|--|---|--|---|--|---|---|---|--|---|---|---|--|--|---|--|--|--|---|
|  | do do   | Qy<br>Dp   | RESULT 2<br>BC028744<br>LOCUS<br>DEFINITION             | ACCESSION<br>VERSION<br>KEYWORDS   | SOURCE  | REFERENCE<br>AUTHORS<br>TITLE<br>JOURNAL  | REMARK  | COMMENT  |   |   |   | FEATURES,<br>SOUTCE  |  | CDS   |  |  |  | BASE COUNT<br>ORIGIN  |
|  |   |  |   |  |   |   |   |  |   |   |   | -  | <u> </u>   |   |  |  |  |   |
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| QQ   | Oy<br>Db  | Oy<br>Dp   | Qy<br>Db  | Qy<br>Dp   | Qy  | Qy  | Qy  | Qy   | Qy  | Qy<br>Db  | Qy  | Qy   | Oy<br>Db   | Qy<br>Db  | Qy<br>Db   | oy<br>qq   | Qy<br>Db   | Oy<br>Dp  |

| Alignment Scores:   0  | GAGCGCAGTGGGGTGGAGTACCGCCTGCTGCCTACCTGTCCAAAGCGGGGCC ValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPherThrValPheSer [ | 1463 AAGCAGATAAATGACCGCATTAAGGACGGCTGCAGTCTTGTTACCGGGGCGAGGCCACG 1522 381 LeuaspLeualaTrpLeuLysValLysaspIleProCysSerSeralaLeuLeuThrile 400 11 | Aspashantullillillillillillillillillillillillilli            | 44   |   |  | Submitted (11-MAT-2001) National instructs of meating Gene Collection (MGC), Cancer Genomics Office, National Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20 USA USA Contact: MGC help desk | Email: cgapbS-r@mail.nin.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC). Gaithersburg, Maryland: http://www.nisc.nih.gov/ | o,Y., W<br>B., Bla<br>N.L., G<br>aduro,C<br>J., Pea<br>E.E., T | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 20 Row: f Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF |
|--|--|---|--|--|---|--|--|---|--|---|
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| ### SCOTEST  ### SCOTEST  ### A57 00  ### CONTESTIVE ### A57 00  ### A57 00  ### A57 00  ### A57 00  ### A57 00  ### A57 00  ### A58 00  # |  |   |  |  |   |  |  |   |  |   |
| O H + O + D + D + D + D + D + D + D + D + D  | Dength: 2020   Dength: 2020   Dength: 457   DO   | 3 ArGAAAGCCATGCCCTGGAACTGGCCTTCTCTCCCACCTCCTCATGGTGGCGTTG 1 GlySerSerThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPhe                      | ValThrPheArgGlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThr | LeuvalthriisgiuthrglyproaspgluaspasnProLyscysTyrProProargile<br> | ValGlurhrCysAsnGluProLeuThrThrAsnAsnValAsnLysMetLeuLeuIlle<br>      | LeuargLeuGluaspLeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeu<br> | TCAGGTGTCAACGAGGGGGTCAGTCTTTGGAGTGATGTCTCCTACAGCAAGCTGGAT ASPLYSLeuphelleAlaThrAlaValAspGlyLySProGluTyrPheProThrIleSer   | 201         SerArgLysLouThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAsp           111111111111111111111111111111111111   | AspileTyrTyrvalTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGln   | 281 ValArgleuCysLysGluAspThralaPheAsnSerTyrValGluValProIleGlyCys   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII  |

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Homo sapiens chromosome 7 clone RP11-198E23, complete sequence.
ACO09785
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Kibukawa, M., Raymond, C.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179145)
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Buckley, D.,
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Unpublished
2 (bases 1 to 179145)
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1 705 C 781 g 788 t
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Conservative:
Mismatches:
Indels:
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1490. .2563
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| Bubb,K.L., Desmarais,C.L., Ramsey,S.A. and Hubley,R.M.<br>Direct Submission<br>Submitted (01-SEP-1999) Human Genome Center, University of                             | be  | between the ex<br>fragments are<br>EcoRI | experimental<br>re separated | rperimental and predicted v<br>separated by dashed lines<br>HindIII | edicted valued in Italian set in Ita |
|---|-----|--|------------------------------|---|--|
| Washington, Box 352145, Seattle, WA 98195, USA<br>3 (bases I to 179145)<br>Raul, R.K., Olson, M.V., Zhou, Y., James, R.A., Raymond, C.,                               | Seg | SeqDerMap F                              | FngrPrnt                     | SeqDerMap   | FngrPrnt   |
| <b>₽</b>  |     | 9698                                     | 8850                         | 399   | <800   |
| USA   | 1   | 9  | <800                         | 6382  | 6347   |
| <pre>Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.</pre>                          | ; I | 1907                                     | 1895                         | 512   | <800   |
|   |     | 1854                                     | 1895                         | 449   | <800   |
| USA<br>Z  | ļ   | 2849                                     | 2922                         | 2322  | 2276   |
| Kaul, K.K., Olson, M.V., Zhou, Y., James, K.A., Kouse, G., Wu, Z.,.<br>Saenphinmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.                       |     | 3722                                     | 3806                         | 5951  | 5995   |
| and haugen, E.D.  Direct Submission  Charlet Interest of Washington   | . ! | 658                                      | <800                         | 7224  | 7291   |
| Submitted (20 mai 2002) Semine Center, Ourversity of massimiscon,  Box 352145, Seattle, Mallon (1820) USA On May 26, 2002 this sequence version replaced di:20066281. |     | 26398                                    | 26593                        | 1005  | 1033   |
| On May 20, 2002 this Sequence related interaction of the Contact of General Average of Washington Genema Center   | ;   | 537                                      | <800                         | 1020  | 1033   |
| Center Code: University of Mashington Genome Context  |     | 1542                                     | 1483                         | 3445  | 3448   |
| web sire: http://www.genome.washington.edu<br>Contact: uwgchtg@u.washington.edu   | į   | 1103                                     | 1096                         | 2131  | 2126   |
| 101   |     | 1928                                     | 2045                         | 2237  | 2276   |
| 323 (djs380)<br>s   |     | 14029                                    | 13827                        | 6625  | 6652   |
| Sequencing vector: plasmid; X52328; 100% of reads<br>Chemistry: Dye-terminator Big Dye; 100% of reads   |     | 6707                                     | 6816                         | 6349  | 6347   |
| Assembly program: Phrap; version 0.990319<br>Consensus quality: 178850 bases at least 040   |     | 1884                                     | 1895                         | 6999  | 6652   |
|   |     | 6048                                     | 6059                         | 1943  | 1916   |
| Insert size: 1/9145; sum-or-contigs Quality coverage: 11.8x in Q20 bases; sum-of-contigs  |     | 2150                                     | 2209                         | 6376  | 6347   |
|   |     | 13944                                    | 13827                        | 5398  | 5641   |
| 5': RP11-341C17 (UMGC:djs301) AC011625 /3322-bp overlap<br>3': RP11-335B7 (UMGC:djs542) AC026239 38206-bp overlap   |     | 4275                                     | 4287                         | 599   | <800   |
|   |     | 2057                                     | 2209                         | 4055  | 4127   |
| This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.   |     | 2293                                     | 2209                         | 299   | <800   |
| All manually edited bases have been reduced to quality zero.<br>Quality levels above 40 are expected to have less than  | 1   | 6448                                     | 6393                         | 20065   | 20079  |
| <pre>1 error in 10,000 bp. Base-by-base quality values are not generally visible from the</pre>   | 1   | 9916                                     | 9943                         | 6964  | 6903   |
| GenBank flat file format but are available as part of this entry's ASN.1 file.  |     | 7673                                     | 7645                         | 5766  | 5641   |
| This sequence was finished as follows unless otherwise noted:   |     | 115                                      | <800                         | 4281  | 4127   |
| all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred   |     | 1490                                     | 1483                         | 7844  | 7901   |
| <pre>quality &gt;= 30); an attempt was made to resolve all sequencing<br/>problems, such as compressions and repeats; all regions were</pre>                          | :   | 1071                                     | 1096                         | 1032  | 1033   |
| subclone or<br>confirmed by   | •   | 18341                                    | 18612                        | 1591  | 1546   |
| Sequence Validation:  | 1   | 7618                                     | 7645                         | 955   | 954  |
| This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest  |     | 1733                                     | 1700                         | 330   | <800   |
| fragments with sequence-predicted fragments is given below.  The electronically-digested sequence consists of both insert and   | ;   | 1478                                     | 1483                         | 1927  | 1916   |
| vector, in order to accurately represent the entire circular BAC. Small fraquents below a variable cutoff (approximately 400-800 bp)                                  | ,   | 7616                                     | 7645                         | 6261  | 6347   |
| are not resolved in the inderprint and hence do not appear<br>in the table. There are no significant remaining discrepancies  |     | 561                                      | <800                         | 445   | <800   |

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| Oy 121 AspTyrLysGluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeu 140   111111111111111111111111111111111111 | Qy         181 AspLysLeuPheilealaThrAlaValaAspGlyLysProGluTyrPheProThrIleSer         200           bb         61256 GACANGCTGTTCATTGCCACGCAGTGGAAGCCCGAGTATTTTCCCACCATCTCC         61197           Qy         201 SerArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAsp         220 | Oy 241 AsplieTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGln 260        | 301 GluargSerGlyValGluTyrargLeuLeuGlnalaAlaTyrLeuSerLysalaGlyAla 320 301 GluargSerGlyValGluTyrargLeuLeuGlnalaAlaTyrLeuSerLysalaGlyAla 320 111111111111111111111111111111111111                          | Oy 341 LysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeu 360 | 381 LeuAspLeuAlaTrpLeuL<br>60656 CTGGACCTGGCTCAGCTCA<br>5<br>AC11625<br>AC11625<br>ION Homo sapiens clone RP<br>NAC011625 | VERSION AC011625.2 GI:6539285 KEYWORDS HTG. ORGANISM Homo sapiens. ORGANISM Homo sapiens. ORGANISM Homo sapiens  ORGANISM Homo sapiens  Eukaryota: Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 188090) AUTHORS Kaul.R.K., Yu.J., Wong.G.KS., Magness,C.L., Green,E.D., Green,P. TITLE Large-scale MCD Mapping and Sequencing of Human Chromosome 7 JOURNAL Unpublished  REFERENCE 2 (bases 1 to 188090) |
|--|--|--|---|---|---|---|
| 19080     18612     3869     3877     9461       114     <800  | 4943 998<br>8931 1318<br>954 94<br>7901 796<br><800 111  | 1905 1916 1029 1011 1905 1916 1491 1485 113 <800 20564 20918 5596 5641 750 735 | FEATURES Location/Qualifiers  Source 1179145  Alignment Scores: 0 Length: 179145  Score: 396.00 Matches: 396  Percent Similarity: 100.00% Conservative: 0  Rest Local Similarity: 100.00% Mismatches: 0 | 20.89% 9 x AC009785 (1  | 21 GlySerSerThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPhe   | Oy 61 G19H1s11e7Fue0G19A19A19A18A18A18A18A18A18A18A18A18A18A18A18A18A   |

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|---|--|--|---|
| Bubb, K.L., Desmarais, C.L., Ramsey, S.A. and Hubley, R.M. Direct Submission Submitted (08-ocr-1999) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA (bases 1 to 188090) Kaul, R.K. and Desmarais, C.L. Direct Submission Submitted (08-DEC-1999) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA on Dec 8, 1999 this sequence version replaced gi:6016750. |  | Quality coverage: 7.78x in Q20 bases; sum-of-contigs  Overlapping Sequences: 5: UWGC:djs302 3': UWGC:djs380  Sequence Quality Assessment: This entry has been annotated with sequence quality astimates computed bases have been reduced to quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file. | Double stranded (DS) coverage: 100.0% Single stranded regions: 0 Single stranded regions: 0 Single stranded regions: 0 Sequence Validation: 0 This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fingerprinting. Comparison of the experimentally derived digest fingerprinting. Comparison of the experimentally derived digest fragments when sequence predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-600 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.  Bgl11 FP Seq FP Seq FP Seq FP Seq PP |

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                                               LeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeu
                                                                                                  SerGlyvalAsnGluSerGlySerValPheGlyvalIleValSerTyrSerAsnLeuAsp
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Primates; Catarrhini; Hominidae; Homo
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Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligo capping; fis (full insert sequence).
Homo sapiens fetal brain cDNA to mRNA, clone_lib:FCBBF3
clone:FCBBF3008362.
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S Isogai. T and Yamamoto, J.

L Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail: genomics@hri.co.jp, Tel: 181-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H., Onogawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E., Kataoka,R., Kuga,N., Kuroda,A., Satoh,I., Kamata,K., Takamahi,E., Terashima,Y., Watanaba,M., Sugiyama,T., Trie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishi,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Watsuo,K., Nakamura,Y., Sekine,M., Kikuch,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., NeDo human cDNA sequencing project
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clone_lib="RPCI-11 Human Male BAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-AUG-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 3, 2000 this sequence version replaced gi:7770419.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13: M77815; 95% of reads
Sequencing vector: Plasmid: n/a: 5% of reads
Chemistry: Dye-primer-amersham: 5% of reads
Chemistry: Dye-terminator Big Dye; 5% of reads
Chemistry: Dye-terminator Big Dye; 5% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 159631 bases at least 040
Consensus quality: 16781 bases at least 020
Insert size: 176000: agarose-fp
Insert size: 176000: agarose-fp
Insert size: 176000: agarose-fp
Ouality coverage: 4.2 in 020 bases
* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3333: contig of 3333 bp in length
                                                                                                                                                           Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-44F19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L1062
Center clone name: 44_F_19
----- Summary Statistics
AC009723.4 GI:9965551
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens.
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                                                                      ORGANISM
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97055
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Homo sapiens mRNA; cDNA DKFZp434G0625 (from clone DKFZp434G0625);
partial_cds.
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases I to 1029)

Ansorge,W., Wirkner,U., Mewes,H.W., Gassenhuber,J. and Wiemann,S. Direct Submission

Submitted (15-JAN-2000) MIPS, Am Klopferspitz 18a, D-82152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      German Genome Project.
This clone (DKFZp434G0625) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is availa
at http://www.mips.biochem.mpg.de/proj/cDNA/.
                                                                                                                                                                                                              97054 AGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCATGTTCGCGTACGTCTTCCATGAT
                                                                                                                                                                         sGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAl
                                                                                                                                                                                                                                                                                                                                    320 aValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPheSe
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                                                                                                          GluPheValAlaSerMetIleLysIleProSer-AspThrPheThrIleIleProAspPh
                                                                                                                      eAspIleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGl
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Homo sapiens
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31544. 37218
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41712 c 41281 g 46388
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HTG 26-JUL-2000
                                                    406 GlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValArgGlyIleProValPhe 425
                                                                  426 ThrGluAspArgAspArgMetThrSerValIleAlaTyrValTyrLysAsnHisSerLeu 445
                                                                                                                            Submitted (12-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 30, 2000 this sequence version replaced gi:7229794.

All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research
             ACU25595 74655 bp DNA linear HTG 26
Homo sapiens clone RPll-24ElO, LOW-PASS SEQUENCE SAMPLING.
AC025595
                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 74655)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-24E10
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                                                                                                                                                                Web site: http://www-seg.wi.mit.edu
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Center project name: L4440
Center clone name: 24_E_10
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Homo sapiens.
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NIASQEQMLCVYLQCSSHKAISDQRVQPLLCCFLNVPGNSS"
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DB108; sites Not1 + Sal1"
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1. 955
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arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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of 742 bp in length
100 bp
of 730 bp in length
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100 bp
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sequencing consortium of the German Genome Project. This clone (DKFZp56600546) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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X1-2blue; sites NotI + SalI"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3556)
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Submitted (19-UUL-2002) 1, D-85764 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email S.wiemann@dkfz-heidelberg.de;
                                                                                                                                                                                                               GlnArgSerPheValThrPheArgGlyGluProAlaGluGlyPheAsnHisLeuValVal
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Ottenwaelder, B., Obermaler, B., Mewes, H.W., Gassenhuber, J. and
                    Length:
Matches:
Conservative:
Mismatches:
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| Int Similarity: 98.99% Conservative: 0  Local Similarity: 98.99% Mismatches: 1  Match: 6.54% Indels: 2  Gaps: 0  1-964-956-13 (1-1896) x AXO88116 (1-601)  503 ThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCysLeuGlySer 522 | 101 GOCCACCCCACTCGCTCGTCTCGTCACACACTTGCACCCGGAAGGACGCGTT 121 12 GOCCACCCCCACTCGCTCGTCTCTCGTCACACACTTGCACCCGGAAGGACGCGTT 121 12 GOCCACCCCCACTCTGCTCTGTCTCTCCACACACTTGCACCCGGAAGGACGCGTT 121 12 GACCGTCCACTGTGTCTTGTTTTTTTTTTTTTTTTTTTT  | •  |
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| Percent Simil-Best Local Signery Match: DB: US-09-964-956 QY 503  | OY  OY  OY  OY  OY  OY  OY  OY  OY  OY   | TITLE<br>JOURNAL<br>REFERENCE  |
| Oy 1693 AspAspLeuPheGluThrIlePheSerThrAlaHisArgGlySerAlaLeuProLeuAla 1712   | 94 175 GLOSTICOGCANTACTOGGAGAGCANTTCCTGCTGCTGGGTTTTGGGTCGACATGAT  175 GLYASARPTCGLRPHVALPABABIHHISLYSANGSTILATTAGGTCGACCATGGTGGT  175 GLYASARACCGCAGTTTTGTGTTTTGACATCACAAGAGCGCTGCTGCTTT  177 TYALVALALGINTHEPHAGATGAGTTGACATCACAAGAGCGCTGGCTGCTTT  178 TYALVALALGINTHEPHAGATGAGTTGACATCACAAGAGCGCTGGCTGCTTT  179 DESPECTORSATAGGACATCTGACATCACACAGAGCCTCCTGCCTTTC  170 TYALVALALGINTHEPHAGATGAGTTGACTTGACATCACAGAGCCTGCTGCTTTC  170 TYALVALALGINTHEPHAGATGAGTTGATTGACTGAAGAGCTGCTGCTTTC  171 TAGAGGTTGACCTCCACACAGTTGATTGACTTGATTGATT | BASE COUNT       124 a 182 c 173 g 122 t         ORIGIN         Alignment Scores:       1.36e-126 Length: 601         Score:       124.00 Matches: 196 |

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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Rattus norvegicus,
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            Direct Submission

L. Submitted (04-Jul-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@Hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
(E-mail:genomics@Hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan: CDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
Construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5' a 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation: clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.

Location/Qualifiers

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/db_xref="taxon:9606"
/clone="FCBBF3022321"
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/clone_lib="FCBBF3"
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Center clone name: CM30-10113
------- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality; 63798 bases at least Q40
Consensus quality: 67738 bases at least Q30
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С οy d οy g ò

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Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Nell,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-A02.2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 21, 2002 this sequence version replaced gi:17061257. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
Naylor, J., Nguyen, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: L18164
Center clone name: 462_0_13
Center clone name: 462_0_13
Center clone name: 462_0_13
Center clone name: 462_0_13
Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 169421 bases at least Q40
Consensus quality: 171821 bases at least Q20
Consensus quality: 171821 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 172885; sum-of-contigs
Quality coverage: 7.1 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
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S (bases 1 to 173385)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Boquslavkiy, L., Boukhgalter, B.,

Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,

Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,

Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,

Ginde, S., Gord, S., Goyette, M., Graham, L., Garad - Piere, N.,

Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,

Jones, C., Kamata, A., Kamatas, A., Kells, C., LaRocque, K.,

Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,

MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,

McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
                       AC102171 173385 bp DNA linear HTG 21-AUG-2002
Mus musculus clone RP23-462013, WORKING DRAFT SEQUENCE, 11
                                                                                               170 eGlyValIleValSerTyrSerAsnLeu-AspAspLysLeuPheIleAlaThrAlaValA 190
                                                                                                                                                                                            190 spGlyLysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSerGluA 210
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Glu-ProTyrHisLysLysGluHisTyrLeuSerGlyValAsnGluSerGlySerValPh 170
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 SerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProProGlySer
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HTG; HTGS_PHASE1; HTGS_FULLTOP.
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Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-462013
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198470 bp DNA linear PRI 17-NOV-2000
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3': RP11-348A15 (UWGC:djs302) AC009364, 64369-bp clone overlap
                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission Salva 2000, Genome Center, University of Washington, Submitted (17-NO2000) Seattle, WA 98195, USA On Jul 28, 2000 this sequence version replaced gi:8050921.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-JUL-2000) Genome Center, University of Washing
Box 352145, Seattle, WA 98195, USA
4 (bases 1 to 198470)
Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and
                                                                                                                                                                                                                                                                                                                                                                                                       and
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Contact: uwgchtgs@u.washington.edu
Contact: uwgchtgs@u.washington.edu
Center project Information
Center project name: HsaChr7
Center project name: RP11-297N5 (djs233)
Center clone name: RP11-297N5 (djs233)
Sequencing vector: M13: X05513; 100% of reads
Sequencing vector: M13: X05513; 100% of reads
Chemistry: Dye-primer-amersham; 1% of reads
Chemistry: Dye-primer-amersham; 1% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 198174 bases at least Q40
Consensus quality: 198402 bases at least Q30
Consensus quality: 198444 bases at least Q20
Insert size: 212411; 7.1% error: agarose-fp
Insert size: 198470; sum-of-contigs
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Quality coverage: 8.02x in Q20 bases; sum-of-contigs
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This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-DEC-1999) Human Genome Center, University Washington, Box 352145, Seattle, WA 98195, USA (bases 1 to 198470)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. Olson,M.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Large-scale Mapping and Sequencing of Human Chromosome Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 198470)
Bubb,K.L., Desmarais,C.L., Ramsey,S.A. and Hubley,R.M.
Direct Submission
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Center Code: UWGC
                                                             Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
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                                                             45187 45266; gap of 100 bp 45287 57434; contig of 12148 bp in length 57435 57534; gap of 100 bp 57535 84630; contig of 27096 bp in length 84731 111275; contig of 26545 bp in length 111276 111375; gap of 100 bp
                                                                                                                                                                                               111276 111375; gap of 100 bp
111376 1134525: contig of 23150 bp in length
134526 134625; gap of 100 bp
134626 170655: contig of 36030 bp in length
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  4837: contig of 1572 bp in length 7: gap of 100 bp 45186: contig of 40249 bp in length
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Conservative:
Mismatches:
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/note="assembly_fragment"
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'note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-462013"
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1360
                                                                                                                                                                                                                                                                                                                                                  source
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ORIGIN .
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0
                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
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δλ pp ò g ò g

GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality, -30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered

| rder  | FngrPrnt  | 4156   | 2070 | 4913 | 2861 | 22935 | 1553 | 925   | 12996 | 5230 | 1322 | <800 | <800 | 11149 | <800 | 4701 | 7301 | 1090  | 4539  | <800 | <800 | 904  | <800 | 774  |
|---|-----------|--------|------|------|------|-------|------|-------|-------|------|------|------|------|-------|------|------|------|-------|-------|------|------|------|------|------|
| н .   | : 유 :     | 3995   | 2067 | 10   | 2868 | 22606 | 1547 | . 924 | 2     |      | 1 50 |      |      | 499   | 43   | 0    | 75   | 110   | 304   | 0    | 14   |      | ' '  | 794  |
| dashed lines.  Bgl  | FigrPrnt  | 14401  | 1148 | 1148 | 6747 | <800  | <800 | 3491  | 1148  | 1148 | <800 | 2607 | 4641 | <800  | 4641 | 3781 | 2967 | 2065  | <800  | 3854 | 7991 | 1173 | 4791 | 2967 |
|   | SeqDerMap | 1430.9 | 1127 | 0.8  |      | 667   | 1.5  | 4     |       | 1167 | 386  |      |      | 68    | 4652 | 3773 | 3018 | 204   |       | 3873 | 8082 | 0    | 4800 | 2919 |
| Derween ine experimental ar<br>fragments are separated by<br>coRI | FngrPrnt  | 8806   | 2841 | 2713 | 8230 | 11374 | 3919 | 795   | 10666 | 2049 | 2261 | 6811 | 920  | 6516  | 4467 | <800 | <800 | 13792 | 12156 | 6516 | 3116 | <800 | 2388 | 2049 |
| fragment<br>EcoRI   | ₹:        | 8696   | 2842 | 74   | 8210 | 11559 | 3869 | 792   | 10723 | 2047 | 2240 | 6878 | 923  | 6549  | 45   | (1)  | 638  | ი ი   | 213   | i Oi | 60   | 1    | 4    | 2058 |

US-09-964-956-13 (1-1896) x AC018643 (1-198470)

|   | 59               | 3609                                   | 33                               | <800   | 3761       | 3904  |
|---|------------------|--|----------------------------------|--|------------|-------|
|   | 1419             | 1403                                   | 3943                             | 3973   | 2990       | 29.74 |
|   | 6733             | 6811                                   | 1335                             | 1324   | 1755       | 1786  |
|   | 11361            | 11374 .                                | 13                               | 1362   | 4506       | 4301  |
|   | 2                | 3919                                   | 125                              | 008>   | 3149       | 3181  |
|   | 728              | 3774                                   | 62                               | 1630   | 95         |       |
|   | 671              | 2713                                   | 9                                | 7991   | ٠ã٥        | 1786  |
|   | 53               | <800                                   | 36                               | 5970   | 1587       | 1553  |
|   | 10               | 2261                                   | 4659                             | 4641   | 778        | 774   |
|   | 9391             | 39409                                  | 418                              |  | 5306       | 5230  |
|   | 712              | 2995                                   | 0                                | 7991   | 449        | <800  |
|   | 37               | <800                                   | 40                               |  | 83         | 4913  |
|   | 77               | 4916                                   | 452                              |  | 88         | 1090  |
|   | 6652             | 6649                                   | 1346                             | 1362   | 6421       | 6427  |
|   | <b>*</b>         | 3 008                                  | 1<br>1<br>1                      | 860  |            | 5230  |
|   | :                | 3323                                   | 9.9                              | 925  |            |       |
|   | 835              | 1818                                   | 3158                             | 3181   |            |       |
|   | 0421             | 1.0389                                 |                                  | 6783   |            |       |
|   | 411              | 2436                                   | · œ                              | 4913   |            |       |
|   | 184              | <800                                   |                                  | 3424   |            | •     |
|   |                  | - 008>                                 | 2929                             | 2974   |            |       |
|   | #<br>!<br>!<br>! | <800                                   | 1243                             | 1220   |            |       |
|   | 88               | <800                                   | æ                                | 2294   |            |       |
|   | 51               | <800                                   | 7                                | <800   |            |       |
|   | 08               | <800                                   | 964                              | 925  |            |       |
|   | 2446             | 2436                                   | 8680                             | 8644   |            |       |
|   | 718              | 1713                                   | 1439                             | 1429   |            |       |
|   | . <del></del>    | 1818                                   |                                  | 3904   |            |       |
|   | 1729             | 1818                                   | 5549                             | 5552   |            |       |
|   | 13               | <800                                   | 37                               | 774  |            |       |
|   | 7684             | 7991                                   | 249                              | <800   |            |       |
| Alignment Sopred. No.:  | cores:           | 1.09e-86                               | rei                              | Length:  | 198470     |       |
| score:<br>Percent Similarity:<br>Best Local Similarit;<br>Query Match:<br>DB: | >-               | 90.00<br>100.008<br>: 100.008<br>4.758 | Matcr<br>Conse<br>Misme<br>Indel | Matches:<br>Conservative:<br>Mismatches:<br>Indels:<br>Gaps: | )<br>00000 |       |
|   |                  | ,                                      |                                  |  | ,          |       |

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|  | 134   |   | 4.  |  |  |   |                    |  |   |     |
|  |   | S.  |   | 2  | 16   |   | 2 <sup>6</sup> .   | -  |   |     |
| 1359   | 69909   | 1379.   | 69849   | 1399   | 68789  | 1419  | 69729              |  | 4                                       | 100 |
| 1340 ValproclyfyrArgGlnGluArgValGluLysGlyLeuLysLeuPheAlaGlnLeuIle 1359 | GTCCCGGCTACCGGCAGAGGCGTGGGAGAAAGGCCTGTAGGCTGTTGGCCCAGGTCATC 65909 | 1360 AsnAsnLysval-PheireuLeuSerPhèileArgIhrieuGluSerGlnArgSerPheSer 1379. | AACAACAAGGTGTTCCTTCTTCTTCTTCTTCTTCATGGGACGCTTGAGTCGGAGCGTAGGTTCTCC 69 | 1380 MetargaspargGlyasnValalaSerLeuileMethrValLeuGinSerLysLeuGlu | ATGCGCGACCGTGGCAACGTGGCGTCATCATGACGGTGGTGGTGGAGGAGCTGGAG 69789 | TyralafıraspvalbeuLyscünbeuLeualaaspbeulleaspLysasnLeugluser 1419 | - (1               | ubeuleuargarg 1429                       | 69728 AAGAACCAGCCTAAGCTGCTCAGGAGG 69699 |     |
| ValProGlyTyrArgGln   | GTCCCGGCTACCGGCAG   | AsnAsnLysVal-Phereul  | AACAACAAGGTGTTCCTG  | MetArgAspArgGLyAsn   | ATGCGCGACCGTGCCAACC  | TyralaThraspValbeul   | TACGCCACTGATGTGCTG | 1420 LysAsnHisProLysLeuBeuLeuArgArg 1429 | AAGAACCAGCCTAAGCTG                      |     |
| 1340   | 89669   | 1360  | 80669   | 1380   | 69848  | 1400  | 88269              | 1420                                     | 69728                                   |     |
|  |   |   |   |  |  |   |                    |  | . 1                                     |     |
| oy.  | qq  | oy<br>Y   | qq  | Qy   | qq   | Qy  | qq                 | OY.                                      | qq.                                     |     |
|  |   | 4   |   |  |  |   |                    |  |   |     |

Search completed: June 28, 2003, 23;01:01 Job time: 12647 secs SUMMARIES

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0 Searched: 2185239 seqs, 1125999159 residues Total number of hits satisfying chosen parameters: 4368727

Word size:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Listing first 45 summaries

| Line par<br>rame+_p2<br>1/USPTC<br>1-/USPTC<br>1 | Database: N_Geneseq_101002:* |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

28-MAR-2002.

XX Od

| scriptio | encodin | brain | bone ma | #11431 | Human bone marrow | #2449 | CDNA en | NOV/F | ncodi | DNA encoding novel | Mouse ischaemic co | phila | CDNA | Nowel human coding | Secret | prostate | prostate |    | e embryoni | brain expre | #24180 | genome-deri | Ψ.  | #11108 | Probe #25106 used | denome- | #12126 | -   | Human tull-length |     | in PR0235 | a      | 2      | CDNA se | PR02    | cDNA enco | n prostate | prostate ex | prosta | brain | Human genome-deriv |  |
|----------|---------|-------|---------|--------|-------------------|-------|---------|-------|-------|--------------------|--------------------|-------|------|--------------------|--------|----------|----------|----|------------|-------------|--------|-------------|-----|--------|-------------------|---------|--------|-----|-------------------|-----|-----------|--------|--------|---------|---------|-----------|------------|-------------|--------|-------|--------------------|--|
| ID       | :       |       |         |        |                   |       |         |       |       |                    |                    |       |      |                    |        |          |          |    |            |             |        |             |     |        | AAT56420          |         |        |     | AAK94356          |     |           | AAC585 | AAA775 | AAS2140 | AAF7240 | AAS0002   | ABV04      | ABV3525     | ABV440 | AAK23 | ABS231             |  |
| bu       |         |       |         |        |                   |       |         |       | 477   | 314                |                    | 382   | 100  |                    | 418    |          |          |    |            |             |        |             |     |        | 201 22            |         |        | 009 | 2414 22           | 844 |           | 477    | 477    | 477     | 477     | 408       |            | n l         | ഹ      | O 1   | ~                  |  |
| ch       |         |       |         |        |                   | -     |         |       | ٠     |                    |                    |       | •    |                    |        |          |          |    | •          |             |        | •           |     |        | 0 0               |         |        |     | •                 | •   |           |        | •      | •       |         | •         |            | •           |        |       | 9.0                |  |
| Score    | . 9     | ~     | /       | 173    | o v               | 2 4   | 2       | 63    | 61    | 61                 | 51                 | 6.    | 7 7  | * *                | 33     | 333      | 33       | 24 | 23         | 18          | 18     | 18          | 200 | 100    | 1 1               | 16      | 16     | 16  | £ [               | 12  | 12        | 12     | 12     | 12      | 12      | 12        | 11         | 11          | 11     | T]    | 11                 |  |
|          | -       |       |         | Ο (    |                   |       |         | 6     | 10    | 11                 | 12                 | 13    | † T  | 15                 | 17     | 18       | 19       | 20 | 21         | 22          | 23     | 24          | 525 | 0 6    | 28                | 29      | 30     | 31  | 32                | 3.4 | 35        | 36     | 37     | 38      | 96.     | 40        | 41         |             |        | 4 4   | 45                 |  |

ALIGNMENTS

| ω̈́× | RESULT 1<br>ABK70006   |                      |
|------|--|----------------------|
| : _  | ABK70006 standard; DNA; 2597 BP.                               |                      |
| ×    |  |                      |
| AC   | ABK70006;  |                      |
| XX   |  |                      |
| DŢ   | 15-JUL-2002 (first entry)                                      |                      |
| ××   |  |                      |
| DE   | cDNA encoding human Pro peptide #46.                           |                      |
| ×    |  |                      |
| ΚW   | Human; ss; gene; PRO; secreted protein; transmembrane protein; | ansmembrane protein; |
| 7    | qenetic disorder; tumour; cancer.                              |                      |
| XX   |  |                      |
| SO   | Homo sapiens.  |                      |
| XX   |  |                      |
| PN   | WO200224888-A2.  |                      |

194 GlufyrPheProThrIleSerSerArgLySLeuThrLySASnSerGluAlaASpGlyMet

```
This invention relates to the cDNA and protein sequences of novel secreted and transmembrane polypeptides PRO polypeptides. The invention also comprises a method for producing the proteins of the invention by recombinant means and antibodies specific for the protein of the invention. The antibody may be used for detecting the PRO polynucleotides may be used as hybridisation probes for a cDNA library to isolate the full-length PRO cDNA or to isolate other cDNAs, to construct hybridisation probes for mapping the gene which encodes that PRO and for genetic analysis of individuals with genetic disorders, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knock-out animals, which in
                                                                                                                                                                                                                                                                                                                                                                                                                                                New PRO polypeptides and polynucleotides encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or for genetic analysis of individuals with genetic disorders
                                                                                                                                                                                                                                                                                                                                                           JC;
Zhang Z;
                                                                                                                                                                                                                                                                                                                                                           Grimaldi .
Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0
                                                                                                                                                                                                                                                                                                                                                           E, Goddard A, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Figure 91; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                          Filvaroff E,
Stephan J,
                                                                                                                                       2001US-264395P.
                                                                                                                                                                                                                               2001US-282199P.
2001US-290589P.
                                                            000US-235147P
                                                                          2000WO-US30873
                                                                                       2001US-261878P.
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2001WO-US19692
                                                                                                                                                                                                                                                                                                         09-JUL-2001; 2001WO-US21735
          2001WO-US27099
                                                                                                                                                                                          2001US-27
                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                           Eaton DL,
Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-362426/39.
P-PSDB; ABG34075.
                                                                                                                           16-JAN-2001;
25-JAN-2001;
02-FEB-2001;
09-FEB-2001;
                                                05-SEP-2000;
22-SEP-2000;
10-NOV-2000;
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16-JAN-2001;
                                                                                                                                                                               28-FEB-2001;
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03-APR-2001;
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01-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                           Baker KP, E
Gurney AL,
Fong S;
                                                                                                                                                                                                                                                                                                29-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                      Fong
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turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides are useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The sequences may also be used to detect overexpression on PRO polypeptides in cancerous tumours and for screening for differentially expressed genes using microarray technology. The present sequence represents a cDNA encoding a human PRO protein of the invention.
```

Length:
Matches:
Conservative:
Mismatches: Indels: 264.00 100.00% 100.00% 13.92% Best Local Similarity: Query Match: Percent Similarity:

.68e-251

US-09-964-956-13 (1-1896) x ABK70006 (1-2597)

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313
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                                             253
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                                                                       62 TTGGGGTAGGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTGGGACACC
                                                                                                                              ValGluValProIleGlyCysGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAla
                                                                                                                                                              CysTyrArgGlyGluGlyThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCys
                                                                                                                                                                                                                                             2 GAGTATTTTCCCACCATCTCCAGCGGAAACTGACCAAGAACTCTGAGGCGGATGCATG
                   PheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAspThr
                                                                                                                                    TyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human brain expressed single exon probe SEQ ID NO: 11113
                                                                                                                                                                                                                                                                                                                                                                                          ВР
                                                                                                                                                                                                                                                                                                                                                                                          AAK11122 standard; DNA; 598
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                    214
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeu 160
                 GlySerSerThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPhe 40
                                                                                                                                                                                                                                                             expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                  NO: 11496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO: 11496; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other;
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1173
0
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0
                                                           SerGlyValAsnGluSerGlySerValPheGlyValIle 173
                                                                                                                                                                                                                                                                            microarray; cancer; leukaemia; lymphoma; myeloma; ss
                                                                         Human bone marrow expressed single exon probe SEQ
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank
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                                                                                                                                               BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W,
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                               standard; DNA; 598
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2000GB-0024263
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                                                                                                                                                                                                     06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                             Human; bone marrow
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Best Local Similarity:
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21-SEP-2000;
27-SEP-2000;
04-0CT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuValThrHisGluThrGlyProAspGluAspAsnProLysCysTyrProProArglle 100
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                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene
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Matches:
Conservative:
Mismatches:
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
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Best Local Similarity:
WO200157275-A2
                                                       30-JAN-2001;
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                                AspTyrLysGluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeu
                                                                                                     GlyHisIleTyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysVal
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ID AA142745 standard; DN
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DE Probe #11431 used to
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W Probe; microarray; hu
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HOMO Sapiens.
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W WO200157272-A2.
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PD 09-AUG-2001.
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PP 09-AUG-2001.
XX
PP 30-JAN-2001; 2001W0-U
XX
PP 30-JAN-2001; 2001W3-U
PP 26-MAY-2000; 2000US-O
PP 26-MAY-2000; 2000US-O
PP 27-SEP-2000; 2000US-O
PR 27-SEP-2000; 2000US-O
PR 27-SEP-2000; 2000US-O
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probes are useful
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expression in samples derived from human placenta. The for antenatal diagnosis of human genetic disorders.
                                                                 598
173
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                                                                                     Percent Similarity:
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Query Match:
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                                 Sequence 598
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                                                       Alignment Scores:
Pred. No.:
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BP.

AAK49882 standard; DNA; 495

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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyHisIleTyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACTACAAGGAGAACAGGCTGATGCCTGTGGGAGCCTGTACCAAGGCATCTGCAAGCTG
                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in
                                                                                                                                                                                       SEQ ID NO: 23783; 650pp + Sequence Listing; English.
                                                                                                                                                                                                             present invention provides a number of single exon
                                                                                                                                                                                                                                                                                                                                    495
1160
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                                                                                                                                                                                                                                                                                                   96 A; 132 C; 153 G; 114 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                       MOLECULAR DYNAMICS INC
                                                                                                             Chen W,
                                                                                                                                                                                                                                                                                                                                  6.7e-149
160.00
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8.44$
                                                                  2000GB-0024263.
  2000US-0180312.
2000US-0207456.
                                  2000US-0632366
2000US-0234687
                                                       2000US-0236359
                        2000US-0608408
                                                                                                             Penn SG, Hanzel DK,
                                                                                                                                  WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                   Sequence 495 BP;
04 - FEB - 2000; 26 - MAY - 2000; 30 - JUN - 2000; 21 - SEP - 2000; 27 - SEP - 2000; 24 - OCT - 2000; 2
                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                        Example 4;
                                                                                                                                                                                                                                                                               invention.
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                                                                                       (MOLE-)
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukable the improved mayeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlySerSerThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValThrPheArgGlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCACATTCCGAGGAGAGCCCGCCGAGGGTTTCAATCACTGGTGGTGGATGAGAGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of single exon nucleic acid
                                                                                         expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                              probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO: 24439; 658pp + Sequence Listing; English.
                                                                  single exon probe SEQ ID NO: 24439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495
160
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                                                                                                   cancer; leukaemia; lymphoma; myeloma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other;
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                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid panalyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 495 BP; 96 A; 132 C; 153 G; 114 T; 0
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Indels:
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Matches:
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2000US-0632366.
2000US-0234687.
2000US-0236359.
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160.00
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                                                                 Human bone marrow expressed
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                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488900/53
                                                                                      Human; bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity:
                                                                                                                                              WO2001.57276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                          30-JAN-2001;
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03-AUG-2000;
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27-SEP-2000;
                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                     04-0CT-2000;
                                                                                                                                                                                                                          26-MAY-2000;
                                         06-NOV-2001
                                                                                                   microarray;
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Pred. No.:
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MetLysAlaMetProTrpAsnTrpThrCysLeuLeuSerHisLeuLeuMetValGlyMet
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Tamagnone L;
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                                                                         LeuValThrHisGluThrGlyProAspGluAspAsnProLysCysTyrProProArgIle 100
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         ValGlnThrCysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuIle
                                              Probe #24492 used to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probes useful for
                                                                                                                                                                                                                                              microarray; human; placenta; antenatal diagnosis;
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160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID No 24492; 654pp; English
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ID AAI55806 standard; DNA; 495
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2000US-0608408.
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2000US-0236359.
                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                     2000US-0180312
                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488897/53
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Best Local Similarity:
                                                                                                                                                                                                                                                        genetic disorder;
                                                                                                                                                                                                                                                                                              WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 495
                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000;
30-JUN-2000;
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US-09-964-956-13 (1-1896) x AAI55806 (1-495)

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182
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                                                                                                                                                                                                                                              Human; Plexin A-4; semaphorin domain; hyperplasia; neoplasia; cancer; neurodegenerative disease; autoimmune disease; lupus; multiple sclerosis; inflammatory bowel disease; diabetes type I; rheumatoid arthritis;
                                          362
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                                                                                                                                                                                                         ValGlnThrCysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuIle
                                                                                                                                                                                 GTCCAGACCTGCAATGAGCCCCTGACCACCAACAATGTCAACAAGATGCTCCTTA
GlySerSerThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPhe
                                  GlyHisIleTyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysVal
                                                                                                                                   LeuValThrHisGluThrGlyProAspGluAspAsnProLysCysTyrProProArgile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goodman CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /partial
/product= "Plexin A-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 2..601
                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                          Human cDNA encoding Plexin A-4.
                                                                                                                                                                                                                                                                                                     AAS00023 standard; cDNA; 601
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                                                                                                                                                                                                                                                                                                                                                                                                      immunogen; antibody; ss.
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CALIFORNIA.
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541 CCATGACCCCAAGACCTGCTCCTTCCAGGAAGGCCGAGTGAAGCTGCCCGAG 592

AAU00018

The sequence encodes Human Plexin A-4. Plexins are large transmembrane proteins whose extracellular domain shares homology with Scatter factor receptors and contain an approximately 500 amino acid Semaphorin domain. The plexin polynucleotides and polypeptides, and plexin-specific binding agents are useful in diagnosis, therapy and in the biopharmaceutical industry. In particular, the plexin polynucleotides and polypeptides are useful for generating compounds (e.g. plexin-specific binding agents or antibodies) for treating or diagnosing a disease or disorder involving herrant call growth (e.g. hyperplasia, neoplasia, cancer or neurodegenerative disease), or diseases or disorders involving aberrant immune regulation (e.g. autoimmune diseases such as lupus, inflammatory bowel disease or Diabetes Type I), or immunosuppressive diseases such as New plexin polynucleotides and polypeptides, useful in diagnosis, therapy and in producing compounds for treating diseases involving aberrant cell growth (e.g. cancer) or immune regulation (e.g. multiple sclerosis or rheumatoid arthritis. 2; Page 69; 79pp; English. autoimmune diseases) Claim 

Sequence 601 BP; 124 A; 182 C; 173 G; 122 T; 0 other;

rGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerValHisAsnSerCy GluArgSerLysGluProArgArgPheAlaSerGluMetLysGlnCysValArgLeuThr pGlyLeuValValGlyAsnGlnIleGlnCysTyrSerProAlaAlaLysGluValProAr gllelleThrGluAsnGlyAspHisHisValValGlnLeuGlnLeuLysSerLysGluTh CGGCATGACCTTCGCCAGCACCAGCTTTGTCTTCTACAATTGCAGCGTCCACAATTCGTG 563 ValHisProAsnAsnIleSerValSerGlnTyrAsnVal-LeuLeuValLeuGluThrTy rHisAspProLysThrCysSerPheGlnGluGlyArgValLysLeuProGlu 601 196 0 2 0 Conservative: Mismatches: Indels: Gaps: Length: Matches: US-09-964-956-13 (1-1896) x AAS00023 (1-601) 4.52e-113 124.00 98.99% 98.99% 6.548 Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: 582 642 421 662 682 543 602 301 622 481 Match: Score: Query g ò pp ò qq Óγ g δy D ò Db ò QQ δ QQ δ q ò

Human; cytokine; cell proliferation; cell differentiation; growth factor; hematcopolasis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematcopoletic disorder; proliferation; cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiaethmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss. SEQ ID NO:773. Human NOV/plexin-Al homologue-encoding cDNA, BP. ABA08997 standard; cDNA; 1088 RT; 03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875. 05-FEE-2001; 2001WO-US03800. (first entry) Pang YT, Liu C, Drmanac WPI; 2001-457740/49. (HYSE-) HYSEQ INC 40200157188-A2. Homo sapiens. 11-JAN-2002 ABA08997 

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer

P-PSDB; ABB11753

61

Claim 1; Page 688; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides of bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities; including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; chamucompodulatory activity; tissue growth activity; immunomodulatory activity; tissue growth activity; chamucotic or chemokinetic activities; hammostatic, thrombotic or thrombolycic activities; nemestation or metastasis.

Conditions, eq., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (eq., myphoid cell cancers, haematopoletic disorders (eq., myphoid cell cancers), chronic inflammatory conditions (eq., nyphoid cell cancers, haematopoletic disorders (eq., myphoid cell cancers, haematopoletic disorders (eq., myphoid cell cancers, haematopoletic disorders (eq., myphoid cell cancers, haematopoletic disorders (eq., myphoid cell cancers, haematopoletic disorders (eq., myphoid cell cancers, haematopoletic disorders), conditions (eq., asthma or arthritis), proliferative retinopathy, atherosclerosis, cononary heart disease,

480

540

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622

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1704
                                                                                                                                                                                                                                                                                                                                                                                            ArgGlySerAlaLeuProLeuAlaIleLysTyrMetPheAspPheLeuAspGluGlnAla 1724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            938
                                                                                                                                              nucleotides
arterial ischaëmia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give ilse to neuroepithalial cells
                                                                                                                                that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotid may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1685 LysGlyThrLeuGlnLysPheValAspAspLeuPheGluThrIlePheSerThrAlaHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                      Sequence 1088 BP; 256 A; 339 C; 310 G; 183 T; 0 other;
                                                                                                                                                                                                                                                               1088
63
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Mismatches:
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Matches:
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63.00
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                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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P-PSDB; ABG04107
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes. (C polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping are also used in diagnostics as expressed sequence tags (C for identifying expressed genes. (I) is useful in gene therapy techniques (C for identifying expressed genes. (I) is useful for generating antibodies against it, detecting or canditating a polypeptide in tissue, as molecular weight markers and as (II). (II) is useful for generating antibodies against it, detecting or canditating a polypeptide in tissue, as molecular weight markers and as following a polypeptide and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical casorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cand to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human cannot be acquences of the invention.

Consideration, but was obtained in electronic format directly from WIPO cannot the product of the format directly from WIPO cannot contact this parent diagnostic contact.
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       useful in
of mutations
           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 477 BP; 108 A; 123 C; 128 G; 118 T; 0 other;
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genee. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the printed diagnostic soft sensits, of sensits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Coming acid sequences AAS6419-AAS4564 represent novel human diagnostic coding sequences of the invention.

Consideration but was obtained in electronic format directly from WIPO
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Matches:
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Best Local Similarity:
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WO200175067-A2
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23-AUG-2000;
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample condition genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compression levels of particular genes (AB19910 to AB19912, encoding expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1785 SerGluHisArgLeuGlyLysAspSerProSerAsnLysLeuLeuTyrAlaLysAspIle
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                                                                                                                                Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease;
                                                                 Mouse ischaemic condition related cDNA sequence SEQ ID NO:479
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.37e-39
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishikawa K, Asai S,
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P-PSD3; ABB57196.
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07-MAR-2002
                                                                                                                                                                                                                                 Mus musculus
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5431 ATAAAGTACATGTTTGATTTTCTTGAC 5457
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                                                                     AAH03972;
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                        RESULT 14
                                    AAH03972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                     5430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                       Drosophila, devėlopmental biology; cell signalling; insecticide;
                                                                                                                               Drosophila melanogaster genomic polynucleotide SEQ ID NO 3268
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 3268; 21pp + Sequence Listing; English.
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Mismatches:
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                                                           ABL17265 standard; DNA; 6382
                                                                                                                                                                                                                                                                                    2000US-191637P.
2000US-0614150.
                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                     pharmaceutical; gene; ds
                                                                                                                                                                                           Drosophila melanogaster.
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11-JUL-2000;
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                                                                                 ABL17265;
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Query Match:
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polynucleotide which comprises a 3'-end sequence, where the polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB02446 to AAH13639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represent oligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                                                                                               Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto J;
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A, Nagai K,
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T, Wakamatsu
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AAH03972 standard; cDNA; 768
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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                                                                                                                       SerIleThrAspAlaCysLeuSerValValAlaGlnThrPheMetAspSerCysSerThr 1784
                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                            234 AGCATCACGGACGCCTCTCTGTGGTGGCCCAGACCTTCATGGACTCTTGTTCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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A, Nagai K,
Gaps:
                             US-09-964-956-13 (1-1896) x AAH03972 (1-768)
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Sugiyama T, Wakamats
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH18742 represent human cDNA sequences; AAB92446 to AAH19632 AAB95893 represent human amino acid sequences; and AAH13639 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                           0 other;
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                                                              of the present invention.
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Best Local Similarity:
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APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
ELLING DATE: October 26, 1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09181706
Patent No. 6130068
GENERAL INFORMATION:
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Robert F. DuBose, Richard S. Johnson
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/958,598 (converted APPLICATION NUMBER: Provisional, see below) FILING DATE: October 28, 1997
US-08-606-322-1
US-09-399-913-31
US-09-399-913-31
US-08-056-200-93
US-08-06-44-93
US-08-627-845-10
US-08-627-845-10
US-08-627-845-10
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US-08-627-845-10
US-08-627-845-10
US-08-627-845-10
US-09-107-109A-3
US-08-68-3-10-277-36-3
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US-09-635-65-30
US-09-585-65-10-10-278-3
US-09-585-65-10-10-278-3
US-09-585-65-10-278-3
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US-08-585-65-10-278-3
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JS-09-605-785-411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  October 28, 1998
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51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTu3_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTu3_COMB.seq:*
                      version 5.1.6
- 2003 Compugen Ltd.
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US-09-459-066-1
US-09-227-357-54
US-09-228-274A-17
US-08-663-310-12
US-09-066-491-12
US-09-335-912
US-08-906-743-1
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US-09-298-731-39
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Maximum DB seq length: 200000000
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1896
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Match
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Database :

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Patent No. 6174689
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
AITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/458,791
FILING DATE: 10-Dec-1999
CLASSIFICATION: <Unknown>
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    APPLICATION NUMBER: 08/958,598
    FILING DATE: 28-007-1997
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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TELEFAX: (206)233-6644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4707 base pairs
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ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                   NAME: Henry, Janis C
REGISTRATION UNBER: 34,347
REFRENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)203-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
100.00%
0.53%
                                                                                                                                                                      LENGTH: 4707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO FEATURE:
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LOCATION:
US-09-181-706-1
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GENERAL INFORMATION:
APPLICANT: Sprigs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
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Mismatches:
Indels:
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Matches:
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/459,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09459066
Patent No. 6187909
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TELECOMMUNICATION INFORMATION
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Janis C. Henry
51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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100.00%
100.00%
0.53%
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EDNESS: double
                                                                                                               NAME/KEY: CDS
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MEDIUM TYPE: 'Floppy
                                                                 HYPOTHETICAL: NO ANTI-SENSE: NO
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Query Match:
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LOCATION:
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FEATURE:
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US-09-459-066-1
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DATE: 1997-08-18

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APPLICANT: Hess, Allan D.
TITLE OF INVENTION: Specificity of Effector T Lymphocytes
TITLE OF INVENTION: inautologous Graft-vs-Host Disease: Role for the MHC Class
TITLE OF INVENTION: inautologous Graft-vs-Host Disease: Role for the MHC Class
TITLE OF INVENTION: In Invariant Chain Peptide
FILE REFERENCE: 01107.73711
CURRENT APPLICATION NUMBER: US-09/028,274A
PRIOR APPLICATION NUMBER: 60/039,032
PRIOR FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEO for Windows Version 3.0

LENGTH: 1353 TYPE: DNA ORGANISM: Rattus rattus

SOFTWARE: 1 SEQ ID NO 17

Sequence 17, Application US/09028274A Patent No. 6326465

JS-09-028-274A-17

GENERAL INFORMATION: APPLICANT: Hess, A

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Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER PILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
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LOCATICN: (1208)
OTHER INFORMATION: n equals a, L, g, or c
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n equals a, L, g, or c
                    FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/056,360
                                                                              EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
60/055,964
                                                               DATE: 1997-08-18
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8.00
100.00$
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0.42$
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver.
SEQ ID NO 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
LOCATION: (1197)
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NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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APPLICANT: MISSARA, NO. 59726901hiko
APPLICANT: KONDO, Keiji
APPLICANT: KAJTWARA, Susumu
APPLICANT: YOKOYAMA, AKIhiro
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/006,491
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Matches:
Conservative:
                                                                                                 US-09-964-956-13 (1-1896) x US-08-663-310-12 (1-1631)
     Conservative:
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                       Mismatches:
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3000 K Street, N.W., Suite 500
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                                           Indels:
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US 08/663,310
FILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
                                                                                                                                     1422 HisProLysLeuLeuLeuArgArg 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 4941/109
TELECOMMUNICATION INFORMATION:
                                                                                                                                                        101 CATCGGAAACTCCTGCTGCGTAGG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTONINY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                ; Sequence 12, Application US/09006491
; Patent No. 5972690
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TELEFAX: (
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STATE:
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                                                                                                                                                                                                                  RESULT 7
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                                                                                                                                          δλ
                                                                                                                                                                            Db
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MISAMA, NO. 58112731hiko
APPLICANT: KONDO, Keiji
APPLICANT: KAJIWARA, SUSUMU
APPLICANT: YOKOYAMA, Akihiro
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSOR
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                                                                                                                                                                                                  US-09-964-956-13 (1-1896) x US-09-028-274A-17 (1-1353)
                                                                                                       Conservative:
                                                                                                                         Mismatches:
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FILING DATE: 23-SEP-1996
FILING DATE: 23-SEP-1996
FILING DATE: 25-SEP-1996
FILING DATE: 26-DEC-1994
FILING DATE: 26-DEC-1994
FILING DATE: 26-DEC-1994
FILING DATE: 26-DEC-1994
FILING DATE: 26-DEC-1994
FILING DATE: D5-SEP-1994
FILING DATE: D5-SEP-1994
FILING DATE: D5-SEP-1994
FILING DATE: 27-DEC-1993
ATTORNEY AGENT INFORMATION:
NAME: BENY: Stephen A.
RESERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELLOCOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                 Length:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08663310 Patent No. 5811273 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 12:
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                                                                                                                                        0.428
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8.00
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EDNESS: double
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20007-51:09
                                                                                                     Percent Similarity:
Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-663-310-12
         JS-09-028-274A-17
                                               Alignment Scores:
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                                                                                                                                              Query Match
                                                                   No.
                                                                                                                                                                                                                                                                                                                   RESULT 6
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Gaps:

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GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: MOLECULES ENCODING HUMAN ENZYME, AND USES THEREOF
TITLE OF INVENTION: MOLECULES ENCODING HUMAN ENZYME, AND USES THEREOF
FILE REFERENCE: CL001181
CURRENT APPLICATION NUMBER: US/09/816,088
                                                                                                                                                                                                                                                                                                                                          SUFTWARE: FASTEM: DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,743
FILING DATE: 06-AUG-1997
PRIOR APPLICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                       ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                        No. 6232097el args
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1422 HisProLysLeuLeuLeuArgArg 1429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9619071.5
FILING DATE: 12-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09816088 Patent No. 6326180
                                                                                                  : Sequence 1, Application US/08906743
: Patent No. 6232097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
                                                                                                                                                 APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6232(
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                    COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1692 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.42%
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                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                             USA
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                                                                                  US-08-906-743-1/c
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                                                                                                                                                                                                                                  APPLICANT: KAJIWARA, Susumu
APPLICANT: KAJIWARA, Susumu
APPLICANT: YOKOYAMA, Akihiro
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,919
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Mismatches:
Indels:
              US-09-964-956-13 (1-1896) x US-09-006-491-12 (1-1631)
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Matches:
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3000 K Street, N.W., Suite 500
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                                              1422 HisProLysLeuLeuLeuArgArg 1429
                                                                                                                                                   Sequence 12, Application US/09335919
Patent No. 6150130
GENERAL INFORMATION:
APPLICANT: MISAWA, NO. 6150130ihiko
APPLICANT: KONDO, Keiji
                                                                  101 CATCCGAAACTCCTGCTGCGTAGG 78
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
...MYTH: 1631 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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EDNESS: double
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Query Match:
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                                                                                                                 RESULT 8
US-09-335-919-12/c
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US-09-335-919-12
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Sequence 39, Application US/09298731

Patent No. 6369197

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMY: KENNETH HODES, MARIA BETTY, HUAI-PING LING, AND FRANK AN TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR FILE REFERENCE: MNI-070
CURRENT APPLICATION NUMBER: US/09/298,731
CURRENT FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 47
SOGTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Crueger, Anneliese; Piepersberg,
APPLICANT: Wolfgang; Distler, Jurgen; and
APPLICANT: Stratmann, Ansgar
APPLICANT: Stratmann, AGRABOSE BIOSYNTHESIS GENES FROM
TITLE OF INVENTION: ACTINOPLANES Sp., PROCESS FOR THE ISOLATION
TITLE OF INVENTION: THEREOF AND THE USE THEREOF
NUMBER OF SEQUENCES:
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Matches:
Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE-DOCKET NUMBER: Bayer 9537-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SPRUNG HORN KRAMER & WOODS STREET: 660 White Plains Road CITY: Tarrytown STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 07 214.6
FILING DATE: 02-MAR-1995
ATTORNEY/AGENT INFORMATION:
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23-FEB-1996
N: 435
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Patent No. 5753501
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OPERATING SYSTEM: DOS
SOFTWARE: WORDERfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
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100.00%
0.42%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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                                                                                                                                                                                                                                            SEQ ID NO 39
LENGTH: 2176
                  US-09-298-731-39
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TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR FILE REPERENCE: MNI-070CP2
CURRENT APPLICATION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR CURRENT APPLICATION NUMBER: US/09/399,913
CURRENT FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: USSN 60/110,277
EARLIER FILING DATE: 1998-11-30
EARLIER FILING DATE: 1998-11-20
EARLIER FILING DATE: 1998-11-20
EARLIER FILING DATE: 1998-11-20
EARLIER FILING DATE: 1999-04-23
EARLIER FILING DATE: 1999-04-23
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: USSN 09/350,614
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER PILING DATE: 1999-07-09
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Matches:
Conservative:
Mismatches:
Indels:
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Indels:
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Matches:
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2071
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Patent No. 6361971
GENERAL INFORMATION:
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APPLICANT: Betty, Maria
APPLICANT: Ling, Huai-Ping
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US-09-399-913-39
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Best Local Similarity:
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                                                                                                          TYPE: DNA
CRGANISM: Human
US-09-816-088-1
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SEQ ID NO 39
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US-09-964-956-13 (1-1896) x US-09-399-913-31 (1-2841)

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Sequence 128, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE:
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Mismatches:
Indels:
Gaps:
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OPERATING SYSTEM: Windows
SOFTWARE: FSSESSO for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE: 23-DEC-1998
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Matches:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA: PP2911
FILING DATE: 01-DEC-1998
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMÁTION:
TELEPHONE: 650-813-5600
TELEFANIOR FOR SEO ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEO ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGRATI HONDER: ACTERISTICS:
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LENGRATI HONDER: A
                                                                            ORGANISM: PORYPHYROMONAS GINGIVALIS
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STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
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HYPOTHETICAL: NO
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LOCATION: 1...4605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Percent Similarity:
Best Local Similarity:
Query Match:
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TOPOLOGY: cir
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Patent No. 6361971

General Information:

APPLICANT: Rhodes, Kenneth
APPLICANT: Ling, Heal-Ping
APPLICANT: Ling, Heal-Ping
APPLICANT: Ling, Heal-Ping
APPLICANT: Ling, Heal-Ping
APPLICANT: Ling, Heal-Ping
APPLICANT: Ling, Heal-Ping
APPLICANT: MI-OFOCP2
CURRENT APPLICATION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
FILE REFERENCE: MNI-OFOCP2
CURRENT APPLICATION NUMBER: US/09/399,913
CURRENT APPLICATION NUMBER: US/N 60/110,277
EARLIER PILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: US/N 60/110,33
EARLIER APPLICATION NUMBER: US/N 60/109,333
EARLIER APPLICATION NUMBER: US/N 60/109,333
EARLIER APPLICATION NUMBER: US/N 60/209
EARLIER PILING DATE: 1998-11-20
EARLIER APPLICATION NUMBER: US/N 69/250,614
EARLIER APPLICATION NUMBER: US/N 69/350,614
EARLIER APPLICATION NUMBER: US/N 69/350,874
EARLIER APPLICATION NUMBER: US/N 69/350,874
EARLIER PILING DATE: 1999-07-09
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ORGANISM: Actinoplanes sp. SE 50/110
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SEQUENCE CHARACTERISTICS:
LENGTH: 2219 Nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                     TOPOLOGY: Linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: No
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TELEFAX: (914) 332-1844
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LENGTH: 2841
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US-09-964-956-13 (1-1896) x US-09-221-017B-128 (1-4605)

Qγ Op

Search completed: June 29, 2003, 00:02:38 Job time: 293 secs:

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APPLICANT: Sulley, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Chang, Zemin
APPLICANT: Eng, Sherman
APPLICANT: Eng, Sherman
APPLICANT: Eng, Sherman
APPLICANT: Eng, Sherman
APPLICANT: Eng, Sherman
APPLICANT: Eng, Sherman
APPLICANT: Eng, Sherman
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT FILING DATE: 2002-09-17
PRIOR PLILING DATE: 2002-07-18
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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US-10-245-883-91
US-10-248-393-91
US-10-238-183-91
US-10-248-375-91
US-10-248-375-91
US-10-248-379-91
US-10-248-379-91
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US-10-247-448-91
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean Phillippe
Watanbe, Colin
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  APPLICANT: Baker, Kevin
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  US-10-245-103-91
  APPLICANT:
APPLICANT:
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-MODEL-frame+ p2n.model -DEV=Xlh
-MODEL-frame+ p2n.model -DEV=Xlh
-Q=/cgn2_1/USPTQ-ppcol/USO9964956/runat_24062003_124832_7501/app_query.fasta_11.2055
-Q=/cgn2_1/USPTQ-spool/USO9964956/runat_24062003_124832_7501/app_query.fasta_11.2055
-DB=Published_Applications_NA -OFMT=fastap -SUFFIX=01i.rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNTS=bits -START=1 -END=-1 -MATRIX=01igo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-quality -THR_MIN=1
-MALGN=15 -MODE=CAGAL -OUTFMT-Pto -NORM-ext -HRAPSIZE=500 -MINLEN-0
-MAXLEN=200000000 -USER=US09564956_GCGN_1_1_376_qcunat_24062003_124832_7501
-NCPU=6 -ICDPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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US-10-245-771-91
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ORGANISM: Homo Sapien
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PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-03
PRIOR PELICATION NUMBER: 60/089801
PRIOR PELICATION NUMBER: 60/09057
PRIOR PELICATION NUMBER: 60/090587
PRIOR PELICATION NUMBER: 60/090689
PRIOR PAPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09089
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                 APPLICATION NUMBER: 60/065027
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ORGANISM: Homo Sapien
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APPLICANT: Abracancy William
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Shong, Sharman
TTTLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPREBENCE: PASORARCTI
CURRENT APPLICATION NUMBER: 10/197942
PRIOR PAPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-24
PRIOR PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/08699
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-18
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 116
SEQ ID NO 91
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Matches:
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
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Sequence 91, Application US/10245107
Publication No. US20030068779A1
GENERAL INFORMATION:
APPLICANT: Baker. Kevin
APPLICANT: Eaton, Dan
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Mismatches:
Indels:
                                                         CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US/10/245,143
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-01-18
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PRIOR APPLICATION NUMBER: 60/05027
PRIOR PLING DATE: 1997-11-10
PRIOR PLING DATE: 1997-11-10
PRIOR PELLING DATE: 1998-03-27
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-18
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Matches:
             APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRAI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C90
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Best Local Similarity:
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ORGANISM: Homo
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                                                                                                                             PheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAsnPhe
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Wood, William
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Publication No. US20030068780A1
GENERAL INFORMATION:
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AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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TyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAsp
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Best Local Similarity:
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US-10-245-851-91
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LENGTH: 2597
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APPLICANT: Zanang, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILLE OF INVENTION: ACIDS ENCODING THE SAME

FILLE PREFERENCE: P3630R1038

CURRENT FILING DATE: 2002-09-16

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-10-14

PRIOR PLICATION NUMBER: 60/065027

PRIOR FILING DATE: 1997-11-10

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-06-22

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-22

PRIOR FILING DATE: 1998-06-22

PRIOR FILING DATE: 1998-06-22

PRIOR FILING DATE: 1998-06-22

PRIOR FILING DATE: 1998-06-22

PRIOR FILING DATE: 1998-06-22
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SEQ ID NO 91
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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APPLICANT: FONG, STREMMAN

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE PS 300 RG/OF

CURRENT APPLICATION NUMBER: US/10/245,883

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: (0/197942

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-10-24

PRIOR PRIOR FILING DATE: 1997-10-24

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PRIOR FILING DATE: 1997-10-24
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                                                                                         ValGluValProlleGlyCysGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAla
                    GlnValTyrThrSerLysLeuValArgLeuCysLysGluAspThrAlaPheAsnSerTyr
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Gurney,Austin
Smith,Victoria
Stephan,Jean-Phillippe
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Filvaroff, Ellen
Goddard, Audrey
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Suith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Abang, Zemin
APPLICANT: Pong, Sherman
APPLICANT: Pong, Sherman
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFREENCE: PASIORICS3
CURRENT APPLICATION NUMBER: US/10/245,851
PRIOR APPLICATION NUMBER: 10/197942
PRIOR PRILING DATE: 2002-09-16
PRIOR PRILING DATE: 1997-09-16
PRIOR FILING DATE: 1997-00-24
PRIOR FILING DATE: 1997-10-10
PRIOR FILING DATE: 1999-10-24
PRIOR FILING DATE: 1999-10-24
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-06-27
PRIOR FILING DATE: 1999-06-18
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PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-24
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Mismatches:
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Matches:
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean Phillippe
Watanbe, Colin
Application US/10245851
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              Publication No. US20030068782A1
GENERAL INFORMATION:
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APPLICANT: Eaton, Dan
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Best Local Similarity:
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APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C3
CURRENT PAPLICATION NUMBER: US/10/237,535
CURRENT FILING DATE: 2002-09-06
PRIOR FILING DATE: 1000-07-18
PRIOR APPLICATION NUMBER: 60/05914
PRIOR PAPLICATION NUMBER: 60/05914
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-10
PRIOR PAPLICATION NUMBER: 60/05027
PRIOR PAPLICATION NUMBER: 60/05027
PRIOR PAPLICATION NUMBER: 60/065027
PRIOR PAPLICATION NUMBER: 60/0809
PRIOR PILING DATE: 1998-05-22
PRIOR PAPLICATION NUMBER: 60/080901
PRIOR PAPLICATION NUMBER: 60/080901
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PRIOR PAPLICATION NUMBER: 60/080901
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PRIOR PAPLICATION NUMBER: 60/090059
                                          PRIOR APPLICATION NUMBER: 60/091978
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-09-10
PRIOR PELING DATE: 1998-10-03
PRIOR PELING DATE: 1998-11-03
PRIOR PAPLICATION NUMBER: 60/11554
PRIOR FILING DATE: 1999-01-12
PRIOR PELING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR PELING DATE: 1999-02-09
PRIOR PELING DATE: 1999-03-07
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PRIOR PELING DATE: 1999-03-12
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FILING DATE: 1999-03-11
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FILING DATE: 1999-04-01
APPLICATION NUMBER: 60/131271
FILING DATE: 1999-04-27
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                                                                                                                                                                                               Sequence 91, Application US/10237535 Publication No. US20030073188A1 GENERAL INFORMATION:
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
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Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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FILING DATE: 1998-07
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PRIOR FILING DATE: 1998-06-18
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|-------------|------------|---------|----------|--------------|-------------------|----------|-------------|--------------|----------|-------|----------|--------------|-------|---------|----------|---------|--------|-------|----------|-----------|---------|--------|--------|-------|-------|-----------|--------|---------|--------|---------|----------|------------|----------|---------|----------|------------|---------|------------|-------------------|--------------|---------|------------|
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274 GlnValTyrThrSerLysLeuValArgLeuCysLysGluAspThrAlaPheAsnSerTyr 293

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TyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAsp
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Conservative:
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         PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
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Query Match:
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LENGTH: 25
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 CAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACACCCTTCAACTCCTAT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS
CURRENT FILE REFERENCE: P5630R1C15
CURRENT FILNG DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
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PRIOR APPLICATION NUMBER: 60/063046
PRIOR FLING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PELING DATE: 1997-11-10
PRIOR PEPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean Phillippe
Watanbe, Colin
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APPLICATION NUMBER: 60/08478
FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/087607
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Publication No. US20030073190A1
GENERAL INFORMATION:
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
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Zhang, Zemin
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LeuLeuPheThrValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGluSer 353
                                                                                                                 ValTyrPheLeuThrLeuGlnProGluMetValSerProProGlySerThrLysGlu 273
                                                                                                                                                                                                                                                                                                               TyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAsp 333
                                                                                                                                                                                                                                                                                                                              SerSerAlaLeuLeuThrIleAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeu 413
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                                                                                                                                                                                                                                                                                                                                                                                                           CTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTCG 481
     CysTyrArgGlyGluGlyThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCys
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APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/10/245,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 91, Application US/10245055; Publication No. US20030073192A1; GENERAL INFORMATION:
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Gurney,Austin
Smith,Victoria
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Watanbe, Colin
Wood, William
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CURRENT FILING DATE: 2002-0
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Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457
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APPLICANT: Eaton, Dan
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APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Lang, Zemin
APPLICANT: Rood, William
APPLICANT: Chang, Zemin
APPLICANT: Pong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1010
CURRENT APPLICATION NUMBER: US/10/238,370
CURRENT PILLING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/059114
PRIOR PILLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/06699
PRIOR FILING DATE: 1998-01-02-4
PRIOR PILLING DATE: 1998-01-02-4
PRIOR PILLING DATE: 1998-01-02-4
PRIOR PILLING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/0869
PRIOR PILLING DATE: 1998-06-18
PRIOR PILLING DATE: 1998-06-18
PRIOR PILLING DATE: 1998-06-18
PRIOR PILLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/0809
PRIOR PILLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/0809
PRIOR PILLING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/0809
PRIOR PILLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/0809
PRIOR PILLING DATE: 1998-06-24
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PRIOR PILLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/0809
PRIOR PILLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/0809
PRIOR PILLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/0809
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PRIOR APPLICATION NUMBER: 60/09069
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                             Sequence 91, Application US/10238370 Publication No. US20030073191A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                         Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
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Filvaroff, Ellen
                                                               LysLeuLysLys 457
                                                                                               AAGCTGAAGAAG 793
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US-10-238-370-91
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APPLICANT: Zhang Zemin
APPLICANT: ENDOG, WILLIAM
APPLICANT: ENDG, Sherman
APPLICANT: FONG, Sherman
APPLICANT: FONG, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C72
CURRENT APPLICATION NUMBER: US/10/245,147
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/06314
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/0669
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR PRILICATION NUMBER: 60/090657
PRIOR PRILICATION NUMBER: 60/090657
PRIOR PRILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-18
                                                                                                                                           434 SerValIleAlaTyrValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGly 453
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                      PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 116
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 91, Application US/10245147 Publication No. US20030073193A1
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Grimaldi, J. Christopher
Gurney, Austin
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Stephan, Jean-Phillippe
Watanbe, Colin
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APPLICANT: Eaton,Dan
APPLICANT: Filvaroff,Ellen
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; ORGANISM: Homo Sapien
US-10-245-147-91
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LENGTH: 2597
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APPLICANT:
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Matches:
Conservative:
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PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 1097-09-17
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/08649
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086769
PRIOR FILING DATE: 1998-06-02
PRIOR PRIOR DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
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ORGANISM: Homo Sapien
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Best Local Similarity:
Query Match:
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                                          US-09-964-956-13 (1-1896) x US-10-245-147-91 (1-2597)
 Matches:
                      Indels:
                             Gaps:
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; Publication No. US20030073194A1
; GENERAL INFORMATION:
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13.92%
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
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      Percent Similarity:
Best Local Similarity:
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APPLICANT: ADARQ, SHERMAN
APPLICANT: ADARQ, SHERMAN
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C85
CURRENT APPLICATION NUMBER: US/10/245,730
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: (0/059114
PRIOR APPLICATION NUMBER: 60/065014
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-25
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Grimaldi,J. Christopher
             Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
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Zhang, Zemin
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                                Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 116
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PRIOR FILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/C PRIOR FILING DATE: 1998-06-25
                                                                                        ORGANISM: Homo Sapien
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Query Match:
                                                      SEQ ID NO 91
LENGTH: 2597
TYPE: DNA
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                        TyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAsp
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCL
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3630R1068
CURRENT APPLICATION NUMBER: U5/10/245,739
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 06/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-10
PRIOR PLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1998-10-24
PRIOR FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-05-23
PRIOR FILING DATE: 1998-05-23
PRIOR FILING DATE: 1998-05-23
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR PULICATION NUMBER: 60/089801
PRIOR PULICATION NUMBER: 60/089801
PRIOR PULICATION NUMBER: 60/089801
PRIOR PULING DATE: 1998-06-18
PRIOR PULING DATE: 1998-06-18
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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Filvaroff, Ellen
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Fong, Sherman
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, E
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Search completed: June 29, 2003, 03:19:12 Job time : 640 secs
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C121

CURRENT APPLICATION NUMBER: US/10/246,210

CURRENT FILING DATE: 2002-09-18

PRIOR APPLICATION NUMBER: 60/06314

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-05-22

PRIOR FILING DATE: 1998-06-02

PRIOR FILING DATE: 1998-06-02

PRIOR FILING DATE: 1998-06-18

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PRIOR FILING DATE: 1998-06-18

PRIOR PRIOR DATE: 1998-06-25

PRIOR FILING DATE: 1998-06-25

PRIOR PRIOR DATE: 1998-06-25
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                                                                                                                                                                               Filvaroff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
                                                                                                 Sequence 91, Application US/10246210 Publication No. US20030073196A1 GENERAL INFORMATION:
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454 LysLeuLysLys 457
                    Watanbe,Colin
Wood,William
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Fong, Sherman
                                                                                                                                                  APPLICANT: Baker, Kevin
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ValTyrPheLeuThrLeuGlnProGluMetValSerProProGlySerThrThrLysGlu
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| Scoring table:                        | OLIGO Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 60.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0 |
| Searched:                             | 16154066 seqs, 8097743376 residues   |
| Word size:                            |  |

Total number of hits satisfying chosen parameters:

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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-O=/CQM_21/USPPO_spool/USO9964956/runat_24062003_124829_7368/app_query.fasta_1.2055
-DB=EST -OFMT=fastap -SUFIX=oli.rst -MINATCH=0.1 -LOOPCL=0 -LOOPCXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
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627 bp mRNA linear EST 26-JAN-2001 H3123F01-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3123F01 5', mRNA sequence. Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 627)
Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka, T.S., Carter, M.G. and Ko, M.S.H. BG086250.1 GI:12568814 house mouse. LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION REFERENCE AUTHORS RESULT 1 BG086250

ALIGNMENTS

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Percent Similarity:
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Query Match:
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and E1.5 female mesonephrosygonad) and one newborn ovary CDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT). Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryousing a 15,000 mouse developmental CDNA microarray, 2000, proc. Nall. Acad. Sci. U S A, 97: 9127.9132; (2)
Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcribts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978.
                                                                                          National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnadlgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3123 row: F column: 01
Seq primer: -21M13 Reverse
High quality sequence stop: 627
POLYA-NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1672 MetValSerGluIleTyrLeuThrArgLeuLeuAlaThrLysGlyThrLeuGlnLysPhe 1691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1692 ValAspAspLeuPheGluThrIlePheSerThrAlaHisArgGlySerAlaLeuProLeu 1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jerification and initial annotation of NIA mouse 15K cDNA clone set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1652 TrpHisLeuValLysAsnHisGluHisGlyAspGlnLysGluGlyAspArgGlySerLys 1671
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                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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Gaps:
                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'lab_host="DH10B"
                                                        Contact: George J. Kargul
Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                         /clone="H3123F01"
                    Unpublished (2001)
Other_ESTs: H3123F01-3
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TITLE
JOURNAL
COMMENT
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483 bp mRNA linear EST 22-MAR-2002 DKF22666H2349_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone AL707761
                                                                                     1771
                                                                                                                                                                                1772 SerValValAlaGlnThrPheMetAspSerCysSerThrSerGluHisArgLeuGlyLys 1791
                                                                                                                                                                                                                                                                     1812 GluArgTyrTyrSerAspIleGlyLysMetProAlaIleSerAspGlnAspMetAsnAla 1831
                                                                                                                                  390
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                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 483)
Mambutt, R., Heubner, D., Mewes, W., Weil, B. and Wiemann, S.
EST (Mambutt, R., Heubner, D., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1832 TyrLeuAlaGluGlnSerArgMetHisMetAsnGluPheAsnThrMetSerAlaLeu 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email S.wiemann@dkfz- heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berlin.
6, 14059
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1732 ProHisValArgHisThrTrpLysSerAsnCysLeuProLeuArgPheTrpValAsnMet
                     1752 IleLysAsnProGlnPheValPheAspIleHisLysAsnSerIleThrAspAlaCysLeu
                                                                                                               This clone (DKFZp686H2349) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerveg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     483
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/dev_stage="adult"
/lab_host="DH10B"
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/clone_lib="686 (synonym: hlcc3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
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Matches:
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/db_xref="taxon:9606"
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Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 512)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValGlyLysTyrSerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysGlyLys 1876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxoc.ugus."
/db_xref="taxoc.ugus."
/clone_lib="%ARC 3BOV"
/clone_lib="%ARC 3BOV"
/tssue_type="pooled"
/lab_host="mil0B"
/note="vector: pCMV SPORT6; Site_l: NotI; Site_2: SalI;
/ibrary made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle.

a 188 c 134 g 106 t
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V2V-NN0229-101100-445-e08 NN0229 Homo sapiens cDNA, mRNA sequence.
BF952116.1 GI:12369391
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Mismatches:
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1. .567
/organism="Bos taurus"
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Best Local Similarity:
Query Match:
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1 (base; Losfo)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casass,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                       GluValIleLysProlleThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyGln 734
                                                                                                                                                                                                                                   ArgGlyTyrGluCysIleLeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArg 754
                                                                                                                                                                                                                                                                                       PheAsnSerSerValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIle 774
                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaGlnAsnLysValHisLeuTyrLysCysGlyAlaMetArgGluSerCysGlyLeuCys 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuLysAlaAspProAspPheAlaCysGlyTrpCysGlnGlyProGlyGlnCysThrLeu 834
                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               normalized bovine cDNA
                                                                Sequence evaluation of four pooled-tissue normalized the libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM105323 567 bp mRNA linear 208753 MARC 3BOY Bos taurus cDNA 5', mRNA sequence. BM105323.1 GI:17036393
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
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Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 3 BM105323

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ORGANISM

REFERENCE AUTHORS JOURNAL MEDLINE COMMENT

TITLE

FEATURES

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                                                                                                                                      Simpson, A.J.
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Query Match:
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                                                             AUTHORS
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/db_xref="taxon:9606"

/clone_lib="NN0229"

/dev_stage="Adult"

/note="Organ: nervous_normal; Vector: pucl8; Site_1: SmaI;

/site_2: SmaI; A mini-library was made by .cloning products
derived from ORESTES PCR (U.S. Letters Patent application
,No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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                                                                                                  Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-NN0229-101100-445-e08&t3=2000-11-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 512.
Location/Qualifiers
I. 1512.
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/_oote=_oogan: nervous_normal; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ONESTBE PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                               Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Balia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 564)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=QV3&t2=QV3-NN0198-III100-373-h10&t3=2000-11-11&t4=1)
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence stop: 556.
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIXEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-171 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . Il (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                   BB656076 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130060F15 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bmail: genome_res@gsc.riken.go.jp,
URL:http://genome_gsc.riken.go.jp/
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.w., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Schences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/note="Site_1: SalI; Site_2: BamHI; cDNA library was
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/lab_host="DH10B"
                                                  ValGlnThrCysAsnGluProLeuThr 109
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/db_xref="taxon:10090"
/clone="D130060F15"
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Contact: Yoshihide Hayashizaki
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Hayashizaki,Y.
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                                                                                        CDNA was
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                                                         contributed to prepare mouse tissues. 1st strand cDNA was
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            Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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232 bp mRNA linear EST 24-SEP-1999
7B44B08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA
AA077700
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//dev_stage="pool of 9 week and 12 week"
//dev_stages="pool of coli strain DH5 alpha"
//note="Organ: brain: Vector: pAWP10; cDNA was generated
from cytoplasmic RNA using a mixture of random DNA
hexamers and oligo(dT). From this pool of cDNA, human
chromosome 7-enriched cDNA was isolated by direct cDNA
selection using chromosome 7 genomic DNA (cosmids)... The
resulting direct-selected cDNA was cloned into a plasmid
vector using a non-directional uracil DNA glycosylase (UDG
)-mediated cloning strategy."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
Tel: 3014020201
                                                    182 CGAGCAGTCGCGGATGCACATGAATGAGTTCAATACGATGAGTGCGCTCTCAGAGATCTT 241
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 232)

Touchman,J.W., Bouffard,G.G., Weintraub,L.A., Idol,J.R., Wang,L.,

Robbins,C.W., Nussbaum,J.C., Lovett,M. and Green,B.D.

2006 expressed-sequence tags derived from human chromosome

7-enriched cDNA libraries

Genome Res. 7 (3), 281-292 (1997)
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/organism="Homo sapiens"
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/clone="7B44808"
/clone="7B44808"
/sex="female and male mixture"
/tissue_type="brain"
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Fax: 3014024735
Email: egreen@hgri.nih.gov
Plate: 44 row: B column: 08
Seg primer: -ZlM13 (ABI).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbsrc@mail.nih.gov
cDNA Library Preparation: M. Bento Soares Laboratory
cDNA Library Prayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing Center (NISC)
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
  EST 04-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Organism="Mus musculus"
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                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I Lo 41. (bases 1 to 41. ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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BG694413 412 bp mRNA linear EST 04-MAY-NISC_iv0lh04.w2 Soares NMBP2 pituitary Mus musculus cDNA clone IMAGE:4316766 5', mRNA sequence.
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Plate: LLAM9919 row: 0 column: 7
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Location/Qualifiers
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98.35$
4.06$
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Unpublished (1997)
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Clark, M. Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
Clark, M., Johnson, S.L., Lehrach, H., J., Beck, C., Wylie, T., Underwood
K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
and Wilson, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                            AW018699 548 bp mRNA linear EST 07-JUN-2001 fd49b01.yl Zebrafish WashU MPIMG EST Danio rerio CDNA clone IMAGE:3733033 5' similar to TR:Q14988 Q14988 OCT PROTEIN ;, mRNA
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GlyvalasncysThrPheGluAspLeuSerGluMetaspGlyLeuValValGlyAsnGln 609
                                                                                         649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missouri (web address: www.genomesystems.com) (email contact: Info@enomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarbatenbank, Berlin, Germany (web address:
                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: zbrafish@watson.wustl.edu
John Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
                                                                                                                                                                                                               /tissue_type="26 somite embryos, adult livers, shield stage embryos"
                                                                                                                                                                                      HisHisValValGlnLeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1998)
Other_ESTS: fd49b01.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                    SerPheValPheTyrAsnCysSerValHisAsnSerCysLeuSerCys 665
                                                                                                                                                                                                                                                                                                             /clone_lib="Zebrafish WashU MPIMG EST"
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High quality sequence stop: 498.
Location/Qualifiers
1. 548
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/clone="IMAGE:3733033"
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sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
Tel: 3014020201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Touchman, J.W., \ Bouffard, G.G., \ Weintraub, L.A., \ Idol, J.R., \ Wang, L., \ Robbins, C.M., \ Nussbaum, J.C., \ Lovett, M. \ and \ Green, E.D. \ 2006 \ expressed-sequence tags derived from human chromosome .
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing In some cases multiple members of the same cluster were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA077556 233 bp mRNA linear EST 24-SEP-17B19F10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B19F10, mRNA sequence.
AA077556 GI:1837030
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/db_xref="taxon:9606"
/clone="7B19F10"
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Plate: 19 row: F column: 10
Seq primer: -21M13 (ABI).
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Best Local Similarity:
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                    /tissue_type="brain"
/tissue_type="brain"
/dev_stage="pool of 9 week and 12 week"
/lab_host="E. coli strain DH5 alpha"
/note="brain" Vector: pAMP10; cDNA was generated
from cytoplasmic RNA using a mixture of random DNA
hexamers and oligo(dT). From this pool of cDNA, human
chromosome 7-enriched cDNA was isolated by direct cDNA
selection using chromosome 7 genomic DNA (cosmids). The
resulting direct-selected cDNA was cloned into a plasmid
vector using a non-directional uracil DNA glycosylase (UDC
)-mediated cloning strategy."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
Tel: 3014020201
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 251)

Touchman, J.W., Bouffard, G.G., Weintraub, L.A., Idol, J.R., Wang, L.,

Robbins, C.M., Nussbaum, J.C., Lovett, M. and Green, E.D.

2006 expressed-sequence tags derived from human chromosome

7-enriched cDNA libraries

Genome Res. 7 (3), 281-292 (1997)
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/clone_lib="Chromosome 7 Fetal Brain cDNA Library"
/sex="female and male mixture"
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Matches:
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Mismatches:
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Bmall: egreen@thgri.nih.gov
Plate: 19 row: H column: 10
Seg primer: -21M13 (ABI).
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Genome Technology Branch
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                                                                                                                                                                                                                                                         3.35e-63
71.00
100.00%
100.00%
3.74%
                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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//dev_stage="pool of 9 week and 12 week"
//dev_stage="pool of 9 week and 12 week"
//dev_stage="coli strain DH5 alpha"
//note="Organ: brain; Vector: pAMP10; cDNA was generated
//note="Organ: brain; Vector: pAMP10; cDNA was generated
from cytoplasmic RNA using a mixture of random DNA
hexamers and oligo(dT). From this pool of cDNA, human
chromosome 7-enriched cDNA was isolated by direct cDNA
selection using chromosome 7 genomic DNA (cosmids). The
resulting direct-selected cDNA was cloned into a plasmid
vector using a non-directional uracil DNA glycosylase (UDG
)-mediated cloning strategy."
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Betheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 493)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagai,M.A., da Silva,W. F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF953008 493 bp mRNA linear EST 22-JAN-2001 QV3-NN0198-111100-373-b07 NN0198 Homo sapiens CDNA, mRNA sequence.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Matches:
Conservative:
Mismatches:
                         /sex="female and male mixture"
/tissue_type="brain"
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/clone_lib="Chromosome
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Fax: +55-11-2707001
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                              /note="Organ: nervous_normal; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES FCR (U.S. Letters Parent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL595528 ACC-gastrula Silurana tropicalis cDNA clone TGas005n23 5', AL595528 XCC-gastrula Silurana tropicalis cDNA clone TGas005n23 5', AL59558
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-NN0198-111100-373-b07&t3=2000-11-11&t4=1)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 650)
HUCKle,E., Taylor,R., McMurray,A., Ashurst,J.L., Zorn,A.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyHisileTyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysVal
|||||||||||
|GGACACATTTA-CTTGGGGCCGTCAATCGGATTTACAAGCTCTCCAGCGACCTGAAGGTC
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Unpublished (2001)
Contact: Huckle E
Sanger Centre
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0198"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
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                                                                         Seq primer: puc 18 forward
High quality sequence stop: 493.
Location/Qualifiers
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1 (Dases 1.to 844)
NIH-MGC http://mgc.ncl.nih.gov/.
NiH-MGC http://mgc.ncl.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1685 LysGlyThrLeuGlnLysPheValAspAspLeuPheGluThrIlePheSerThrAlaHis
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Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropésanger.ac.uk
Sanger xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas005n23.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencial by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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5', mRNA sequence.
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/clone_1bb=NIH_MGC_71"
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/clone_1bb=NIH_MGC_71"
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/clone_1bbest=NIHOB (phage resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2.1 kb. " 256 c 246 g 140 t
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gow.k.column: 22
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Matches:
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Mismatches:
http://image.llnl.gov
Plate: LLAM13500 row: h column: 19
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/organism="Homo sapiens"
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-964-956-13 (1-1896) x BQ434703 (1-844)
                               High quality sequence stop: 597
Location/Qualifiers
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Location/Qualifiers
                                                                                               /db_xref="taxon:9606
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Tissue Procurement: DCTD/DTP
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Best Local Similarity:
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AUTHORS
TITLE
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                                                FEATURES
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/tissue__rype="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="organ: skin; Vector: pOTB7; Site_1: XhOI; Site_2:
ECORI; CDNA made by Oligo-dr priming. Directionally cloned
into ECORI/XhOI sites using the following 5' adaptor:
GGCAGGGG(). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1685 LysGlyThrLeuGlnLysPheValAspAspLeuPheGluThrIlePheSerThrAlaHis 1704
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Matches:
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/clone_lib="NIH_MGC_112"
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he : 5367 secs
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X87852 H.sapiens m
D86950 Mus musculu
X87832 Homo sapien
X87831 Homo sapien
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AL807376 Mus muscu
L44140 Homo sapien
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AX305728 Sequence
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-MODEL=frame+p2n.model -DEV=x1h
-MODEL=frame+p2n.model -DEV=x1h
-MODEL=frame+p2n.model -DEV=x1h
-MODEL=frame+p2n.model -DEV=x1h
-MODEL=frame+p2n.model -DEV=x1h
-DE-GORD_1/USPTO_spool/US09964956/runat_24062003_124338_5205/app_query.fasta_1.2055
-DB-GenEmbl -OFMT-fastap -SUBFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -TRR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM-ext -HEAPSIXE=500 -MINENEN=0 -MAXEN=200000000
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-NO_MMAP -LARGEGUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -KGAPDP=10 -KGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                        June 28, 2003, 04:02:59 ; Search time 10687 Seconds
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                              nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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CLSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIPSYKSWVERYYADIAKLPAISDQ
DMNAYLAEQSRLHAVEFNMLSALNEIYSYVSKYSEELIGALEQDEQARRQRLAYKVEQ
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QVICISPGPKDVPVIPLDQDWFGLELQLRSKETGKIFVSTEFKFYNCSAHQLCLSCVN
SAFRCHWCKYRNLCTHDPTTCSFQEGRINISEDCPQLVPTEEILIPVGEVKPITLKAR
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DLDRSGIPYLDYRTYAMRVLFPGIEDHPVLRELEVQGNGQQHVEKALKLFAQLINNKV
FLLTFIRTLELQRSFSMRDRGNVASLIMTGLQGRLEYATDVLKQLLSDLIDKNLENKN
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VWNGNFI I DNPQDLKVHLYKCAAQRESCGLCLKADRKFECGWCSGERRCTLHOHCTSP
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YNDTKFIYYPNPTFELLSPTGVLDQKPGSPIILKGKNLCPPASGGAKLNYTYLLGETP
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EEDNKSCYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLACGSLYQGVCKLLRLDDL
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EGNLELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLILYTTSRDRMTSV
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SLNPIRGPESGGTMVTITGHYLGAGSSVAVYLGNQTCEFYGRSMSEIVCVSPPSSNGL
                                                                                                                                                                                                                                                        Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F., Xue,A.J., Yang,Y., Wehrman,T. and Drmanac,R.T.
Novel nucleic acids and polypeptides
Patent: WO 0222660-A 310 21-MAR-2002;
HYSEQ, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSTHRSRLLTAAPLSMEQROPWPRALEVDSRSVVLLSVVWVLLA
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     PAT 14-JUN-2002
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 310 from Patent WO0222660.
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/db_xref="GI:21439230"
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| SIIèLeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArgPheAsnSerSel:::   | 2550 CGTTCAGTGTCAGAACAGCTCGTACCAGTATGATGAGGCATGGACATCAGCAATCTGGCCGT 2609 779 IGLULeuThrValValTrpAsnGlyHisPheAsnIieAspAsnProAlaGlnAsnLysVa 799 1::: | 799 1HisLeuTyrLysCysGlyAlaMetArgGluSerCysGlyLeuCysLeuLysAlaAspPr 819 | 2730 GAAGTTTGAGTGGCTGGTGCGGGGGGGGGGGGGGGCAGCTCCACCACCAGCAGTAC 2789 839 OAlaGlnGluSerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnProAr 859 ::: | 9 gilethrGluileileProvalThrGlyProArgGluGlyGlyThrLysValThrileAr<br>:      | geryeru<br>   <br>  TGGCGTG                                  | 2970 GCCCTGCACGCCCTCCCAGGGAATACATCATCGCTCAGCACATTGTCTGTGAGATGGG 3029 919 yGluAlaLysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgPr 939 | 939 oGluPheMetAlaArgSerSerGlnLeuTyrTyrPheMetThfLeuThrLeuSerAspLe 959 | uLysProSerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLe                | uAsnAlaGlySerAsnValValWetPheGlyLySGlnProCysLeuPheHisArgAr 999<br>            | 999 gSerProSerTyrIleValCysAsnThrThrSerSerAspGluValLeuGluMetLy 1018<br>   | 1018 svalServalGlnValAspArgAlaLysIleHisGlnAspLeuValPheGlnTyrValGl 1038<br> | 1038 uAspProThrIleValArgIleGluProGluTrpSerIleValSerGlyAsnThrProIl 1058 : | 1058 eAlaValTrpGJyThrHisLeuAspLeuIleGlnAsnProGlnIleArgAlaLysHisGl 1078 :::     :::   | 1078 yGlyLysGLuHisIleAsnIleCysGluValLeuAsnAlaThrGluMetThrCysGlnAl 1098<br> |
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| OY OY   | 90 VV G  | oy Db  | do dy do  | ov e   | S 6 S  | qa da   | QY   | da  | QQ<br>Dp   | QQ<br>QD   | QQ<br>QQ   | qa<br>Ko   | Qy<br>Qu   | qa<br>qa   |
| GAGGGCAA 1412 LeuThril 400 . :::       GTCCCCAT 1472 MetValar 420   | <br> CAGTGGA 1532<br> YrValTy 440<br> -       <br> ACGTTTA 1592  | rgva 46  | spproG1 479   | lucy<br>      <br>   |  | Incysva   |  |   | .euLysSe 639<br>  :::  <br>:TGAGGTC 2189                                     | ervalhi 659 .<br>        <br> Grgccca 2249   | yrargH1 679<br>     ::<br> ACCGCAA 2309                                    | rogl<br>  <br> CAGA  | leLysPr 719<br>::     <br>TAAAGCC 2429   | lucy<br>     <br>AGTG  |
| GCAGTCCTGCTACCAGGGCGAGG eProcysSerSerAlaLeuLeuT :         : : :         : : :                                       |  | rLysasnHisSerLeualaPheValGlyThrLysSerGlyLysLeuLysLyslleArgVa         | IASp61yProArgG1yAsnAlaLeuG1nTyrG1uThrValG1nValVal AspP  | uArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyG<br>         ::: | SLeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsnThrCysThrArgLy | SullargySellargSellySelluProArgArgPheAlaSerGluMetLySGlnCySVa :::::::   ::::::::::   | uGluThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThrPheGluAspLeuSe<br>     | rGluMetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSerProAlaAlaLysGl<br>     :::::: | isValValGlnLeuGlnLeuLysSe<br>:::::         ::  <br>TTGGGCTGGAGCTACAGCTGAGGTC | SGluThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerV<br>           <br> GGAGACAGGGAAGATATTTGTCAGCACCCAGTTCAAGTTTTACAACTGCAGTG | ysteuSerCysValGluSerProTyrargCysHisTrpCysLysTyrArgHi<br>                   | SVALCYSThrHisAspProLysThrCysSerPheGlnGluGlyArgValLysLeuP<br>:::::        | ysproGinLeuLeuArgValAspLysIleLeuValProValGluValIleLyspr<br>              ::<br> GTCCCCAGGTGGTGCCCACAGAGGAGATCTTGATTCCAGTCGGGGAAGTAAAGC | ollethrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyGlnArgGlyTyrG<br>               |
| GCAGATCAAGGAGCGCCTGC. pLeuLysValLysAspileP.   |  | aPheValGlyThrLysS  | indlaLeuGlnTyrGluT<br>:::          <br>::GGGGTCCATACGAGA<br>  | nProvalGluSerCysG<br>                    <br> ccccGTGGAGTCATGTG          | OHisCysGlyTrpCysV  | rLysGluProArgArgPr<br>: 1   | CGluLeuSerAlaGlyV.   | ValGlyAsnGlnIleG<br>  | rgileileThrGluAsnGlyAspHisHis'<br>:::   <br>GTCATCCCGCTGGATCAAGACTGGTTT      | I  | 'sValGluSerProTyra<br>          ::: <br>sTGTCAACAGCGCCTTCC                 | COLYSThrCysSerPheG   | euArgValAspLysIleL<br>::::::    <br>rGCCCACAGAGGAGATCT   | /sAsnLeuProGlnProG<br>::   |
| 1353 CCGGCCCATCAACTTGCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCC 380 rLeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaLeu | 1473 CGATGATAACTTCTGTGG<br>420 gGlylleProvalPheTh<br>1533 GGGCTGACCCTGACACA  | 0 m  | 460 1AspGlyProArgGlyAs<br>1111111<br>1653 CGACGGTCCCCCCATCG<br>479 yProValLeuArgAspMe<br>1713 CCCCATCCTCCGGAAN                              | 499 uArgGlnLeuThrArgVa<br>          <br>1773 GAGACAGGTCACCAGGGT          | 0 6 6  | 559 LARGLEUTH STATES  1893 GGACAAATGCCAACAGGC  559 LARGLEUTH VALHISPE  1953 GACCATTGCAACTGCONTCONT  | 79   | 599 rGluMetAspGlyLeuVa<br>:   :::::      <br>2073 AGAGGTGGAGGGCAGGT         | 619 uValProArgileileTh<br>:      <br>2133 TGTCCTGTCATCCC                     | 639 rLysGluThrGlyMetTh<br>                <br>2190 CAAGGAGACAGGGAAGAT  | 659 sAsnSerCysLeuSerCy<br>   | 679 sValCysThrHisAspPr<br>:::  | 699 uAspCysProGlnLeuLe<br>   | 719 ollethrLeuLysAlaLy<br>   |
| Db<br>Qy<br>Oy  |  |  |   |  |  |   |  |   | •  |  |  |  |  |  |

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|--|--------------------------------------|--------------------------------------|--|---|---|--|---|
| AlaLeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPh 1118 ACCACGGACTACCGCCTGGCCTGGACCTGTGGAACGCCCAGTGAGTT 3629 LeuAspAsnValGlnSerLeuLeulleLeuAsnLysThrAsnPheThrTy 1138 ::: |                                      | 1231<br>398<br>1251<br>404           | yrLysargLysSerArgGluSerAspLeuThrLeuLysArgLeuGlnMetGlnMe 1278 | raspileHisGluLeuThrSeraspLeuAspGlyAlaGlyIleProPheLeuAspTyrAr 1318 | SLeuphealaGlnLe 1358 [                            | ethrgaspargGlyasnValalaSerLeuIleMetThrValLeuGlnSerLysLe 1398 | erLysasnHisProLysLeuLeuLeuArgargThrGluSerValalaGluLysMetLe 1438 ::                  |
| aproAlaLeuala<br>    :::  <br> ACCTCTCTGACC<br>eGlyPheIleLeu<br>      ::<br> TGATTTGTTTT<br>TTYPPOASNPTC<br>   | YThrProll  :::        ATGCCCAT       | yMetG<br>    <br> GATGG<br>allev<br> | eAlaT<br>      <br>TGCCT<br>tASPA<br>                        |   | uGl<br>   <br> <br> <br> <br> <br> <br> <br> <br> | eserM<br>      <br> CTCCA<br>uGluT<br>                       | 8 uSerLysAsi<br> :::     <br>7 GAACAAGAA<br>8 uThrAsnTr<br>         <br>7 GACCAATIG |
| 3570<br>1118<br>3630<br>1138<br>3690   | 3750<br>1178<br>3807<br>1198<br>3867 | 1218<br>3927<br>1238<br>3987         | 1258<br>4047<br>1278<br>4107                                 | 1298<br>4167<br>1318<br>4227                                      | 1338<br>4287<br>1358<br>4347                      | 1378<br>4407<br>1398<br>4467                                 | 1418<br>4527<br>1438<br>4587<br>1458  |

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1818 5726 1838 5656 1618 1778 9909 5126 1638 5186 1658 5246 1678 5306 1698 5366 1718 5426 1738 5486 1758 5546 1798 1578 5006 1598 1518 1558 4946 1538 4886 eMetAspSerCysSerThrSerGluHisArgLeuGlyLysAspSerProSerAsnLysLe uthrargleuteualathriysglythrieuglniysphevalaspaspleuphegluth pLysSerAsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnProGlnPheVa yser GlyAlaArgMetIleLeuGlnAspGluAspIleThrThrLysIleGluAsnAspTrsThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLy 1718 1798 5667 1818 1698 5427 1738 5487 1778 5607 1598 2067 1618 5127 1638 5187 5247 1678 5307 5367 1558 4947 1578 5007 1658 4647 4707 4767 1518 4827 1478 1498 pp αd g δy qq οy g QY ÓΣ δ q qq qq QΣ g ōλ qq δ g Qγ QY qq q QΥ Qγ q δ ΩD Qγ Ω οy D οy QΥ

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QANITSQDDVLFAIFSKGKQYHHPPDDSALCAFTIRAINLQIKGRLQSCYQGEGN
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YNGYSVYVFVGTKSRKKIRADPHGGVOYEMVSVLKDGSPILRDMAFSIDDRYLYV
MSERQVTRVPVESCEQYTTCGECLSSGDPHCGWCALHNMCSRRDKCQQAWEDNRFAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seki, N., Ohira, M., Nagase, T., Ishikawa, K., Miyajima, N., Nakajima, D., Nomura, N. and Ohara, O. Characterization of CDNA clones in size-fractionated cDNA libraries from human brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHWCKYRNLCTHDPTTCSFQEGRINISEDCPQLVPTEEILIPVGEVKPTTLKARNLPQ
PQSGQRGYECVLNIQGAIHRVPALRFNSSSVQCQNSSYQYDGMDISNLAVDFAVVWNG
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CGCCAAGCTCCCAGCCATCAGTGACCAGGACATGAATGCCTACCTCGCCGAGCAGTCCCG 5786
                                                                                                         1858 yLysTyrSerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysGlyLysGlnLy 1878
                                                                                                                                   PRI 13-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (08-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mall:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="GFGRLPDSELRAGRGASRRPQQPAAAEVDRAGTEGGTDVAELES
CEGQPGKVEQMSTHRSRLLTAAPLSMEQRRPWPRALEVDSRSVVLLSVVWVLLAPPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GMPQFSTFHSENRDWTFNHLITVHQGTGAVYVGAINRVYKLTGNLTIQVAHKTGPEBDN
KSCYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLACGSLYQGVCKLLRLDDLFILV
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ESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFLTVQPETPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISQCVSLAVHPSSISVSEHSRLLSLVVSDAPDLSAGIACAFGNLTEVEGQVSGSQVIC
ISPGPKDVPVIPLDQDWFGLELQLRSKETGKIFVSTEFKFYNCSAHQLCLSCVNSAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                 KIAA0463 protein.
Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII
plus clone:HG0942.
                                                                                                                                                                                       sLeuAlaTyrLysLeuGluGlnValIleThrLeuMetSerLeuAspSer 1894
                                                                                                                                                                                                             авии/уз2 6263 bp mRNA linear l
Homo sapiens mRNA for KIAA0463 protein, partial cds.
AB007932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
1. .6263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=3
/product="KIAA0463 protein"
/protein_id="BAA32308.1"
/db_xref="G1:3413888"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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VERSION
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REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                 RESULT 2
AB007932
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IVITULIAYKRKSRENDLTLKRLOMONDNLESRVALECKEAFAELOTDINELTSDLDR
SEDYLDYRTYAMRULPGIEDHPVURELEVOGROGOHVERALKLFGOLINRKYELLT
FIRTLELORSESMENGRONASLIHMTGLOGRESYATDVLKGLLSDLIDRNLERKHPRL
LILRRTESVAEKMLTNWFAFLLHKFLKECAGEDLFMLYCAIKOOMEKGPIDAITGEARY
SLEBEKLIROKOJISKYTOLINGVNPDNENSPEIPSVYLMCDTITOVRKRILDAVYKNVP
YSQRPRAVDNDLEMGORIARVLODEDITTKIEGDMKRLNTLMHYOYSDRSVALVP
KQTSSYNIPASASISRTSISRYDSSFRYTGSPDSLRSRAPMITPDLESGVKWWHLVKN
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KFIYYPNPTFELLSPTGVLDQKPGSPI1LKGKNLCPPASGGAKLNYTVLIGETPCAVT
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VSVSVDRAHVDSNLQFEYIDDPRVQRIEPEWSIASGHTPLTITGFNLDVIQEPRIRVK
                                                                                                                                                                                                                                                                                        HDHGDQKEGDRGSKMVSEIYLTRLLATKGTLQKFVDDLFETLFSTVHRGSALPLAIKY
MFDFLDEQADRHSIHDTDVRHTWKSNCLPLRFWVNVIKNPQFVFDIHKGSITDACLSV
                                                                                                                                                                                                                                                                                                                                      VAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIPSYKSWVERYYADIAKLPAISDQDMNA
YLAEQSRLHAVEFNMLSALNEIYSYVSKYSEELIGALEQDEQARRQRLAYKVEQLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTGAGAATCGTGACCTTCAACCACTTGACCGTCCACCAAGGGACGGGGCCGT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 TCATAAGACAGGCCAGAAGAGGACAACAAGTCTTGTTACCCGCCCTCATCGTGCAGCC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rCysAsnGluProLeuThrThrAsnAsnValAsnLysMetLeuLeuIleAspTyrLy 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    515 CTGCAGCGAAGTGCTCACCCTCACCAACAATGTCAACAAGCTGCTCATCATTGACTACTC 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sGluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLe 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAspAspLysLe 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSer-PheValThrPheAr 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProTrpAsnTrpThrCysLeuLeuSerHisLeuLeuMetValGlyMetGlySerSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gGlyGluProAlaGlu---GlyPheAsnHisLeuValValAspGluArgThrGlyHisIl
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Mismatches:
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203

sLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheVa 223

uPhelleAlaThrAlaValAspGlyLysProGluTyrPheProThrIleSerSerArgLy

|      |  |  |  |   | •                                |   | -  |   |   |                  |  |  |                          | -  |     |  |  |  |  |   |   |   | ·  |   |                      |   | _                                       |   |  |   |  |  |  |   |
|------|--|--|--|---|----------------------------------|---|--|---|---|------------------|--|--|--------------------------|--|-----|--|--|--|--|---|---|---|--|---|----------------------|---|---|---|--|---|--|--|--|---|
| 874  | 243  | 934  | 263  | 5   | 200                              | _   | 00   | 1108  | 320   | 1168             | 340  | 1228   | 360                      | 1288   | 380 | 1348   | 400  | 1408   | 420  | 1468  | 440 .   | 1528  | 460  | 1588  | 479                  | 1648  | 499                                     | 1708  | 519  | 1768  | 539  | 1828   | 559<br>1888  | 579   |
|      | laSerMetIleLysIleProSerAspThrPheThrIleIleI | TCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCCACTTTGACAT | rTyrValfyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMe | TACAIC TACGGC TITGC TAGGGGGGCTTTG TC TACTITC TCACTGGCCCCGAG | ValSerProProG1ySerThrThrLysG1uG1 | -ACCCTGAGGGTGTGGCCATCACTCCGCTGGAGACCTCTTCTACACCTCACGC | ValArgLeuCysLysGluAspThrAlaPheAsnSerTyrValGluValProlleGlyC<br>               ::: | 3CGGCTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGC | sGluArgSerGlyValGluTyrArgLeuCeuGlnAlaAlaTyrLeuSerLysAlaGl | seccessistations | aValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThr | CTCACTGGCCCAGGCCTTCAATATCACCAGGCCAGGACGATGTACTCTTTGCCATCTTCT | rLysGlyGlnLysArgLysMetLy | CAAAGGGCAGAAGCAGTATCACCACCGCCCGATGACTCTGCCCTGTGTTCCC | _   | ccggccdatcaacttgcagatcaagggccgcctacagtctgctaccagggcgaggg | rLeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaLeuLe | CCTGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGGTGCACCAAGGCGCCTGTCCC | eAspaspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValAr | CGATGATAACTICTGTGGACTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGT | gGlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAl | GGGCCTGACCCTGTACACCACCACCACCACGAGGACCGCATGACTTCTGTGTGTTTTTTTT | rLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysLleArgVa | CAACGCTACAGCGTGTTTTTGTGGGGACTAAGAGTGGCAAGCTGAAAAAAATTCG | lAspGlyProArgGlyAsnA | CGACGGTCCCCCCCATGGTGGGGTCCAGTACGAGATGGTCTCTGTGC | yProvalLeuArgAspMetAlaPheSerLysAspHisGl | CCCCATCCTCCGGGGACATGGCCTTCTCCATTGATCAGCGCTACCTGTACGTCATGTCTGT | uArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCy | GAGACAGGTCACCAGGGTCCCCGTGGAGTCATGTGAGCAGTATACGACTTGTGGG | sLeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsnTh | CIGAGCICIGGGGACCCICACIGIGGCIGGIGIGCCCIGCACAACAIGIGCICC | sGludrgCysGludrgSerLysGluDrodrgArgPheAlaSerGluMetLysGlnCysVa ::::::    ::::: | ArgLeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeuLeuVal |
| 815  | 223  | 875  | 243  | 2 1   | ، ف                              | σ   | 280  | 1049  | 300   | 1109             | 320  | 1169   | 340                      | 1229   | 360 | 1289   | 380  | 1349   | 400  | 1409  | 420   | 1469  | 440  | 1529  | 460                  | 1589  | 479                                     | 1649  | 499  | 1709  | 519  | 1769   | 539  | L)  |
| qa · | QY   | qa   | oy<br>F  | an .  | ο <sub>λ</sub>                   | qq  | Qy   | Db  | Qy  | QQ               | Qy   | QQ   | Qy                       | q <sub>Q</sub>                                       | ογ  | qq   | Οy   | qq   | Qy   | QQ  | Oy  | QQ  | Qy   | qq  | Qy                   | Dp  | Qy                                      | đọ.   | οy   | qa  | οy   | QQ   | . Qy   | Qy  |

2485 2545 2605 2725 2905 2962 3025 2365 2245 2425 .889 GAGCCTTGCAGTGCATCCCAGCAGCATCTCAGTATCTGAGCACAGCCGGTTGCTTAGCCT 1948 899 919 939 629 839 759 779 2246 CCTCTGCACTCATGACCCCACCACCACCTCCTTCCAGGAGGGCCGGATCATATTCAGA lHisLeuTyrLysCysGlyAlaMetArgGluSerCysGlyLeuCysLeuLysAlaAspPr uGluThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThrPheGluAspLeuSe rLysGluThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerValHi uAspCysProGlnLeuLeuArgValAspLySIleLeuValProValGluValIleLysPr sIleLeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArgPheAsnSerSerSe rValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIleAsnAsnLeuProVa lGluLeuThrValValTrpAsnGlyHisPheAsnIleAspAsnProAlaGlnAsnLysVa 2546 GGATTTCGCTGTGGTGTGGAACGGCAATTTCATCATTGACAACCCTCAGGACCTGAAAGT oAspPheAlaCysGlyTrpCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCysPr 839 oAlaGluSerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnProAr 1GluCysSerProLeuValAspGlyTyrIleProAlaGluGlnIleValCysGluMetGl yGluAlaLysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgPr rGluMetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSerProAlaAlaLysGl uValProArgIleIleThrGluAsnGlyAspHisHisValValGlnLeuGlnLeuLysSe 679 sValCysThrHisAspProLysThrCysSerPheGlnGluGlyArgValLysLeuProGl 739 779 2606 819 859 2786 879 2846 799 899 919 1949 579 599 619 g qq g qq g g g  $\dot{\Omega}$ g δ Qγ g δ Db QΥ Q qq QQ g ò οy ŏ οy qq δ Dp Qγ Ω QΥ qq δ qq ò δy δy δý

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| OGluPheMetAlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLe | gSerProSerTyrIleValCysAsnThrThrSerSerAspGluValLeuGluMetLy | yGlyLysGluHisTleAsnIleCysGluValLeuAsnAlaThrGluMetThrCysGlnAl                    | alleyabserlievalavaladelyGiyueubeulielleyabalavalledillillillillillillillillillillillillill |
| 8 2 3 8 7 4  | 999<br>3206<br>1018<br>3266<br>1038<br>3326<br>1058       | 444<br>444<br>1111<br>1111<br>1111<br>1111<br>1111<br>1111                      | 1238<br>3923<br>1258<br>3983<br>1278  |
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1518 4282 1378 4342 4402 1418 4462 1438 1458 4582 1478 4642 1498 4702 1558 4942 5002 1618 uGluValProGlyTyrArgGlnGluArgValGluLysGlyLeuLysLeuPheAlaGlnLe 1SerLysGlnValThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThrSerAl rAspIleHisGluLeuThrSerAspLeuAspGlyAlaGlyIleProPheLeuAspTyrAr uThrAsnTrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGluProLe sGluHisGlyAspGlnLysGluGlyAspArgGlySerLysMetValSerGluIleTyrLe sAsnValProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGl 4283 ( 4703 ( 1598 1298 1318 4163 1338 4223 1358 1378 4343 1398 4.103 1.138 4523 1458 4583 1498 1518 4763 1538 1558 1578 4943 5003 51.23 1658 g Ω Dp ōλ g QY Db O.Y D.b ΟŊ qq δy Db Q Db Qγ Д οy д οy g ò qq QY Op Οý qq QY οg Qγ οp Ω Db οy QQ Ω

| Percent Similarity: 80.24% Conservative: 239 Best Local Similarity: 67.52% Mismatches: 357 Query Match: 67.72% Indels: 14 DB: 6 Gaps: 8 US-09-964-956-13 (1-1896) x AX305728 (1-6730) | Oy 25 LeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPheValThrPheArg 44 | Oy 45 GlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThrGlyHisIle 63            | Qy 64 TyrLeuGlyAlaValAsnArglleTyrLysLeuSerSerAspLeuLysValLeuValThr 83     | Qy 84 HisGluThrGlyProAspGluAspAsnProLysCysTyrProProArgileValGlnThr 103    | Qy 104 CysAsnGluProLeuThrThrAsnAsnAsnLysWetLeuLeuLeasPTyrLys 123          | Oy 124 GluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeu 143   | Qy 144 GluaspLeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeuSerGlyVal 163 :::           | Qy 164 AsnGluSerGlySerValPheGlyVallleValSerTyrSerAsnLeuAspAspLysLeu 183   | 0y 184 PhellealathralavalaspGlyLysProGluTyrPheProThr11eSerSerArgLys 203   | Oy 204 LeuthrLysAsiSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheVal 223                              | Oy 224 AlaSerMetileLysileProSerAspThrPheThrileIleProAspPheAspIleTyr 243  :::   :::  | 264 ValSerProProGlySerThrThrLysGluGlnValTyrThrSerLysLeu 280 :::             :::::: | Oy 281 ValargLeuCysLysGluaspThralaPheasnSerTyrValGluValProlleGlyCys 300  | Oy 301 GluargserGlyValGluTyrargLeuGeuGlnAlaAlaTyrLeuSerLysAlaGlyAla 320   11:::                                    | Qy 321 ValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPheSer 340             | 341  |
|---|---|---|---|---|---|---|---|---|---|--|---|--|--|--|---|--|
|   | 1698  | Qy 1718 pPheLeuaspGluGlnalaaspLysHisGlyIleHisaspProHisValargHisThrTr 1738<br> | Qy 1738 pLysSerAsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnProGlnPheVa 1758 | Oy 1758 1PheaspileHisLysAsnSerIleThrAspalaCysLeuSerValValalaGlnThrPh 1778 | Qy 1778 eMetAspSerCysSerThrSerGluHisArgLeuGlyLysAspSerProSerAsnLysLe 1798 | Qy 1798 uLeuTyrAlaLysAspIleProSerTyrLysAsnTrpValGluArgTyrTyrSerAspIl 1818 | Oy 1818 eGlyLysMetProalaIleSerAspGlnAspMetAsnAlaTyrLeuAlaGluGlnSerAr 1838<br>       - | Qy 1838 gMetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSerTyrValG1 1858 | Oy 1858 yLysTyrSerGlugluIleLeuGlyProLeuAspHisAspAspGlnCysGlyLysGlnLy 1878 | Oy 1878 sLeuahaTyrLysLeuGluGlnVallleThrLeuMetSerLeuaspSer 1894   11111111111111111111111111111111111 | RESULT 3 AX305728 LOCUS AX305728 LOCUS DEFINITION SEQUENCE 479 from Patent WO0188188. ACCESSION AX305728 ACCESSION AX305728 G1:17645146 |  | REFERENCE 1<br>AUTHORS ISHIKawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.<br>TITLE Method for examining ischemic conditions<br>JOURNAL Patent: WO 0188188-A 479 22-NOV-2001; | School Juridical Person Nihon University (JP) FEATURES Location/Qualifiers Source 1. 6730 /organism="Mus musculus" | /db_xref="taxon:10090"<br>BASE COUNT 1656 a 1850 c 1740 g 1482 t 2 others<br>ORIGIN | Alignment Scores:  Pred. No.:  Score:  6730  Matches: 1268 |

| 720 IleThrLeuLysAlaLysA<br>  | 2887 GACTTTGCTGTAGTATGGA 800 HisLeuTyrLySCySGJyA 2947 CATCTTACAAGTGTGCAG 820 ASPPHAAlaCYSGJYTTPC 810 AAGTTCCAGTGTGGCTGTGTGCAG 840 AlaGlnGluSerGlnTrpL | 3 AGCP<br>0 Ile1<br>1  |  | 980 AsnAlaGlySerAsnValV 3487 GGTGCTGGGACCAGTGTGG 1000 SerProSerTyrIleValC 1000 SerProSerTyrIleValC 1019 ValSerValGlnValAspA 1019 ValSerValGlnValAspA 1019 AspProThrIleValArgI 1039 AspProThrIleValArgI 1059 AlaValTrpGlyThrHisL 1059 AlaValTrpGlyThrHisL 1059 AlaValTrpGlyThrHisL 1059 AlaValTrpGlyThrHisL 1059 AlaValTrpGlyThrHisL 1059 AlaValTrpGlyThrHisL   |
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| 361 LysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThr 380 361 LysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThr 380 362 LysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThr 380 363 CGGGCCATCAATTCAAGGAGGGGGTTGCAGTCTGCTACCAGGAGGGGCAAC 1689 381 LeuAspLeuAlaTTpLeuLysValLysAspIleProCysSerSerAlaLeuLeuThrile 400 111:::: | 18<br>46<br>19<br>19  | 480 ProvalLeukargAspMetAlaPheSerLysAspHisGluGlnLeuTyrlleNetSerclu 499 111::: | 540 GluArgCysGluArgSerLysGluProArgArgPheAlaSerGluMetLysGlnCysVal 559 :::::   :::   :::   :::    :::    ::: | 620 ValproargilelleThrGludsnGlyAspHisHisValValGluLeuGluCeuLysSer 639 [1111]   1    1    1        1      1      1      1      1      1      1      1        1        1        1        1        1        1 |
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CACCAGCAGTATACTTTTGTGAATCCTTCTGTGCTGTCACTC 3426 Cys---AsnThrThrSerSerAspGluValLeuGluMetLys 1018 ArgAlaLySIleHisGlnAspLeuValPheGlnTyrValGlu 1038 ATTGAGCCAGAGTGGAGTATCACTAGTGGGCACACCCCCTA 3726 MeuGluLeuSerGlyAlaLysSerLysCysThrAsnProArg 859 WalThrGlyProArgGluGlyGlyThrLysValThrIleArg 879 MetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeu 979 ValValMetPheGlyLysGlnProCysLeuPheHisArgArg 999 AlaMetArgGluSerCysGlyLeuCysLeuLysAlaAspPro OCYSGlnGlyProGlyGlnCysThrLeuArgGlnHisCysPro HisAlaGlyPheValGluIleCysValAlaValCysArgPro SerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeu

|   | 759 PheaspleHisty 824 TTTGACATCCACAA 779 MetaspSerCysSe 111111111111111111111111111111111111 |
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| 1079 GIJUJSGLUHIAILEARNILECYSCINVALLEUNASNALATHUCHUMETTHUCYSGLDAIA 1098   11111111   111111111111111111111111 |  |
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snTrpValGluArgTyrTyrSerAspile 1818 lehisaspProHisValargHisThrTrp 1738 ||||||||| rccacGacacaGarGTGCGGCACACCTGG 5763 alAsnMetIleLysAsnProGlnPheVal 1758 nAsnSerThrValSerArgThrSerAla 1618 allysMetTrpHisLeuValLysAsnHis ||||||:::|||||||||| |TCAAGGTTTGGCATCTGGTGAAGAATCAT nalaasnSerProGluValProValLys | ||||||||||||| TGAGAACAGCCCAGAGATCCCAGTGAAA CTGAAGGAGTGTGCTGGGGAACCACTC

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RLOMOMDNIESRVALECKEAFAELQTDINELTSDLDRSGIPYLDYRTYAMRVLFPGIE
PHPVLRELEVORSCONFAKAIKLFAGLINNKYELLTFTRLELGASFSERBRCHVAS
LIMTGLQGRLEYATVVLKOLLSDLINKNENNHPKLLIRRTESVARKMLTNNFAFLL
HYFLKECAGEPLFMLYCAIKQOMEKGPIDAITGEARYSLSEDKLIRQOIEYKTLILC
VNDDBNSPRETPVKJAKOTTTOVREKTLDAVYKNPYSORPRAVDMLEWRGGRIAR
VVLDDEDITTKIEGDELMHYQVOSDRSVVALVRGTSSYNIBASAISFTSR
YDGSFRYTGSPDSLRSRVPMITPDLESCVKVWHLVKNHHGDOKEGDRGSKMVSEIYG
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TWKSNCLPLEWVNVIKNDGPYFDIHKGSITDACLSVVAQTPWDSCSTSEHRLGKDSP
SNKLLYAKDIPPSYKNWVERYADIAKLPAISDODMNAYLAEGSRLHATEFNMLSALNE
IYSYVSKYSKELLEQDEQARRQRLAYKVEHLINMASIES"

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                                                                             PRVORIEPEWSTTSGHTPLTITGFNLDVIQEPRVRVKFNGKESVNVCTVVNTTTLFCL
PRSLTSDYFREGLDTVERPDEFGELFWNVOSLLLINDTKRIYTPRHTELLSPTGLL
RPGSPI ILKGKNLCPPASGGARLNTVWIGERPCTVYVSETQLLCEPPNLTGGHKVMV
HVGGNVFSPGSVSVISDSLLTLPAIISIAAGGSLLLIIVIIVLIYLIYKRKSRENDLTKR
                     SGPPEGGTRVTIHGVNLGLDFSEIAHHVQVAGVPCTPIPGEYIIAEQIVCEMGHAVIG
TTSGPVRLCIGECKPEFMTKSHQQYTFVNPSVLSLSPIRGPESGGTMVTITGHYLGAG
                                                              SSVAVYLGNQTCEFYGRSMNEIVCVSPPSSNGLGPVPVSVSVDRARVDSSLQFEYIDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 HisGluThrGlyProAspGluAspAsnProLysCysTyrProProArgIleValGlnThr 103
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LOCRSKETGK IFVSTERFFYNCSAHQLCLSCYNSAFRCHWGXTRULCTHDPTTCSFQE
GRINVSEDCPGLYFEELLIPVEGEKP ITLKARNLFOPGSGGRGYECVLSIGGAVHRV
PALRFNSSSVQCOPFSELLIPVEGEKPATANDFAVENINGPPSIDNRQDLKVHLYKCAAQR
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DPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGEALAQAFNISSDEDVLFAIFSKGQK
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NFCGLDINQPLGGSTPVEGLTLYTTSRDRLTSVASYVYNGYSVVFVGTKSGKLKKIRA
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ECLSSGDPHCGWCALHNMCSRRDKCQRAWEANRFAASISQCMSLEVHPNSISVSDHSR
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5944 CTCTATGCCAAGGATATCCCCAGTTATAAGAACTGGGTAGAAAGATACTATGCAGATATT 6003
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                    1839 MetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSerTyrValGly
                                                                                                                                      6124 AAGTACAGTGAGGACTCATCGGGGCACTAGAGCAGGATGAACAGGCCCGACGGCAACGA
                                                                                                                                                                                                  LysTyrSerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysGlyLysGlnLys
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                                                                                                                                                                                                                                                                                                           Submitted (07-AUG-1996) Hajime Fujisawa, Nagoya University G. School of Science, Division of Biological Science: Furo-cho, Chikua-ku, Nagoya, Alchi 464-01, Japan (E-mail:fujisawa@bio.nagoya-u.ac.jp, Tel:052-789-2978, Fax:052-2978)
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Hirata,T. and Fujisawa,H.
Identification of plexin family molecules in mice
Biochem. Blophys. Res. Commun. 226 (2), 396-402 (1996)
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/organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="brain"
/dev_stage="E17.5"
580. 6234
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/protein_id="BAA13189.1"
/db_xref="G1:1655432"
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SerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgPro ArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeu CTCCCAACCTCTGAAGGTATTGCTTGTGCCTTTGGGAATCTGACT .euValValGlyAsnGlnIleGlnCysTyrSerProAlaAlaLysGlu ||| ||| |||:::||||::: ||| ||||||| |AGGTATCTGGGAGTCAAGTCTGCATCTGCACCTGGACCCAAGGAT seuLeuArgValAspLysIleLeuValProValGluValIleLysPro ValTrpAsnGlyHisPheAsnIleAspAsnProAlaGlnAsnLysVal

us-09-964-956-13.p2n.rge

| 1319   ThrTyrThrMetArgValLeuPheProGlyIleGluAspHisProValLeuArgAspLeu   1338 | 1379   SerMetargAspargGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLySLeu   | 1419 SerLysAsnHisProLysLeuLeuArgArgThrGluSerValAlaGluLysMetLeu 1438 ::: | 1459 PheserLeupheCysalaIleLysGlnGlnMetGluLysGlyProIleAspalaIleThr 1478  | 1499 ThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLys 1518   | 539 ASNVAlProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGly 155  | 4 CGGATTGCCAGAGTGGTGTTGCAGGACGAAGACATTACCACCAAAATAGAGGG 9 LysArgLeuAsnThrLeuAlaHisTyrGlnValProAspGlySerValValAl  | GAGACCTCCTCCTACACATCCCTGCCTGCCAGCTTCTCTGCAGCATCTCTTCTGCAGCATCTCTTCTGCAGCATCTCTGCTGCAGCATCTCTGCTGCAGCAGCCATCTTCTTCAGGTACACAGGCAGCCCAGACAGCCTTCCTT | 1539 ProMetIleThrProAspLeuGluSerGlyValLySMetTrpHisLeuValLySASnHis 1658 | istráaccadaagdaggtaaccggggcagcaaaaatggrgtcr<br>.euLeualathrLysGlyThrLeuGlnLysPheValaspasf |
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| 60 G G G G G G G G G G G G G G G G G G G                                   | . 0y<br>0y<br>0y  | Oy<br>Oy<br>Oy  | oy<br>oy<br>oy  | 0y<br>0b<br>0y   | . da oy   | Db<br>Qy<br>Qy   | Db<br>Qy a   | oy<br>Oy   | Db  |
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| 960 LysProSerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeu 979   11  | ValSerValGlnValAspargAlaLysIleHisGlnAspLeuValPheGlnTyrValGlu 103  ValSerValGlnValAspargAlaLysIleHisGlnAspLeuValPheGlnTyrValGlu 103  GTCTCCGTGAGTGTCGACAGAGCCCGGGTGGATAGCAGTTCGAGTATATAGAT 366  AspProThrIleValArgIleGluProGluTrpSerIleValSerGlyAsnThrProIle 105  GAGCCGACCGCGTAACCAGAACCAGAACCAGAACCAGAACCAGAACAACCAGAACAAC | AlaValTrpGlyThrHisLeuAspLeuIleGlnAsnProGlnIleArgAlaLysHisGly 107  ::    | ProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPhe 111    ::: | TyrProAsnProValPheGluAlaPheGlyProSerGlyIleLeuGluLeuLysProGly 115  TyrProAsnProValPheGluAlaPheGlyProSerGlyIleLeuGluLeuLysProGly 115  TACCCCAACCCAACGTTTGAACTGCTCAGCCCCACTGGAATCTTGGATCAGAAGCCAGGC 402  ThrProIleIleLeuLysGlyLysAsnLeuIleProProValAlaGlyGlyAsnValLys 117 | Leucartantericateassecandanicitericatecretecrescriftsasses Geo-<br>LeuasnTyrThrValLeuValGlyGluLysProCysThrValThrValSerAspVal<br>[                 :::::      <br>  CTCAACTACACAGTAATGATTGGAGACACCTTGTACAGTCACTGTGTGTG | 4144 CTGCTTTGTGAACCTCCAACGGCAGCACAAGGTCATGGTTTCGTGGGCGGG 4203 1219 MetGluTyrSerProGlyMetValTyrIleAlaProAspSerProLeuSerLeuProAla 1238 1219 MetGluTyrSerProGlyMetValTyrIleAlaProAspSerProLeuSerLeuProAla 1238 1219 ArGGTGTTCTCACCTGGCTCGTGAGCGTCATCTCCGACACCTGTTGACCCTGCCAGCGCACACTGTTGACCTGCCAGCGAGCG |  | Thr 129<br>   <br>  ACA 444  |   |

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Submitted (09-SEP-1994) Kunimasa Ohta, Kumamoto University Graduate
School of Medical Sciences, Dept. of Neuroscience and Immunology;
4-24-1 Kuhonji, Kumamoto, Kumamoto 862, Japan
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                                                     6004 GCCAAGCTCCCAGCCATTAGTGACCAAGATATGAATGCCTACCTCGCGGAGCAGTCCCGC
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Obta.K., Mizutani,A., Kawakami,A., Murakami,Y., Kasuya,Y.,
Takagi,S., Tanaka,H. and Fujisawa,H.
Plexin: a novel neuronal cell surface molecule that mediate
adhesion via a homophilic binding mechanism in the presence
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membrane protein.
Xenopus laevis cDNA to mRNA,
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Xenopus laevis mRNA for D38175
D38175.1, GI:961514
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DTTWYCLAESVDNPLRSPPRGDREDEIGFIMDNVARLLIVWTTSELYYPDPVFEPLT
SGONELEKPSSPLIIKGRNLIPAAPGNPRLNYTVLIGDTPCALTVSETYLLCESPNLT
GOHKVTIKAGGFFEVSPGTLOIYSDSLLTLRAIIGIGGGGGLLLLIIIVLIAVKRKSR
DADRTLKRLQLQMDNLESRVALECKEAFAELQTDIHELTNDLDGAGIPFLEYRTYAMR
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QLKIPSDTLSKFPTFDIYYVYSFSSEGFVYYLTLQLDTQLTSPDSTGEQFFTSKIVRL
CVDDPKFYSYVEFPIGCMKDGVEYRLIQDAYLSKPGKRLAKELGISEREDILFTVFSQ
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IDDNECGOPROPLGGTVT LEGTPLELDKEDGMTSVAAYDYRGHTVVRAGTREGENKK
ILVDLSASSSHLVOQYENVYHEGRALLEDLULSPDRQ I TAMTEKQVTRVPUESCEQ
YESCOTCLGSRDPHGGWCVLNINGCSRDRCERADELFFTSDQRQCVOLTYRVPUESCEG
TVSEVPMYLQARNYPDLSAGVNCSFEDFTEMEGRILDGK I YCTSPSAKEV I PITTRGHG
DKRVVKLY LKSKETGKKFASVDFVYRCSVHQSCLSCVNGSPCHWCK THVANA
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KCSALRESCCLCLKSDRRFECGWCVSEKKCTLRONCPTLENPWMHASTANSRCTDPK I
TKLFPETGPROGGTRLT I TGENLGLRFEDI RFGVRVGHVMCVPVESEY I SAEQI VCEI
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GNYLNAGSDVSVAIGGRPCMFSWRTAKEIRCKTPQGPSTGKAEIQILINRATMNNSEV
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FLLYKFLKECAGEPLFMLHCAIKQQMEKGPIDAITGEARYSLSEDKLIRQQIDYKTLN
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PKONSAYNISNSSTFTKSLSRYESMLRTASSPDSLRSRTPMITPDLESGTKLWHLVKN
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TTNNVNKLLLIDYSDNRLIAGGSASQGIOQFLRLDDLFKLGEPHHRKEHYLSSVNESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCSFQEGRVNMSEDCPQILPSSQIYIPVGVVKPITLTAKNLPQPQSGQRNYECIFHIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLFPGIEDHPVLKEMEVQANVEKSLTLFGQLLTKKHFLLTFIRTLEAQRSFSMRDRGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCADDVGLSDESCCRSPQTLNCVNPENENAPE1PVKVLNCDT1TQVKEKLLDAVYKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLAEQSRLHLSQFNSMSALHEIYSYITKYRDEILTALEKDEQARRQRLRSKLEQVIDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 TrpAsnTrpThrCysLeuLeuSerHisLeuLeuMetValGlyMetGlySerSerThrLeu
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(E-mail:ohta9203@gpo.kumamoto-u.ac.jp, Tel:096-373-5294
Fax:096-364-3554)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 rggactttttagtttrgcttggttcctggattgcaacaggggatgggtcr
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Mismatches:
Indels:
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Matches:

    .6163
/organism="Xenopus laevis"

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                                                                                                                                                                                                                                                                                  /product="plexin"
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                                                                                                                                                                       /db_xref="taxon:8355"
                                                                          Location/Qualifiers
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198. .5825
/product="plexin"
a 1502 c 1506 g
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/codon_start=1
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|---|--|--|--|--|--|--|---|--|--|---|---|--|---|---|---|---|---|---|
| 2498  | 820<br>2558  | 840<br>2618  | 860<br>2678  | 880<br>2738  | 900  | 920<br>2858  | 939<br>2918   | 959<br>2978  | 979<br>3038  | 999<br>3098   | 1019<br>3158  | 1038<br>3218   | 1058<br>3278  | 1078<br>3338  | 1098<br>3398  | 3449  | 1135<br>3509  | 1155<br>3569  |
| 2439 TTATCTGTGGTCTGGAATGGGCACTTTGTCATAGACAACCCTCAAAACATTCAAGCTCAT ' | 801 LeutyrLysCysGlyalaMetArgGluSerCysGlyLeuCysLeuLysAlaAspProAsp E<br> | 821 PhealacysGlyTrpCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCysProAla 8<br> | 841 GInGluSerGInTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnProArÿlle 8 | 861 ThrGluIleIleProValThrGlyProArgGluGlyGlyThrLysValThrIleArgGly | 881 GluasnLeuGlyLeuGluPheArgAspIlealaSerHisValLysValAlaGlyValGlu<br> | 901 CysSerProLeuValAspGlyTyrIleProAlaGluGlnIleValCysGluMetGlyGlu<br> | 921 AlaLysProSerGlnHisAlaGlyPheValGlulleCysValAlaValCysArgPro | 940 GlupheMetalaargSerSerGlnLeuTyrTyrPheWetThrLeuThrLeuSeraspLeu ::::: | 960 LysproSerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeu<br> | 980 ASNAIAGIYSErASNVAIVAIVAIVAIMETPHEGIYLYSGINProCySLeuPheHisArgArg<br> | 1000 SerProSerTyrIleValCysAsnThrThrSerSerAspGluValLeuGluMetLysVal ::: | 1020 SerValGlnValAspArgAlaLysIleHisGlnAspLeuValPheGlnTyrValGlu ::::::        ::::: | 1039 AspProThrIleValArgIleGluProGluTrpSerIleValSerGlyAsnThrProIle | 1059 AlaValTrpGlyThrHisLeuAspLeuIleGlnAsnProGlnIleArgAlaLySHisGly | 1079 GlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMetThrCysGlnAla<br> | 1099 ProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGluArgPro   11   1   1   1   1   1   1   1   1 | 1116 GluGluPheGlyPheIleLeuAspAsnValGlnSerLeuLeuIeLeuAsnLySThrAsn::: | 1136 PheThrTyrTyrProAsnProValPheGluAlaPheGlyProSerGlyIleLeuGluLeu<br> |
|   |  |  |  |  |  |  |   |  |  |   |   |  |   |   |   |   |   |   |

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|                              | KMLTNWFTFLLYKFLKECAGEPLFMLYCAIKQQMEKGPIDAITGEARYSLSEDKLIRQ<br>OIDYKTIJTIMOVNPFHFNABPYDVKGINCONVTONKEKIJIDAVYKOVPKSORPKAGDM   | QY      | 259 Leu         |
|------------------------------|--|---------|-----------------|
|                              | DEEMROGRMARITIQDEDYTKIDNDWRRLNTLAHYQYTDGSSVALVPRQTSAYNISN<br>CERPRIKET EDYBEWIT DAS CEDRET ERDEN TRODITECTRY BUILT VRAITHITOPECTED   | o<br>QQ | 1039 CTG        |
|                              | GSKMVSEIYLPRILATKGTVE COJKONTENTI EDIBOTKENILA KRAIDINGVECON<br>GSKMVSEIYLPRILATKGTVE KVODILFETI ESTAHRGSALPLATKY MPETEDBOADK<br>HOTTINGVECKTI DI DEGAMAT VRIDORIDENE TRIPACT GYNAOTRANGCE   | QY      | 277 Thr         |
|                              | HQIHDDUKHIWASUULKINNUN INNEQEEDIOMASI IONUNSYEMETOOMASI ENDSUSI<br>SEHKIGKOSPONUKLYAKOIPNYKSWVERTYADIAKMASI SOOMASYLAEQSKIHIS<br>VORMANGAT HITUGUTA VAKAPITTIVA PROROKABDOI DEKT FONUMMAI GE   | qa      | 1093 ACC        |
| BASE COUNT                   | 1379 8   | Qy      | 297 Pro         |
| ORIGIN                       | į  | qa      | 1153 CCC        |
| No.                          | scores: 0 Length:  | ΟŊ      | 317 Lys         |
| ent                          | nilarity: 77.52% Conservative:   | qa      | 1213 CGG        |
| Best Local S<br>Query Match: | imilarity: 63.50% Mismatche 63.43% Indels:   | QY      | 337 Thr         |
|                              | i dapa i dagada i daga i i ci daga   | qa .    | 1273 ACT        |
| US-09-964-                   | 956-13 (1-1896) X D86948 (1-6466)  | Qy      | 357 Ile         |
| Ολ                           | MetLysAlaMetProTrpAsnTrpThrCysLeuLeuSerHisLeuLeuMetValGlyMet<br>     ::::::  | qq      | 1333 CTG        |
| QQ                           | ATGCCACTGCCACCTCTGAGCTCTCGGACACTGCTGCTGCTGCTCTTGCTGCTGCTGGTGAGG  | Qy      | 377 Gly         |
| ΟŸ                           | <pre>GlySerSerThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPhe    </pre>  | qq      | 111<br>1393 GGA |
| QQ                           |  | Qy      | 397 Leu         |
| Qy                           | ValThrPheArgGlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThr<br>   | QQ      | 1453 CCC        |
| qa                           | 382 CGCACCITTGTGGCCCAGTGAC-:-TGGGGCCTCACTCACTGGTGGTTCACGAACAGACA 438   | ۸٥      | 417 ASE         |
| Qy                           | 61 GlyHisIleTyrLeuGlyAlaNalAsnArgIleTyrLysLeuSerSerAspLeuLysVal 80   | ı q     |                 |
| qq                           | 439 GGAGAGGTATATGTTGGCGCTGTGAACCGTATTTACAAGCTGTCGGGGAACCTAACCCTG 498   |         |                 |
| Qy                           | 81 LeuvalThrHisGluThrGlyProAspGluAspAsnProLysCysTyrProProArg1le 100  | S t     |                 |
| Dp                           | 499 CITCGGGCCCAIGTGACAGGCCCTGTAGAAGACAATGGTACCCACCCCCCCAGT 558   | an i    |                 |
| 0y                           | 101 ValGlnThrCysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuIeuIle 120   | δ i     |                 |
| qq                           |  | an o    |                 |
| Qy                           | 121 ASPTyrLysGluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeu 140   | δŽ      |                 |
| · qq                         |  | DÞ      | 1693 GTG        |
| ì                            | TonardianGluzenIonDhoIveTonCluGluDroTvrHielveClveGluHieTvrIon 16   | ΟŊ      | 494 Leu         |
| ें द                         |  | QQ      | 1753 CTC        |
| 2 2                          | Corc] vVa  | Qy      | 514 Glr         |
| 5 6                          |  | QQ      | 1813 AC         |
| 2 6                          | 0. MENATORIO NO MENATORIO DE LO CARROLLO DE LA CARROLLO DEL CARROLLO DE LA CARROLLO DE LA CARROLLO DE LA CARROLLO DE LA CARROLLO DE LA CARROLLO DE LA CARROLLO DE LA CARROLLO DE LA CARROLLO DE LA CARROLLO DE LA CARROLLO DE LA CARROLLO DE LA CARROLLO DEL CARROLLO DE LA CARROLLO DEL CARROLLO D | Qy      | 534 Asr         |
| δλ                           | LeuaspaspLysLeukheiteatainfalavalaspUjuyskioolulyfriekioinf 19<br>   | Db      | 1873 AGC        |
| an i                         | GGCCAGGCCAAGCTCTTCGTGGGCACACCCATCGATGGCAAATACTTCCCCACT   | QY      | 554 Glu         |
| ογ                           | <pre>11eSerSerArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPhe 21 :::          :::    :::           </pre>  | QQ      | 1933 GAC        |
| qq                           | 9 CIGICCAGICGCCGCCICAIGGCCAACGAGGAGAIGCIGACAIGIIIIGGCIIIGIGIAC 91  | Oy      | 574 AS          |
| δλ                           | 9 HisaspGluPheValAlaSerMetIleLysIleProSerAspThrPheThrIleIlePro   | . qa    | 1993 CAC        |
| QQ                           | 9 CAGGATGAGTTTGTGTCATCTCAGGTCCCTTCAGACACATTGTCCAAGTTCCCA   | Qy      | 594 Th          |
| δλ<br>to                     | 9 AspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThr<br>   | QQ      | 2053 TCC        |
| QQ                           | 979 GCCTTTGACATCTACTATGTGTACAGTTTCCGCAGCAGCAGTTCGTATACTACCTCACC 1038   | QY      | 614 Se          |

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uGln-----ProGluMetValSerProProGlySerThrThrLysGluGlnValTyr 276
                                                                               sAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPhe
                                                                                                                                  pMetValArgGlyIleProValPheThrGluAspArgAspArgMetThrSerValIle
                                                                                                                                                                                                                                                                                                                                                                      snThrCysThrArgLysGluArgCysGluArgSerLysGluProArgArgPheAlaSer
                                       rSerLysLeuValArgLeuCysLysGluAspThrAlaPheAsnSerTyrValGluVal
                                                                                                                                                                                                                                                                                                  rslleArgValAsp-----GlyProArgGlyAsn---AlaLeuGlnTyrGluThrVal
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| Oy 1711 LeualaileLysTyrMetPheAspPheLeu/                                    | 5455   | 5515   | 5575   | 1791 5635         | 5695   | 5755 G   | 5815 C   | 1871 AspaspGlnCysGlyL<br>111:::111<br>5875 GATGAACAGGCTCGA:            |  | RESULT 7 RESULT 7 RESULT 7 RESEXGENE 6039 bp DEFINITION H.sapiens mRNA for SEX gene. | ACLESION AG70234 VERGION X87852.1 GI:1200234 KEYWORDS Sex gene. SOURCE human | Eukaryota; Metazoa; Chordata<br>Eukaryota; Metazoa; Chordata<br>Mammalia; Eutheria; Primates<br>E 1 (bases I to 6039)<br>Macetrini F Tamannone I. | TITLE A novel family of transmembrane company of transmembrane company of transmembrane company of transmembrane company transmembra | AUTHORS Toniolo,D. TITLE Direct Submission                             | KNAL SUBMITTER (09-50N-1295) D. Blochimica ed Evoluzionisti Pavia, ITALY This entry extends and repl | irce   | / Cilousoume_ A / / map="q28"  |
|--|--|--|--|-------------------|--|--|--|--|--|--|--|---|--|--|--|--|--|
| 1351 GlyLeuLysLeuPheAlaGinLeuIleAsnAsnLysValPheLeuLeuSerPheIleArg 1370<br> | 1371 ThrLeuGluSerGlnArgSerPheSerMetArgAspArgGlyAsnValAlaSerLeuIle 1390 | 1391 MetThrvalLeuGlnSerLysLeuGluTyralaThrAspvalLeuLysGlnLeuLeuala 1410 | 1411 AspLeufleAspLysAsnLeuGluSerLysAsnHisProLysLeuLeuLeuArgArgThr 1430 | cValAlaGluLys<br> | 1451 LysGluCysAlaGlyGluProLeuPheSerLeuPheCysAlaIleLysGlnGlnMetGlu 1470<br> | 1471 LysGlyProlleAspAlaileThrGlyGluAlaArgTyrSerLeuSerGluAspLysLeu 1490<br> | 1491 IleargGlnGlnIleAspTyrLysThrLeuValLeuSerCysValSerProAspAsnAla 1510 | 1511 AsnSerProGluvalProvalLysIleLeuAsnCysAspThrIleThrGlnValLysGlu 1530 | 1531 LysIleLeuaspalaIlePheLysAsnValProCysSerHisArgProLysAlaalaasp 1550 | 1551 MetaspleuGluTrpargGlnGlySerGlyalaargMetIleLeuGlnAspGluAspIle 1570<br>           | 1571 ThrThrLysIleGluAsnAspTrpLysArgLeuAsnThrLeuAlaHisTyrGlnValPro 1590       | 1591 AspGlySerValValAlaLeuValSerLysGlnValThrAlaTyrAsnAlaValAsnAsnAsn 1610   | 1611 SerThrValSerArgThrSerAlaSerLysTyrGluAsnMetlleArgTyrThrGlySer 1630   | 1631 ProaspSerLeuargSerargThrProwetlleThrProaspLeuGluSerGlyValLys 1650 | 1651 MetTrpHisLeuValLysasnHisGluHisGlyAspGlnLysGluGlyAspArgGlySer 1670 :::                           | 1671 LysMetValSerGlulleTyrLeuThrArgLeuLeuAlaThrLysGlyThrLeuGlnLys 1690<br> | 1691 PhevalaspaspLeuPheGluThrIlePheSerThrAlaHisargGlySerAlaLeuPro 1710<br> |
| oy<br>Db   | Oy<br>Dp   | Qy<br>Db   | Qy   | Qy<br>Db          | QY<br>Db   | δy   | Oy<br>DP   | Qy   | Qy   | Qy   | Ογ<br>Db   | Oy<br>Dp  | Qy   | Qy   | Qy   | Qy   | QY   |

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ralalysaspileProSerTyrLysasnTrp 1810
                                                                                                                                                           rSerGluGluIleLeuGlyProLeuAspHis 1870
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Latarrhini; Hominidae; Homo.
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Toniolo,D. and Comoglio,P.M.
proteins with homology to the
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CNR, Via Abbiategrasso 207, 27100
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VDDLFETVFSTAHRGSALPLAIKYMFDFLDEQADQRQISDPDVRHTWKSNCLPLRFWV
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                                                                                                                                                                                                                                                                                                                                                                                                                     KSWVERYYRDIAKMASISDQDMDAYLVEQSRLHASDFSVLSALNELYFYVTKYRQEIL
TALDRDASCRKHKLRQKLEQIISLVSSDS" 2 others
                                                                                                                                    YPALDIYYIYGFVSASFVYELTLQLDTQQTLLDTAGEKFFTSKIVRMCAGDSEFYSYV
EFPIGCSWRGVEYRLVQSAHLAKPGLLLAQALGVPADEDVLFTIFSQGGKNRASPPRQ
TILCLFTLSNINAHIRRRIQSCYRGEGTLALPWLLNKELPCINTPXQINGNFCGLVLN
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                                                                                                                                                                                                          SerGlyValAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAsp 180
                                                                                                                                                                                                                                                                                                                      SerArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAsp
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TCGGGGGCCCAGGACCCGACTCCATGGCTGTCATTGTGGAGCAGGGCCCAGGGGCCC
                                                                                                                                                                                                                                                                               TCCCGCAAGCTCATCAGTGATGAAGACAGCGCGGACATGTTCAGTCTCGTGTACCAGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaLeuLeuThrIle
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|---|--|---|--|--|---|--|--|---|---------|---|---|--|--|--|---|---|--|---|-------------|
| 1510                                    | 480  | 500<br>1627   | 520<br>1687  | 540  | 560   | 580<br>1867  | 600  | 619   | 639     | 659   | 2107  | 679<br>2167  | 699.   | 719  | 739   | 759   | 779  | 799   | 819<br>2587 |
| CGCCAGCACTCTGTGGTCTTCATTGGCACGCGCAGCGCA | AspelyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValValAspProGlyPro<br> | ValLeuargaspMetalaPheSerLysaspHisGluGlnLeuTyrIleMetSerGluarg   :::           :::: | 1 GInLeuthrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCysLeu | GlyserGlyaspProHisCysGlyTrpCysValLeuHisAsnThrCysThrArgLysGlu<br> | ArgCysdluArgSerLysGluProArgArgPheAlaSerGluMetLysGlnCysValAr<br> | LeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeuLeuVais: | 1 ThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThrPheGluAspLeuSerGlu ::: | 1 MetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSerProAlaAlaLysGlu ::: |         | <pre>0 LysGluThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerValHis                                      </pre> | 8 AAGGAGACAGGCGGAGGTTTGCCGGTGCTGACTTTGTCTTCTACAACTGCAGCGTCCTC | 0 AsnSerCysLeuSerCysValGluSerProfyrArgCysHisTrpCysLysTyrArgHis<br> | 0 ValCysThrHisAspProLysThrCysSerPheGlnGluGlyArgValLysLeuProGlu<br> | 0 AspCysProGlnLeuLeuArgValAspLysIleLeuValProValGluValIleLysPro | 0 IlethriculysalalysasnicuproginProginSerglyglnArgGlyTyrGluCys:::       ::: | 0 IleLeuksnileGlnGlySerGluGlnArgValProAlaLeukrgPheksnSerSerser::::::::::::::::::::::::::::::: | 0 ValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIleAsnAsnLeuProVal | 0 GluLeuThrValValTrpAsnGlyHisPheAsnIleAspAsnProAlaGlnAsnLysVal ::: :: |             |
| 1451                                    | 461  | 481   | 501  | 52Í<br>1688  |   | 561  | 581  | 601   | 62      | 1986  | 2048  | 2108   | 680<br>2168  | 700  | 720   | 74(   | 760  | 780   | 800         |
| qq                                      | Oy<br>Db   | Oy .  | Qy<br>Db   | Qy<br>da   | S 64 G  | Qy<br>Db   | Oy<br>Ob   | Qy<br>Db  | oy<br>S | Qy  | qq  | Qy .<br>Db   | Qy<br>Db   | Qy<br>Db   | Q.y<br>Db   | Qy  | Qy<br>Db   | Oy<br>Ob  | Qy .<br>Db  |

1076 1096 1116 1136 1156 1036 1056 3301 3421 3481 3541 3601 1017 3241 3361 2647 2767 2821 3121 3181 2707 2881 3001 3061 916 938 839 879 978 866 2822 CGTTGCAACTCCATTCCGGCCGAGTACATCAGTGCTGAGAGGATCGTGTGTGGAGGAG 2882 GAGTCGCTGGTGCCCAGCCCGCCGGGGCCCGTGGACTGTGTGGGGGTGACTGTTCA 1057 ProllealavalTrpGlyThrHisLeuAspLeuIleGlnAsnProGlnIleArgAlaLys 3302 GCCATCACTGTGAGTGGGACCCACCTGCTGACGGTCCAGGAGCCCCGGGTCCGTGCCAAG GlnAlaProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGluArgProGlu 820 AspPheAlaCysGlyTrpCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCysPro AlaGlnGluSerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnProArg 860 IleThrGluIleIleProValThrGlyProArgGluGlyGlyThrLysValThrIleArg 900 GluCysSerProLeuValAspGlyTyrIleProAlaGluGlnIleValCysGluMetGly 920 GluAla---LysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArg 939 ProGluPheMetAlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAsp LeuAsnAlaGlySerAsnValValValMetPheGlyLysGlnProCysLeuPheHisArg ArgSerProSerTyrIleValCys -- - AsnThrThrSerSerAspGluValLeuGluMet 1018 LysValSerValGlnValAspArgAlaLysIleHisGln---AspLeuValPheGlnTyr 1037 ValGluAspProThrIleValArgIleGluProGluTrpSerIleValSerGlyAsnThr HisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMetThrCys GluPheGlyPheIleLeuAspAsnValGlnSerLeuLeuIleLeuAsnLysThrAsnPhe ThrTyrTyrProAsnProValPheGluAlaPheGlyProSerGlyIleLeuGluLeuLys 666 1077 1097 1117 3482 1137 3542 1157 3602 979 840 g qq g qq QΥ g δy g Dp qq g δy g g ò P ŏ δ ŏ. g óγ В Q QQ Ω qq ōλ Q Ω δλ q δ ò ŏ Qλ

| ### ##################################                                     | AspTrpLysArgLeuAsnThrLeuAlaHisTyrGlnValProAspGlySerValValAla 159<br> | LeuvalSerLysGinvalThrAlaTyrAsnAlavalAsnAsnAsnCerThrValSerArgThr 161<br> | SerAlaSerLysTyrGluAsnMetIleArgTyrThrGlySerFroAspSerLeuArgSer<br>           | 1637 ArgThrFrometIleThrProAspLeuGluSerGlyValLysMetTrpHisLeuValLys 1656 1:1 | 1657 AsnHisGluHisGlyAspGlnLySGluGlyAspArgGlySerLySMetValSerGluIle 1676   1657   11   11   11   11   11   11   11 | 1677 TyrLeuThrArgLeuLeuAlaThrLysGlyThrLeuGlnLysPheValAspAspLeuPhe 1696 | 1697 GluthrilePheSerThralaHisArgGlySerAlaLeuProLeuAlaIleLySTyrMet 1716 | 1717 PheaspPheLeudspGluGlnalaaspLysHisGlyIleHisAspPrOHisValargHis 1736   1717 PheaspPheLeudspGluGlnalaaspLysHisGlyIleHis   1717 | 1737 ThrTrpLysSerAsnCysLeuProLeuArgPheTrpValAsnMetileLysAsnProGln 1756   1737 ThrTrpLysSerAsnCysLeuProLeuArgPheTrpValAsnMetileLysAsnProGln 1756   11111111111111111111111111111111111 | 1757 PhevalPheaspileHisLysasnSerIleThraspalacysLeuServalvalalaGln 1776   1757   11   11   11   11   11   11 | 1777 ThrPheMetAspSerCysSerThrSerGluHisArgLeuGlyLysAspSerProSerAsn 1796 [   | 1797 LysLeuLeuTyrAlaLysAspIleProSerTyrLysAsnTrpValGluArgTyrTyrSer 1816<br> | 1817 AspileGlyLysMetProAlaileSerAspGlnAspMetAsnAlaTyrLeuAlaGluGln 1836<br>               ::: | 1837 SerargMetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSerTyr 1856   1811 | 1857 ValGlyLysTyrSerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysGlyLys 1876 | 1677 GlnLysLeuAlaTyrLysLeuGluGlnVallleThrLeuMetSerLeuAspSer 1894<br> | FT 8  |
|--|--|---|--|--|--|--|--|---|---|---|--|--|--|---|--|--|---|
| da<br>Qy   | Qy<br>Db   | oy<br>Db  | oy oy  | oy<br>Oy   | Qy   | Qy   | Qy<br>Dp   | Oy<br>Dp  | Qy  | Qy  | Qy<br>Db   | Qy   | qa<br>Kö   | oy<br>Oy  | Qy<br>Db   | Qy<br>Db   | RESULT<br>D86950  |
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| 1177 ValLysLeuAsnTyrThrValLeuValGlyGluLysProCysThrValThrValSerAsp 1196 ::: | 7 GlyGlyMetGluTyrSerProGlyMetValTyrIlealaProAspSerProLeuSerLeu 123   | 1237 ProhlaileValSerileAlaValAlaGlyGlyLeuLeuleIlePheileValAlaVal 1256   | 1257 LeullealaTyrLysArgLysSerArgGluSerAspLeuThrLeuLysArgLeuGlnMet 1276<br> | 1277 GlnMetAspAsnLeuGluSerArgValAlaLeuGluCysLysGluAlaPheAlaGluLeu 1296<br> | Asp<br>    <br> GAC  | JArg<br> :::   | eAla<br> <br> GGG  | GlnLeulleAsnAsnLysValPheLeuLeuSerPhelleArgThrLeuGluSerGlnArg<br>        :::::::::::::     :::    :::  | PARGGIYASNVALALASETLEUILEMETTHRVALLEUGLINSER 139<br>  | LysLeuGluTyrAlaThrAspValLeuLysGlnLeuLeuAlaAspLeuIleAspLysAsn:::    :::                                      | 1417 LeuGluSerLysAsnHisProLysLeuLeuLeuArgArgThrGluSerValAlaGluLys 1436<br> | METLEUTHRASITEPPHETHEPHELEULEUTYELYSPHELEULYSG1UCYSALGG1VG1U<br>           | PAla<br>   | IleThrGlyGlualaArgTyrSerLeuSerGluAspLysLeulleArgGlnGlnIleAsp 149              | 1Pro   | ValLysIleLeuAsnCysAspThrIleThrGlnValLysGluLysIleLeuAspAlaIle         | oo, oranasirticantisisataanatataataataanataasaataanataasaataataataataataataataataataataataa |

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LeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeu:160
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                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (07-MUG-1996) Hajime Fujisawa, Nagoya University Graduate School of Science, Division of Biological Science; Furo-cho, Chikua-ku, Nagoya, Aichi 464-01, Japan (E-mail:fujisawa@bio.nagoya-u.ac.jp, Tel:052-789-2978,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGPSKLFVGTAVDGKSEYFPTLSSRKLIDDEDSGDMFSLVYQDEFVSSQIKIPSDTLS
LYPAFDIYYIYGFVSASFVYFLTLQLDTQQTLLDTAGEKFFTSKIVRMCAGDSEFYSY
VEFPIGCSWRGVEYRLVQSAHLAKPGLLLAQALGVPADEDVLFTIFSQGOKNRANPPR
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NQPLGGLHVIEGLPLLADSTDGMASVAAYTYHQHSVVFIGTRSGNLKKVRVDGSQDAQ
LYETVSVVQGSPILRDLLFSPDHRHIYLLSEKQVSQLPVETCEQYLSCAACLGSGDPH
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HPQPRAQGEHPDEFGFLLDHVQAARSLNRSSFTYYPDPSFEPLGPSGVLDVKPGSHVV
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WLGTLHITTADRALTLPAMVGLAAGGGLLLLAITVVLVAYKRKTQDADRTLKRLQLQMD
NLESRVALECKEAFAELQTDINELTNHMDGVQIPFLDYRTYAVRVLFPGIEAHPVLKE
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YATGLLKQLLADLIEKNLESKNHPKLLLRRTESVAEKMLTNWFTFLLHKFLKECAGEP
LFLLYCAIKQOMEKGPIDAITGEARYSLSEDKLIRQQIDYKTLTLHCVCPESEGSAQV
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SLRSRAPMLTPDQEAGTKLWHLVRNHDHTDHREGDRGSKMVSEIYLTRLLATKGTLQK
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VNVIKNPOFVFDIHKNSITDACLSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIPN
YKSWYERYRDIAKMASISDOMDATIVEGSRLHANDFNVLSALSELYFYVTKYRQEI
LTSLDRDASCRKHKLRQKPEQIITLVSSSS" 1 others
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IDYAARRLVACGSIWQGICQFLRLDDLFKLGEPHHRKEHYLSGAQEPDSMAGVIVEQV
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TGVRPAGVDFVFYNCSALQSCMSCVGSPYPCHWCKYRHVCTSHPHECSFQEGRVHSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCPETLPQGDLLIPVGVMQPLTLRAKNLPQPQSGQKNYECVVRVQGRQHRVPAVRFNS
SSVQCQNASYFYEGDEFGDTELDFSVVWDGDFPIDKPPSFRALLYKCWAQRPSCGLCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KADPRFNCGWCISEHRCQLRAHCPAPKSNWMHPSQKGARCSHPRITQIHPLTGPKEGG
TRVTIVGENLGLISREVGLRVAGVRCNSIPTEYVSAERIVCEMEESLVPSPPPGPAEL
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                                                                                                                                               Mus
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                                                                                                                               Eukaryota; Metązoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                  Kameyama,T., Murakami,Y., Suto,F., Kawakami,A., Takagi,S.
Hirata,T. and Fujisawa,H.
Hirata,T. and Fujisawa,H.
Identification of plexin family molecules in mice
Biochem. Biophys. Res. Commun. 226 (2), 396-402 (1996)
   ROD
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Shimizu,M., Murakami,Y., Suto,F. and Fujisawa,H.
Determination of cell adhesion sites of neuropilin-1
20191894
   linear
cds.
 mRNA
complete
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3,
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5982
mRNA for plexin
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Fujisawa, H.
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200 692 220 752 812 260 872 320

| 1056<br>3263<br>1076<br>3323<br>1096<br>3383  | 13<br>13<br>15<br>17<br>17<br>62   | 1196<br>3680<br>1216<br>3740<br>1236<br>3800   | 1256<br>3860<br>1276<br>3920<br>1296<br>3980<br>1316         | 333<br>33<br>37<br>37<br>39<br>39  |
|---|--|--|--|--|
| ValGluAspProThrileValArglieGluProGluTrpSerlleValSerGlyAsnTh ACCCAGGACCTACACACACACACACACACACACAGCACACACA | ### STATE OF THE PROPERTY OF T | ValLysLeuAsnTyrThrValLeuVal<br>:::            :::<br>CGCCTACTACAGGTGTTGATT<br>ValGlnLeuLeuCysGluSerProAsn<br>             :::      :::<br>ACTCAACTTCTGTGTGATTCCCCAAGG<br>GlyGlyMetGluTyrSerProGlyMet<br>      ::   ::: | ProblatievalSerIlealavalalaGlyGlyLeuLeuIleIlePheIlevalalaval | TyrArgThrTyrThrMetArgValLeuPheProGlylleGluAspHisProVall TACGGACCTATGCTGCTGCTTTCCTGGCATCGAGGCTCACCCAGTG TACCGGACCTATGCTGCGCGTGCTTTTCCTGGCATCGAGGCTCACCCAGTG AspLeuGluValProGlyTyrArgGlnGluArgValGluLysGlyLeuLysLeuF ::: |
| 1037<br>3204<br>1057<br>3264<br>1077<br>1097  | 11.<br>11.<br>13.<br>15.<br>56.  | 3624<br>1197<br>3681<br>1217<br>3741   | 1237<br>3801<br>1257<br>3861<br>1277<br>3921<br>1297         | 33.<br>33.<br>33.<br>33.<br>35.<br>37.   |
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1496 1696 1716 5285 1756 4568 1516 1536 4803 1636 4985 5165 LeuValSerLysGlnValThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThr 1616 PheAspPheLeuAspGluGlnAlaAspLysHisGlyIleHisAspProHisValArgHis 1736 PheValPheAspIleHisLysAsnSerIleThrAspAlaCysLeuSerValValAlaGln 1776 GlnGlySerGlyAlaargMetIleLeuGlnAspGluAspIleThrThrLysIleGluAsn ||||||| CAGGGCCGCATGGCCCGAATCATCCTCCAAGATGAGGACATCACTACAAAGATTGAGTT TyrLysThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerProGluValPro SerAlaSerLysTyrGluAsnMetIleArgTyrThrGlySerProAspSerLeuArgSer GluThrIlePheSerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysTyrMet LysLeuGluTyrAlaThrAspValLeuLysGlnLeuLeuAlaAspLeuIleAspLysAsn LeuGluSerLysAsnHisProLysLeuLeuLeuArgArgThrGluSerValAlaGluLys 4449 4569 4629 1537 4689 4749 1617 4986 5106 5166 5226 1757 4389 1477 4509 1497 1557 1597 4869 4926 1637 1677 1697 1717 1517 1577 4809 1397 4269 4329 1437 1457 1417 Db qq QYqq Dp δy qq Ω qq δy qq Qγ QQ  $\delta \lambda$ qq δλ g δ qq δλ οg  $\underline{o}_{\underline{\lambda}}$ Db Ω Op δ qq Qγ ΩD δλ Db qq QY δ Óγ Qγ

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VPDLGAGVNCSFEDFFESSULEDGRIHCRSPRAREVAPITROGGDRVVKLYXKSKE
TGKRFRASUPVFYNCSVHOSCLSCVWGSFPCHURCKYRHVCTHWADCAFLEGRYNVSE
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1723 C 1561 g 939 t 6 others
                                                                                                                                                                                                                                                                                                                                                   AFDIYYYSFRSEGEVYTLTLOLDTQLTSPDAAGEHFFTSKIVRLCVDDPKFYSYVEF
PIGCDSQUSVERLOVDAYLSREGRALAHOLGLABDEDVLFYPROGORNRVPRESA
LCLFTLRAIKEKINESYERTOSYSFEGKLSLPWLLNKELGCINSPLOIDDPFRODFRODF
LGGTVTIEGTPLFVDKDDGLTAVAAYDYRGFTVVFAGTRSGRIRKILVDLSNPGGRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPVRSPPELGERPDELGFVMDNVRSLLVLNSTSFLYYPDPVLEPLSPTGLLELKPSSP
LILKGRNLLPPAPGNSRLNYTVLIGSTPCTLTVSETQLLCEAPNLTGQHKVTVRAGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFSPGTLÖVY SDSLLTLPA I VGIGGGGGLLLLVI VAVLIAY KRKSRDADRTLKRLQLQ
MDNLESRVALECK EA PAELQTDI HELTNDLDGAGI PFLDY RTY AMRVLPPGI EDHPVL
KEMEVQANVEKSLTLFGQLLTKKHFLLTFI RTLEAQRSFSMRDRGNVASLI MTALQGE
                                                                                                                                                                                                                                                                                 AVNRIYKLSGNLTLLRAHVTGPVEDNEKCYPPPXVQSCPHGLGNTDNVNKLLLLDYAA
NRLLACGSASQGICQSLRLDXLFKLGEPHHRKEHYLSSVQEAGSMAGVLIAGPPGQGQ
AKLFVGTPIDGKSEYFPTLSSRRLMANEEDADMFGFVYQDEFVSSQLKIPSDTLSKFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAYESVVAQEGSPILRDLVLSPNHQYLYAMTEKQVTRVPVESCVQYTSCELCLGSRDP
HCGWCVLHSICSRRDACERADEPQRFAADLLQCVQLTVQPRNVSVTMSQVPLVLQAMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDPEWSINSGGTLLTVTGTNLATVREPRIRAKYGGIERENGCLVYNDTTMVCRAPSVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 AspLeuLysValLeuValThrHisGluThrGlyProAspGluAspAsnProLysCysTyr 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AspGluArgThrGlyHisIleTyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACCTGACACTGCTGCGGGCCCACGTCACGGGCCCTGTGGAGGGCCAACGAGAAGTGCTAC
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11114
237
378
19
                                                                                                                                                                                        /product="NOV/plexin-Al protein"
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Conservative:
                           muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
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                                                                                             LysLeuLeuTyrAlaLysAspIleProSerTyrLysAsnTrpValGluArgTyrTyrSer 1816
                                                                                                                                                                                        AspIleGlyLysMetProAlaIleSerAspGlnAspMetAsnAlaTyrLeuAlaGluGln 1836
                                                                                                                                                                                                                                                                                   SerArgMetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSerTyr 1856
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Catarrhini; Hominidae; Homo.
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Januayuovic.
Submitted (27-AUG-1998) L. Tamagnone, University of Torino, IRCC,
SP 142, 10060 Candiolo, Torino, ITALY
On Oct 4, 1999 this sequence version replaced gi:1247575.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-JUN-1995) D. Toniolo, Instituto di Genetica
Biochimica ed Evoluzionistica, CNR, Via Abbiategrasso 207, 27100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5706 CACAAGCTTCGACAGAAGCCTGAGCAGATCATCACCCTGGTGTCCAGCAGCAGC 5759
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NOV/plexin-Al gene; transmembrane receptor.
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Mammalia; Eutheria; Primates;
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| qq       | 284 CTGCTGCTGCTGGACTATGCCGCTAA   | CTGCTGCTGCTGGACTATGCCGCTAACCGCCTGGTGGCCTGTGGCAGCGCCTCCCAGGGC 343  |   |
|----------|--|---|---|
| Qy<br>Db | 137 IleCysLysLeuLeuArgLeuGluAs;  | IleCysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHisLysLys 156  |   |
| Qy<br>Db | 157 GluHiSTyrLeuSerGlyValAsnGl<br>   | GluHisTyrLeuSerGlyValAsnGluSerGlySerValPheGlyValIleValSer 175<br>   | . <u>.                                   </u> |
| δ, d     | 176TyrSerAsnLeuAspAspLysLe   | TyrSerAsnLeuAspAspLysLeuPhelleAlaThrAlaValAspGlyLysProGlu 194   |   |
| oy y     |  | 21,   |   |
| oy<br>Oy | 524 TACTTCCCCACACTGTCCAGCCGTCG   | TACTICCCCACACTGTCCAGCCGTCGGCTCATGGCCAACGAGGAGGATGCCGACATGTIC 583  AlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAspThrPhe 234                          |   |
| Db       | 584 GGCTTCGTGTACCAGGATGAGTTTGT   | STCATCACAGCTCCAAGATCCCTTCGGACACGCTG 643   | ·   |
| Oy<br>Db | 235 ThrileileProAspPheAspileTy:::  | ThrileileproaspPheaspIleTyrTyrValTyrGlyPheSerSerGlyAsnPheVal 254 :::  | · · · · · ·                                   |
| Qy<br>Dh | 255 TyrPheLeuThrLeuGlnProGluMetValSerPro   | TyrPheLeuThrLeuGlnProGluMetValSerProProGlySerThrThrLys 272  |   |
| 3 8      |  |   |   |
| a a      | 00   | GAGCACTTCTTCACGTCCAAGATCGTGCGCTCTGTGTGGACCACCCCAAATTCTACTCG 817   |   |
| oy<br>Db | 293 TyrValGluValProlleGlyCysGl<br>   | TyrValGluValProIleGlyCysGluArgSerGlyValGluTyrArgLeuLeuGlnAla 312<br>  | ·   |
| Qy<br>Db | 313 AlaryrLeuSerLysAlaGlyAlaVa<br>   | AlaryrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAsp 332  | je:   |
| . Ko qu  | 333 AspLeuLeuPheThrValPheSerLy<br>   :::   | AspLeuLeuPheThrValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGlu 352  |   |
| Qy<br>Db |  | SeralaLeuCysIlePheIleLeuLysGlnIleAsnAspArgIleLysGluArgLeuGln 372<br>                  :::   <br>TCAGCACTGTGCCTGTTCAGGGCCATCAAGAGAAGATTAAGGAGGCGCATCCAG 1057 |   |
| Qy<br>Dp | 373 SerCysTyrArgGlyGluGlyThrLe   | SerCysTyrArgGlyGluGlyThrLeuAspLeuAlaTrpLeuLysValLysAspIloPro 392<br>  |   |
| o vy     | 393 CysSerSerAlaLeuLeuThrIleAs<br>        :::::  | CysSerSerAlaLeuLeuThrIleAspAsnPheCysGlyLeuAspMetAsnAlaPro 412<br>   |   |
| . o      |  |   | ·   |
| oy<br>Oy | 11/8 CIGGGGGGCACAGICACCAIlGAGGGGGGGGGGGGGGGGG  | CIGGGGGGGCACACATIGAGGGACGCCCCIGIICGIGGGACAAGGGIGAIGGGCCIG 1237<br>ThrSerVallleAlaTyrValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSer 452                          |   |
| Db       | 1238 ACCGCCGTGCCTGCCTATGACTATCG  | :::                ::    <br>accgccgtgcctaftgactaftcgcgccgcactgtggtattcgccgcacacgcaagt 1297   |   |
| oy<br>Db | 453 GlyLysLeuLysLyslleArgYalAs<br>   :::::::             <br> 1298 GGCGCATCCGCAAGATTCTGGTGGA | GlyLysLeuLysLysIleArgValAspGlyProArgGlyAsńAlaLeuGln 469<br>    ::::::::   | 7   |
| oy<br>S  | 70   | TyrGluThrValGlnValValAspProGlyProValLeuArgAspMetAlaPheSerLys 489  | 1   |
| ΩΩ       | 1358 TACGAGAGCGTCGTGGCCCAGGAGGG  | CAGCCCCATCCTGCGAGACCTCGTCCTCAGCCCC 1417   | -   |

2137 1777 1957 2017 2077 2257 2317 2377 2437 2438 CGCCGNTGCTCCCTGCGACACCACCACCTGCGACACACCTGCATCGTGGATGCACGC 2497 1657 1837 2197 589 649 699 689 709 729 749 809 769 789 590 GlyvalAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGln 609 CysValLeuHisAsnThrCysThrArgLysGluArgCysGluArgSerLysGluProArg ValSerGlnTyrAsnValLeuLeuValLeuGluThrTyrAsnValProGluLeuSerAla 610 IleGlnCysTyrSerProAlaAlaLysGluValProArgIleIleThrGluAsnGlyAsp 630 HisHisValValGlnLeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThr 670 TyrArgCysHisTrpCysLysTyrArgHisValCysThrHisAspProLysThrCysSer 690 PheGlnGluGlyArgValLysLeuProGluAspCysProGlnLeuLeuArgValAspLys 710 IleLeuValProValGluValIleLysProIleThrLeuLysAlaLysAsnLeuProGln 750 ValProAlaLeuArgPheAsnSerSerSerValGlnCysGlnAsnThrSerTyrSerTyr GluGlyMetGluIleAsnAsnLeuProValGluLeuThrValValTrpAsnGlyHisPhe 790 AsnileAspAsnProAlaGlnAsnLysValHisLeuTyrLysCysGlyAlaMetArgGlu 830 GlyGlnCysThrLeuArgGlnHisCysProAlaGln---GluSerGlnTrpLeuGluLeu ArgPheAlaSerGluMetLysGlnCysValArgLeuThrValHisProAsnAsnIleSer AspHisGluGlnLeuTyrIleMetSerGluArgGlnLeuThrArgValProValGluSer 1418 1478 1538 770 490 510 530 550 570 qq OD Óλ Ωp δ В οy Db  $_{\rm QY}$ Db δ a Ω qq Q qq δ Db δX qq δ ď Q q Q qq οy δλ Вp ΩŽ q Ω d δy d Q

| 899 GETCH/ANIALySteritys/grafthAsinProvigilethriciunietiefrovalritricity 868 899 GETCACCOGGACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC   |  | 1267 SerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeuGluSerArgValAla 1286 ::::        | 1307 LeuaspGlyalaclyIleProPheLeuaspTyrargThrTyrThrMetargValLeuPhe 1326 | 347<br>983<br>367 | 4643 ACCTICATION TO THE CONTROL OF T | 1407 GlnieuLeuAlaAspLeuIleAspLysAsnLeuGluSerLysAsnHisProLysLeuLeu 1426  | 4223 CTGCGCCGGACTGGCTGGCAGAGAAGACTAACTAACTACTCCTTCTTG 4282 1447 TyrLysPheLeuLysGluCysAlaGlyGluProLeuPheSerLeuPheCysAlaIleLys 1466 | GlnGlnMetGlubysGlyProIleAspAlaIleThrGlyGluAlaArgTyrSerLeuSer<br> | GluasplysLeulleArgGlnGlnIleAspTyrLysThrLeuValLeuSerCysValSer<br> | 1507 ProAspAsnAlaAsnSerProGluValProValLysIleLeuAsnCysAspThrIleThr 1526<br> | 1527 GlnValLysGluLysIleLeuAspAlaIlePheLysAsnValProCysSerHisArgPro 1546 | 1547 LysalaalaaspwetaspteuGluTrpargGlnGlySerGlyalaargwetIleLeuGln 1566<br> | 1567 AspGluAspIleThrThrLysIleGluAsnAspTrpLysArgLeuAsnThrLeuAlaHis 1586<br> |
|---|--|--|--|-------------------|--|---|---|--|--|--|--|--|--|
| SerGlyAlaLySearLySCySThrAsnProArgllethrGlutLelleProvalThrGly  CGTCACGGCACACACGACCCCAACCCCAACCCCCAACCGCC  ProArgGluGlyGlyThrLySValThrIleArgGlyGluAsnLeuGlyLeuGlubheArg  CCGACGCACCACCACCCCCCAACCCCCAACCCCCCCCC | . qa a   | 97<br>90<br>97   | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                  | oy<br>Oy          | da<br>Qy<br>Db   | oy o  | d Qy  | Qy<br>Db   | Qy<br>dū   | Oy<br>Dp   | Qy   | Qy<br>Db   | Qy   |
| SerGlyAlaLySearLySCySThrAsnProArgllethrGlutLelleProvalThrGly CGTCACGGCACACACGCCCCAACCCCCAACCCCCAACCGCCCCCC  |  |  |  |                   |  |   |   |  |  |  |  |  |  |
|   | ThrasnProArgileThrGluileIleProValThrGly    :::   :::    :::      ACCGACCCAAGATCCTCAAGCTGTCCCCCGAGACGGGC ValThrIleArgGlyGluAsnLeuGlyLeuGluPheArg  ::: | aLysProSerGlnHisAla :::         CAGCTCCGTGCGTGCCCATGAC  UPheMetAlaArgSerSerGln ::: | etSer<br>::   <br>TGTCA  | ysAsn<br>         | CCCCCCAG  IArgileGlu   | sanccencences casomics of a salaval representation of the salaval | IleasnileCys<br>    <br>    <br>    <br>  | valgln<br>   :::<br>GrgcGC                                       | roValPheGluAla<br>      <br> CGTACTGGAGCCA                       | elleLeuLysGlyLys<br>:           :::<br>CATCCTCAAGGGCCGG                    | rThrValLeuValGly<br>           <br>cacGGTGCTCATCGGC                    | Leu  | Val  |

27100

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ITGEARYSLSEDKLIRQQIEYKTLILNCVNPDNENSPEIPVKVLNCDTITQVKEKILD
AVYKNVPYSQRPRAVDMDLEWRQGRIARVVLQDEDITTKIEGDWKRLNTLMHYQVSDR
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VWHLVKNHOHGDQKEGDRGSKMVSETYLTRLLATKGTLQKFVDDLFETLFSTVHRGSA
LPLAIKYMFDFLDEQADRHSIHDTDVRHTWKSNCLPLRFWVNVIKNPQFVFDIHKGSI
TDACLSVV" 820 t
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Location/Qualifiers
                                                                                                               Submitted (08-JUN-1995) D. Toniolo, Instituto di Genetica
Biochimica ed Evoluzionistica, CNR, Via Abbiategrasso 207,
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Mismatches:
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/clone_lib="lambda GT10"
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                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
SEX/plexin receptor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="OCT/plexin-A2"
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/gene="OCT/plexin-A2"
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5 (bases 1 to 3985)
Tamagnone, L.
                                          4 (bases 1 to 3985)
Toniolo, D.
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                                               1747 PheTrpValAsnMetIleLysAsnProGlnPheValPheAspIleHisLysAsnSerIle 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRI 06-OCT-1999
4643 GACGAGGACGTCACCACCACGAGATTGACAACGATTGGAAGAGGCTGAACACACTGGCTCAC 4702
                                                                                                                                                                                                                                      TyrThrGlySerProAspSerLeuArgSerArgThrProMetIleThrProAspLeuGlu 1646
                                                                                                                                                                                                                                                                                                                                    SerGlyValLysMetTrpHisLeuValLysAsnHisGluHisGlyAspGlnLysGluGly 1666
                                                                                                                                                                                                                                                                                                                                                                                                                             AspArgGlySerLysMetValSerGluIleTyrLeuThrArgLeuLeuAlaThrLysGly 1686
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J. (bases 1 to 3985)
Maestrini, E., Tamagnone, L., Longati, P., Cremona, O., Gulisano, M.,
Blone, S., Tamanini, P., Neel, B.G., Toniolo, D. and Comoglio, P.M.
Afamily of transmembrane proteins with homology to the
Proc. Natl. Acad. Sci. U.S.A. 93 (2), 674-678 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bione, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4820 ACGCCCACCACCACCACACACACCCCGCACCATGATCACGCCCGACCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrLeuGlnLysPheValAspAspLeuPheGluThrIlePheSerThrAlaHisArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1607 AlaValAsnAsnSerThrValSerArgThrSerAlaSerLysTyrGluAsnMetIleArg
                                                                                                                                                                                                                                                                                                                                                          5000 ACACTGCAGAAGTTTGTGGACGACCTGTTTGAGACCATCTTCAGCACGGCACACCGGGGC
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Angelinie, P., Artigiani, S., Tamagnone, L., Maestrini, E.,
Toniolo, D. and Comoglio, P.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSOCTPROT 3985 bp mRNA linear
Homo sapiens mRNA for partial OCT/plexin-A2 protein.
X87831
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Homo sapiens.
Homo sapiens
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|------------|--|--------------|------------|
| qq         | 62 GGGGTCCAGTACGAGATGGTCTCTGTGCTCAAGGACGGAAGCCCCATCCTCCGGGACATG 121  | ٥            | 846 Leu    |
| QY         | 486 AlaPheSerLysAspHisGluGlnLeuTyrIleMetSerGluArgGlnLeuThrArgVal 505 | Z 6          |            |
| qq         | 122 GCCTTCTCCATTGATCAGGGCTACCTGTAGTCTGTGAGAGACAGGTCACCAGGGTC 181     | Q :0         |            |
| Οy         | 506 ProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCysLeuGlySerGlyAspPro 525 | Š) í         |            |
| qa         | 182 CCCGTGGAGTCATGTGAGCAGTATACGACTTGTGGGGAGTGCCTGAGCTCTGGGGACCCT 241 | <b>a</b>     | י תכ       |
| Οy         | 526 HisCysGlyTrpCysValLeuHisAsnThrCysThrArgLysGluArgCysGluArgSer 545 | λo t         |            |
| qq         | 242 CACTGTGGCTGGTGTGCCCTGCACAACATGTGCTCCCGCAGGGACAAATGCCAACAGGCC 301 | gg ÷         |            |
| Qy         | 546 LysGluProArgPheAlaSerGluMetLysGlnCysValArgLeuThrValHisPro 565    | λ̈́O         | .0         |
| qa         | 302 TGGGAACCFAATCGATTGCTGCCAGCGACCAGTGTGAGCCTTGCAGTGCATCCC 361       | <b>q</b> a . | 6<br>6     |
| οy         | 566 AsnAsnIleSerValSerGlnTyrAsnValLeuLeuValLeuGluThrTyrAsnValPro 585 | Oy           |            |
| Dp         | ::::::   | qa           | 1439 ACC   |
| δÿ         | 586 GluLeuSerAlaGlyValAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuVal 605 | QY           | 946 Ser    |
| qq         |  | qa           | 1499 CAT   |
| ΛO         | ValGlvAsnGlnIleGlnCvsTvrSerProAlaAlaLvsGluValProArglleThr 6          | . Оу         | 966 Met    |
| 면          |  | qq           | 1559 GAG   |
| ٥٥         | GluAsnGlvAspHisHisValValValCinfenGlnfenIvsQerIvsGluAbrGlvMorThr      | Qy           | 986 Val    |
| 7 qa       | CTGGATCAAGACTGGTTTGGGCTGGAGCTAAGAGTCCAAGAAAGA                        | qa .         | 1619 GCA   |
| è          |  | Oy           | 1006 Cys   |
| Š 2        | o Filestassettiitseelrijevalrijetytässetvaltissasiseelväleivys       | qq           | 1679 TGT   |
| g<br>G     | 1116ICAGCACCGAGTICAAGITTTACAACTGCAGTGCCCACCAACCGTGCCTGTCCTGT         | δλ           | 1025 Arg   |
| δy         | 66 ValGluSerProTyrArgCysHisTrpCysLysTyrargHisValCysThrHisAspPro      | : qa         | 1139 CGA   |
| đ          | 0  | ò            | 'n         |
| δλ         | 686 LysThrCysSerPheGlnGluGlyArgValLysLeuProGluAspCysProGlnLeuLeu 705 | 3 6          | 110001     |
| QQ         | 719 ACCACCTGCTCCTTCCAGGAGGGCCGGATCAATATTTCAGAGGACTGTCCCCAGCTGGTG 778 | 2 6          |            |
| Οy         | 706 ArgValAspLysIleLeuValProValGluValIleLysProIleThrLeuLysAlaLys 725 | δ            | 9 <u> </u> |
| qq         | ::::::       ::  | අු           | on .       |
| δλ         | 726 AsnLeuProGlnProGlnSerGlyGlnArqGlyTyrGluCysIleLeuAsnIleGlnGly 745 | QY           | 1685 Ile   |
| QQ         |  | Op           | 1919 GTG   |
| δý         |  | Qy           | 1105 Pro   |
| · q0       | :::  | qa           | 1979 TAC   |
| ۸ò         | SerTyrSerTyrGluGlyMetGluIleAsnAsnLeuProValGluLeuThrValValTrr 7       | Qy           | 1125 Val   |
| 7 원        |  | qa           | 2039 GTC   |
| }          | 86 AenGluHieDhabenIlabenbenDroblaGlnbenIweValuieIawwwwineCuerche Ons | Qy           | 1145 Glu   |
| 7.<br>QO   |  | qq           | 2099 GAA   |
| <b>^</b> 0 | AlaMetArdGluSerCvsGlvLeuCvsLeuLvsAlaAspProAspPheAlaCvsGlvTrp 825     | Qy           | 1165 Gly   |
| . qa       | GCCCAGCGGGAAGTGCCTCTAAAGGCCGGAAAGTTTGAGTTGGCTTGG                     | QQ           | 2159 GGG   |
| ΛO         | S CVSG DG VProG VG DCVSThrLenAraG DHisCVSProAlaG DG DSarG DTrn 845   | Oy .         | 1185 val   |
| 7 A        |  | qq           | 2216 ATC   |
| 1          |  |              |            |

1164 VICAGCAGTACACCTTCGTGAACCCTTCTGTGCTGTCACTCAACCCAATCCGAGGTCCC 1558 s---AsnThrThrSerSerAspGluValLeuGluMetLysValSerValGlnValAsp 1024 gAlaLysIleHisGlnAspLeuValPheGlnTyrValGluAspProThrIleValArg 1044 wAspLeuIleGlnAsnProGlnIleArgAlaLysHisGlyGlyLysGluHisIleAsn 1084 oAspHisGlnSerAspLeuThrGluArgProGluGluPheGlyPheIleLeuAspAsn 1124 eGluProGluTrpSerIleValSerGlyAsnThrProIleAlaValTrpGlyThrHis 1064 eCysGluValLeuAsnAlaThrGluMetThrCysGlnAlaProAlaLeuAlaLeuGly 1104 uGluLeuSerGlyAlaLysSerLysCysThrAsnProArgIleThrGluIleIlePro 865 yLysAsnLeuIleProProValAlaGlyGlyAsnValLysLeuAsnTyrThrValLeu pGlyTyr11eProAlaGluGlnIleValCysGluMetGlyGluAlaLysProSerGln srGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSerArgGlyPro tSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAlaGlySerAsnVal uAlaPheGlyProSerGlyIleLeuGluLeuLysProGlyThrProIleIleLeuLys sAlaGlyPheValGluIleCysValAlaValCysArgProGluPheMetAlaArgSer

| 35910 CTCTGTCCTGGTCTCAGGTGCGGGTCGATGGCTCTCAGGATGCCCAGCTA 35966 470 TyrGluThrValGlnValValAspProGlyProValLeuArgAspMetAlaPheSerLys 489 | OVAIGLUSEACCYSGLYGINTYCLINESSECYSGLYGLUCYSLEGGLYSETGLYASPPROHI 526          ::: | 36267 GTGGGCTCCCTGGGGCCATTATCTTGGGAGACAGAGGATTTAGGAGGACCTTGCCAGCTG 36326 534   | 534  | 540 uArgCysGluArgSerLysGluProArgArgPheAlaSerGluMetLysGlnCysValAr 560  1 |   |
|---|---|--|--|---|---|
|   | 30  | 35191 CGACTTTCCATCCCAGTCCCATGGGGTCCTAGGGGAAACAAAC  | AspasaphecysGlyLeuAspMetAsnAlaProleuGlyValSerAspMetValArgGly 421 | AGA 3554' ACA 3560' ACA 3560' ACT 3566'                                 | 35670 CCAAGAACTGGATCCTTTGGTGGCTCCTCTGCCATCTGCTGGCATTGT 35729  457 |
| 97<br>97<br>97<br>97<br>97  | qa oy   | \( \delta \) \( \d | 6  | 0   | 0   |

| 1004         DD         40333           39316         QY         1198           1004         DD         40393           39376         QY         1213           1042         DD         40453           39436         QY         1214           1052         DD         40573           39436         QY         1231           1052         DD         40573           39555         QY         1231           1052         DD         40573           39615         DD         40633           39735         QY         1291           1054         DD         40813           39975         DD         40873           1068         QY         1341           1107         DD         40993           39975         DD         40993           40035         DD         40993           1107         DD         41153           40095         QY         1356           1164         DD         41173           40215         QY         1356           1164         DD         41173           4021  |   | 3931  | ď           | 40333 CGCCTCAACTACACAG |
|--|---|---|-------------|------------------------|
| 998  |   |   | 3           |                        |
| 19317   GEOMOGICANTENGECTIANCECTRACTIONAGIANACHOCCAMAGRAPHY  |   |   | Qy<br>Db    |                        |
| 1000 VALCES - ABSTRACTA ESPERANCE   1014   1015   1014   |   | 3937  | ò           |                        |
| 1947   STATESTANCTCACCTGGGCCCCARTCACACCTGCCACCTGCCACC 39436   Oy   1214   October   124   Oc |   | ValCysAsnThrThrSerSerAspGluValLeuGluMetLysValSerValGlnVal         | Z da        |                        |
| 1024   ASPACAGOALACAMENTOCAMOCACAGOACACAGOACACAGOACACAGOACACAGOACACAGOACACAGOACACAGOACACAGOACACAGOACACAGOACACAGOACACAGOACACACAGOACACAGOACACAGOACACAGOACACAGOACACAGOACACAGOACACAGOACACAGOACACACAGOACACACAGOACACACAGOACACACAGOACACACAGOACACACAC  |   | GTGTGTATCTCACCTGTCTCCACCCTGGGCCCCAGTCAGAGCCCTATCACCCTTGCCATC      | l ò         |                        |
| 19437 GHTCHECCARCHACTCRACACTATATACTACACCAGGACCCTACGATC 39496   09417 GHTCHECCARCCACACTACCTACACCTACGACCCTACACACCCCACACACCTACACACAC  |   | AspargalaLysIleHisGlnAspLeuValPheGlnTyrValGluAspProThrIle         | Z qq        | CTTAC                  |
| 1043 ValArgitLeGAGCCCACCIGGAGCATCAT-CAAGTCAGCAGCAATGGGGTTGA 39555   D9 40573   D9 4057 |   | GATCATGCCAACATCCCAACACTGGAGTCATCTATACCTACACCCAGGACCTACGGTC        | } &         |                        |
| 19497   ACACACCTTGAGCCCTGGAGCATCAT-CANGTORACCCTGAGGGCTTTGGTCAT 39555   1951   1952   1955   |   |   | Z qa        |                        |
| 1052   1052   1053   1054   1055    |   | ACACACCTTGAGCCCACCTGGAGCATCAT-CAAGTGAGACCCTGAGGAGAATGGGGTTGA      | l ò         |                        |
| 1052   1052   1052   1053   1054   1055    |   |   | <i>∓</i> 16 |                        |
| 1052   1052   1052   1053   1054   1055    |   | 3961  | ì ô         |                        |
| 39616 CANGTGGTTCCTCCTGGAGCCCTCATCAGGAGCCCTCATA 39675  1052   |   |   | 7 E         |                        |
| 1052   1053   1054   1057   1058   1059    | • |   | 2 8         |                        |
| 39676 TAGAGGCTGGCACCTGCAAGGCTCTGAGGTCTCAGAAAATCCT 39735 U752  1053   | • |   | Z 2         |                        |
| 1053   | • |   | an a        |                        |
| 1055 Asnthrerollacladalurgocococococococococococococococococococ   | • | SerGly  | ži<br>O     |                        |
| 1055 ASMTHEPTOILEALAVALTEGLYAPELILEGIAASPERULIEGIAASPERGE   1074   110   | • |   | gg<br>O     |                        |
| 39796 AGCACCTCATCATCATCATCATCATCATCATCATCATCATCA   |   |   | δō          |                        |
| 1075 AlalysHisGlyGlyLysGluHisIleAsnIle   | • |   | 20 6        |                        |
| 9856 GCCAAGTACCGTGGTTTTTTTTTTTTTTTTTTTTTTTTT   |   |   | Š t         |                        |
| 1086   | • |   | G :         |                        |
| 39916 CATTGCTACTAGGCTTCATGCGCTGAGACTGCTGG 39975  1088 ValLeudanAlarhrCyGCInAlaProAlaLeudlyProAspHis 1107  1088 ValLeudanAlarhrCyGCInAlaProAlaLeudlyProAspHis 1107  1108 Ill:::   |   | CysG1u  | Š á         |                        |
| 1088 ValLeuAsnAlaThrGluMetThrCysGlnAlaLeuGlyProAspHis 1107 1108 GTGATCAACGACACTGCAATGCTAGGCCCTTGGCACCCTCG 40035 1108 GInSerAspLeuThrGluArgProGluGluPheGlyPheTleLeuAspAsnValGlnSer 1127 1108 GInSerAspLeuThrGluArgProGluGluPheGlyPheTleLeuAspAsnValGlnSer 1127 1108 GInSerAspLeuThrGluArgProGluGluPheGlyPheTleLeuAspAsnValGlnSer 1127 1108 GInSerAspLeuThrGluArgProGluGluPheGlyPheTleLeuAspAsnValGlnSer 1127 1108 CTCGGGCCCAAGGCACCTGACGAGTTTGGTTGGCTTTTGTTGGTGGAGA 40095 11128 LeuLeuIleLeuAspLySThrAsnPheThrTyTTyTProAsnProValPheGluAlaPhe 1147 1128 LeuLeuIleLeuAspCTTTCTTCTTCTTCACCTGATCCAGCTTTGAACCACTTTGAACCACTTTTGAACCACTTTTGAACCACTTTTGAACCACTTTTTT 40156 1148 GlyProSerGlyIleLeuGluLEuLySProGlyThrProIleIleLeuLyST   |   | CATTGCTACTCATGGCTTCATGCGCTGAGATGATTGCTGTTGTCTTCACAGACATGCCAG 3997 | <b>a</b> 8  |                        |
| 39976 GTGATCAACGCACTGCAATGTTTTTTTTTTTTTTTTTTT  |   |   | Š 2         |                        |
| 108 GINSerAspLeuThrGludrgProGluGluPheGlyPheIleLeuAspAsnValGlnSer 1127 40036 CCTCGGGCCCAAGGCGAGCACCTGACGACTTTGTGCTGGACCACGTGCAGGCA 40095 40036 CCTCGGGCCCAAGGCGAGCACCTTGACGACTTTGTTGTTGGTGGACCACGTGCAGGCA 40095 40096 GCCCGTCCTTAAACGTTTTTTTTTTTTTTTTTTTTTTTT   |   |   | an d        |                        |
| 40036 CCTCGGGCCCAAGGCAGTTTTGTTTTTTTTTTTTTTTTT  |   | GlnSerAspLeuThrGluArgProGluGluPheGlyPheIleLeuAspAsnValGlnSer      | δ, δ        |                        |
| 1128   LeuLeuIleLeuAsnLysThrAsnPheThrTyTTyTPTOASnProValPheGluAlaPhe   1147   |   | CTCGGGCCCCAAGGCGAGCACCTGACGAGTTTGGCTTCTTGCTGGACCACGTGCAGGCA 4009  | a d         |                        |
| 40096 GCCGCTCCCTCAACGTTTTCTTTTTTTTTTTTTTTTTTT  |   | LeuLeuileLeuAsnLysThrAsnPheThrTyrTyrProAsnProValPheGluAlaPhe      | QY          |                        |
| 1148 GlyProSerGlyIleLeuGluLeuLysProGlyThrProlleIleLeuLys   |   | GCCCCTCCCTCAACCGTTCTTCCTTCACCTACCACCTGATCCCAGCTTTGAACCACTT 4015   | ga (        |                        |
| 40156 GGGCCTCTGGTGTGTGTGTTGTTGTTGTTGTGTGGGG 40215  1164  |   | GlyProSerGlyIleLeuGluLeuLysProGlyThrProIleIleLeuLys               | Š ź         |                        |
| 1164 1164 Db 14129 40216 ATAAGGATAGGAGAGAGAGAGAGAGCTGGAGTGCTTGACTGTTTCT 40275 Qy 1428 1165   |   | GGGCCCTCTGGTGTGCTAGATGTCAAACCTGGTTCACATGTTGTATTGAAGGTGCTGGG       | <b>a</b> 3  |                        |
| 40216 ATAAGGATAGGAGTAGAAAGGAGGGAAGAACTGAGAGTGCTTGACTGTTTCT 40275  Qy 1428  1165  |   |   | 5 2         |                        |
| 1165   |   | ATAAGGATAGGGAGTAGAAAGGAGGGGAAGAACTGAGAGCTGGAGTGCTTGACTGTTTCT 4027 | 3 6         |                        |
|  |   |   | 3 2         | 77E78 77E77E775 85E18  |

|          | 40276 | GTGTGGGTTATCCACTACTAGGGCAAGAACCTGATCCCTGCTGCAGCTGGCAGCTCC 40335                     |          |
|----------|-------|---|----------|
|          | ~     | SLeuAsnTyrThrValLeuValGlyGluLysProCysThrValThrValSerAspVal                          |          |
| _        | 40333 | GGAGGACAGCCATGTGCACTGTCTCAGATACT 4039   |          |
|          | 1198  | LeuLeuCysGluSerProAsnLeuIleGlyArg   |          |
|          | 40393 | AACTICIGIGATICCCCAAGCCAGACAGGCGGGCAGCCIGITATGGTGGGTAIGGGC 4045                      |          |
|          | 1213  | ,   |          |
| _        | 40453 | CAAGAGGCCACCAGGGCAGCCCTGGCTGTGCATGGGAGTTGGTTCACCTCAAGCTTGCC 4051                    |          |
|          | 21    | AlaArg-ValGlyGlyMetGluTyrSerProGlyMetValTyrIleAlaProAs 1231                         | $\vdash$ |
| ^        | 40513 | rgggrggccrggagttcrggrrgggcacgcrgcacarcacrgcrga 4057                                 |          |
|          | 123   | pSerProLeuSerLeuProAlaIleValSerIleAlaValAlaGlyGlyLeuLeuIleIl 1251                   | - 6      |
| 0        | 27    | TCGGGCACTGACCTTACCAGCTATGGTGGGGCTAGCAGCAGGGGGGGG                                    |          |
|          | 1251  | ePheileValalaValLeuileAlaTyrLySArgLySSerArgGluSerAspLeuThrLe 1271 :                 |          |
| Α.       | 1271  | uLysArgLeuGlnMetGlnMetAspAsnLeuGluSerArgValAlaLeuGluCysLysG                         | 1        |
| ^        | 9     |   |          |
| ν.       | 1291  | 3-  | 1        |
| •        | 40753 | i<br>AGGIGCCIAAAAGCAGGGGGIGIACCACATIGIGIGAGAGGIGAGGGACTTTCCTGCTTCT 4081             | 112      |
|          | 1292  |   | 11       |
| •        | 40813 | TGTTCAACTCACTCTACCGTATTGTTTCCCAGCCTTTGCTGAGCTGCAGACTGATATCAA 4087                   |          |
| ~ 0      | 1301  | sGluLeuThrSerAspLeuAspGlyAlaGlyIleProPheLeüAspTyrArgThrTyrTh 1321:           :::::: |          |
| . ~      | 3     | rMetargValLeuPheProGly1leGluAspHisProValLeuArgAspLeuGluVa                           |          |
| 0        | σ     | :::   |          |
| _        | 1341  | roGlyTyrArgGlnGlu   |          |
| 0        | 6     | CCTCCTACCCCCAAAGCCTGCCCATATTCTGTTTTCCCCAGAGCCACCACTACCTAC                           |          |
| ~        | 1347  |   | 9        |
| 0        | 41053 | CIGAGATICCCIGGICCCCACAGACICCCCCCAATGIGGAGAAGGCCCIGCGICTATIIG 4111                   |          |
| <i>,</i> | 135   | laGlnLeulleAsnAsnLysValPheLeuLeuSerPheIleArgThrLeuGluSerGlnA 137                    | o i      |
| 0        |       | GACAGTTGCTGCACAGCCGTGCCTTCCTGCTCACCTTTATCCACACTTTGGAGGCCCAGA 411                    |          |
| 5~       | 37    | rgSerPheSerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnS 139                    | 9        |
| o        | 41173 | GTAGTTTCTCCATGCGTGACCGTGGTACTGTGGCCTCACCTCACCATGGTGGCCCTGCAGA 412                   |          |
| >-       | 1396  | erLysLeuGluTyrAlaThrAspValLeuLysGlnLeuLeuAlaAspLeuIleAspLysA 1410                   | 9        |
| ٥        | 41233 | GCCGGCTTGACTATGCCACTGGGCTCCTCAAGCAACTGCTGGCTG                                       |          |
| >-       | 141   | snLeuGluSerLysAsnHisProLysLeuLeuArg   |          |
| o.       | 7 .   | ACCITICAGAGCAAGCAACCACCCAAAGCAAGCAGCAAGCAAGAAAGAAG                                  | i a      |
| >-       | 42    | 7.47  | o d      |
| Ω        | 41353 | GCCTCTCCCTCCAGTCCTGCTTCCATTTCCTGCTTGGGCCCCTACCTCTGTTCAAGTCTC 4141                   |          |

| TITLE Direct Submission  Cambridgeshire, CB10 15A, UK. E-mail enquiries:     humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk     conher on Aug 15, 2002 this sequence version replaced gi:21628092.  COMMENT On Aug 15, 2002 this sequence version replaced gi:21628092.  Center: Wellcome Trust Sanger Institute Center code: SC     web site: http://www.sanger.ac.uk     contact: humquery@sanger.ac.uk     contact: humquery@sanger.ac.uk     contact: humquery@sanger.ac.uk     contact: humquery@sanger.ac.uk     contact: project Information     Center project name: bM436K3     contact: project name: bM436K3     contact: sudality: 203854 bases at least Q40     consensus quality: 203854 bases at least Q20     Insert size: 203924; sum-of-contigs Quality     coverage: 8.28x in Q20 bases; sum-of-contigs Quality     coverage: 8.28x in Q20 bases; agarose-fp |   | source 1.24432.    Joganism="Mus musculus"     Ab_xref="taxon:10090"     Clone="RP23-436K3"     Clone=lib="RPGT-23"     J. 1898 | Alignment Scores:  Pred. No.:  A403.00  Matches: 1115  Score:  A403.00  Matches: 1115  Percent Similarity: 37.79%  Conservative: 292  Mismatches: 1897  Query Match: 2 |
|--|---|---|--|
| Db         43569 ATAGAAGGTGGTGCTGGGTTGTGCAGATGGAAGTGCTAGTCTAGCACTGGGATTG 43628           Oy         1741   | 1745 LeuargPheTrpValasnMetIleLysAsnProGlnPheValPheAspIleHisLysAsn | 0y 1812   | Oy 1847 tSerAlaLeuSerGluIlePheSerTyrValGlyLysTyrSerGluGluIle 1864  1   |

| 276 TyrThrSerLysLeuValArgLeuCysLysGluAspThrAlaPheAsnSerTyrValGlu 295 :::           ::: | TITELLI III IIIIIIIIIIIIIIIIIIIIIIIIIIII                             | 392  | 88511 TTCTCTTGGCCAGTGTCCTGTTTGTATACTGCCATTTTCCTTTTCTGCCTCTATATTCAT 88512 392 | 392   | AspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValArgGly | 442 ASNHiSSErLeuAlaPheValGlyThrLysSerGlyLysLeuLysLys                 |
|--|--|--|--|---|--|--|
| 6  | 6                              | çò da co da co   | q  | 90 OV   | ko qa ko qa .  | 90 OO OO   |
| 41<br>90187<br>61<br>90130<br>81<br>90070<br>101                                       | 121 AspTyrLysGluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeu 140 | 181 AspLysLeuPheIlealaThralaValaspGlyLysProGluTyrPheProThrIleSer 200   1 | 89650 GTTGCTTTTGTCTTTCCCCTGGTTCTTATGAGCCCAGGTCTTATTCACTCCTTTCTC 89 214       | 89530 ACTGTCACATAGATGTAGACCAGCTGTTGAGGACAGGAAGATGGGCAGAGTTTACCTGTG 89471  214 | 215  | 236 IleileProAspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyr ::: |
|  |  | oy<br>Oy<br>Oy<br>Oy   | oy oy oy   | 8 8 8 8   |  | oy<br>da<br>oy   |

| _              | 86955   | GGTGCGGGTCCGTCCCAATAATGTGTCAGTGACATCCTCTGGGGTGCA-GGTAAGTGACA                            | 86897        |
|----------------|---------|---|--------------|
| ,              | 3       |   | ,            |
| <b>~</b>       | <u></u> | 1   | ٥            |
| 0              | 96898   | TAGAGGATACTTGGCCCTGTATATGCTTCATGAGGGAGGG  | 86837        |
| 5.             | 577     |   | 92           |
| 0              | 86836   | CTGCCTTCCCCAGCTGACCGTAGCCCATGCGCAACGTGCCAGACCTCAGTGTGGGTGTGAG                           | 86777        |
| > (            | 592     | nCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIleGl                               | 6111         |
| n.             | 0       |   | - 6          |
| 5- 1           | 611     | nCysTyrSerProAlaAlaLysGluValProArgIleIleThrGluAsnGlyAsp :             :   :           : | 629<br>86657 |
| د ۵            | 20      | 17C11CACCA1CCA1CACACACACACACACACACACACAC  | 29           |
| , G            | 10      | GGGGCAATCTGGGGTGTTGTGGGGCAGGGCAGAATTCCAGACTAGTTGGCAATAGCCA                              | 9            |
| ı :            | 630     | TheuGlnLeuLvsSerLvsGluThr   | 43           |
| . <sub>γ</sub> | 96      |   | 9            |
| >              | 43      | rAsnCysSer  | 657          |
| فد             | m       | :::   | 86477        |
| *              | 657     |   | 657          |
| q              | 86476   | CCTGGTCCAGAATCTGTCCCTAGCCCTGGGGATAGTAGAAAAGTGCTCTG                                      | 86417        |
| <b>≻</b>       | 657     |   | 657          |
| Q              | 86416   | AATTGCACTGTAACTTTCTCTAGGGTTCAGGGGTGAGTTGTTGGGACTTCCTGC                                  | 86357        |
| ≻₁             | 658     | eA  | 658          |
| ą              | 86356   | ATGTGCCCTATGTGCCTTGGGCAGGTTCTGCC  | 86297        |
| λ              | 658     | IHis  | 629          |
| ٩              | 86296   | CCAATGTGT   | 86237        |
| Ž              | 099     | AsnSerCysLeuSerCysValGluSerProTyrArgCysHi   | 673          |
| ð              | 86236   | TTCTAAAGCTACTCCCCCCCCCCCGGTGTATGTCCTGTGTTGGCAGCCCTTACCCCTGCCA                           | 86177        |
| ¥              | 673     | rpCysLysTyrArgHisVa   | 693          |
| ð              | 86176   | AGCCACCCACAC  | 86117        |
| λi             | 693     | ArgValLysLeuProGluAs  | 700          |
| q              | 86116   | <br>GTCCACAGCCCTGAGGT-GAGGTGGTGCAGCGTGGAAGAGGCTGG                                       | 86058        |
| λi             | 700     |   | 700          |
| ą              | 86057   | GCTGGCCTCTCACATTTTTTGTTTGACCTCCC  | 85658        |
| λ              | 701     | CysProGlnLeuAr  | 902          |
| q              | 85997   | PAACAAG   | 85938        |
| λ              | 206     | gValAspLysIleLeuValProValGluValIleLysProIleThrLeuLysAlaLysAs                            | 726          |
| q              | 85937   | AGGGGACCTCTTGATTCCTGTGGGTGTCATGCAGCCTCTAACTCTGC   | 82878        |
| ίγ             | 726     | nLeuProGinProGinSerGlyGinArgGlyTyrGiuCysIleLeuAsnIleGinGlyS                             | 746          |
| qo             | 85877   | cereceacaecereaer   | 85818        |

| 920 GlualaLysProSerGlnHisAlaGlyPheValGlulleCysValAlaValCysArg 938<br> | ProGluPheMetalaArgSerSerGlnLeuTyrTyrPheMet | 4 GCTGACTTCCGCACACAGTCCCAGCAACTCTACAGCTTTGTGGTGCGTGGTCTAACTAGC | 952     | CCCTTCCCCTTCCCTATCTGGGAAAATGTGGAGTGTCCCTTGGATCAGGCTGCCTTCTAC           | 953     | CICCICICAAGGGCIGCIICIICAGACCCCIACAACCGIGIGAGICCCICICG        | 903 9G1VPTOMETSETG1VG1V1NThTG1NVALThTIEThTG1VThTAShleuAshAlaG1ySe 983 | GGGCCCAGCTTCTGGAGGCACTCGGCTTACCATCTCTGGAATTTCTCTGGATGCCGGCAG        | 983 rAsnValValMetPheGIyLysGlnProCysLeuPheHis997<br> |        | AAGCCATCTGGAGTTGAGCACTGATTGTGTGAAAGACTATGGGGGGCAGGGTAGGTGAAGG | 998   | TICCAGGCCATCTCATCATCCTACCTGCTTACCTGTGTGAGGAGATCCGGAGGCAATTACCTGTGTGTAGGAGAGATCTGCAAGGAAAGCAAGGCAATTACCTGTGTGTAGGAAGAGAAGAGAAGAAGAAGAAAGA | OV2   Over and American Conference of the live of the | CVALCYS ASHIII III III SALASVALLAVALLAVALLAVALLAVALLAVALSVALJOH VALGETIVA | Acadata   Acad | INSPARJONATELYSTIE HISCHINASPHEUCHINTY MALGELUASPHOOHITI<br> | eValArdTleGluDroGluTrnGerTleVal   | :::   | 1052 1052   | 84086 AGGACTGAGTTGGGGCTCTGAGAGTCTTGGGGCCTTACTACTAGGGGCCTTGGGTCA 84027     | 1052 1052  | 84026 TCAAGTGGTTCCTCCTTCCTGAGCCCTCATCAGTAGGGGCCACAGAGTTGTCCTGCCCAT 83967 | 1052 1052 | 83966 ATAGAGCCTGGCACCTGCTGAATGAACCAAGGTCAGAGGCTCTGAGGTCTCAGAAAATCC 83907 | 1053SerGl 1054 | 83906 TTGGTAACTTTGGACAGGGGGAAGGGAGTCTGAGCTCTTTACCCCATCTCTGCAGTGG 83847 | 1054 yAsnThrProlleAlaValTrpGlyThrHisLeuAspLeuileGlnAsnProGlnIleAr 1074  ::: | ANGCALCICCATICACTOTORS LOGANCCCATICTOCTONCAGIT CANGGANCCCCGTGTACG | 10/4 9/10/15/2017/01/2017/01/2010/15/11/01/2017/01/2017/01/2017/01/2017/01/2017/01/2017/01/2017/01/2017/01/2017/01/2017/01/2017/2017 |       |   | . 1087 uValLeuAsnAlaThrGluMetThrCysGlnAlaProAlaLeuAlaLeuGlyProAspHi 1107 |
|---|--|--|---------|--|---------|--|---|---|---|--------|---|-------|--|---|---|--|--|---|---|---|---|--|--|-----------|--|----------------|--|---|---|--|-------|---|--|
| Qy  | Qy   | qq   | Oy      | QQ   | Vy dy   | 20 6   | λο · δ  | ag (  | λδ  | -      | qq  |       | - qd   |   | ₹ £   | 3 8  | S de   | <u> </u>  | ැ අ   | Oy  | qa  | Qy   | qa   | Qy        | qa   | Qy             | qa   | oy d  |   | 2 dd   | ^0    | · qa  | Qy   |
| 746 rGluGlnArgValProAlaLeuArgPheAsnSerSerSerValGlnCysGlnAsnThrSe :::  | 766 F                                      | <br>85757 GGTAAGACCCAGAGGTGCAGGCCAGCCAGGAATAATTTGTTTG          | 992 392 | 85697 GTTTTATTTTGTGTTTTGTGTGTGTGTGTGTGTGTGTGCGTGTAATATTTTACTGTAT 85638 | 766 766 | 85637 TTTGTATTTGGTTGGTTTTGGTCTATGCCTTACTTATCTGGAAACCTTTTTTTT | 992 1992  | 85577 TTTTTTTTTTTTTTTTATAAGGGATTCCTAAAGTGGGCAAGGATTTTGCTCATCT 85518 | 767   |        | 776 snLeuProValGluLeuThrValValTrpAsnGlyHisPheAsnIleAspAsnPro  | 85457 | 794  | 85397 GCTTCCGAGGTGAGGGGTGACATGGGGCCAAGGAGCATGGCTCCTGGGGCAGGATTGGCA 85338  | 795AlaGlnAsnLysValH 800   | 85337 CIGCIGGGGCCAAGICIGIAGGICCIAGAGCCCCCIGCIIITCIGCCAT-TGCCIGC  | 800 is   | 85278 ATCAGIAGICTCCTGTGCCTGCAGCCCTTCTTACAAGTGCTGGGCTCAGCGGCCTAGCT 85219 | 811 ysGlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGlnGlyProGlyG 831. | 031 ) ACCOMPLET CONCENTRATION OF THE CONTRACT | osi incystiiledukigeintiseyskioaladindinsektrinirphedelubebergiya 851<br> | 851 JalvsSerivsThrAsnDroArdTeathrile-10-10-10-10-10-10-10-10-10-10-10-10-10- | 85098 AGGGTGCCGATCCATCCGGATCCGGATCGTAACTTAACT                            | 798       | 85038 TIGCTICTIAGGCAIGTGTGAGTCTGGCCTGATCTTCTTGCTTCTTCTCCTGCTCTGCAG       | 882            | 84978 ATTCATCCACTTACAGGACCCCAAGGAGGTGCCACCCGGGTCACCACTTGTGGGTGAGAAC    | 902   | 84918 CTGGGCCTCACTTCCCGTGAGGTTGGCCTTCGAGTAGCTGGTGTACGTGCAAC 84865 |  | 84864 | 913Glumetcly 919 919 919 919 919 919 919 919 919 91 | 04004  |
| oy d  | δ δ  | qq   | Qy      | QQ   | Οy      | DP   | Qy  | QQ  | Qy  | Q<br>D | δŏ  | gg    | δy   | qq  | Qγ  | qq   | Οy   | q<br>C  | Qy<br>dq  | 3 8   | d<br>d  | ò  | 7 음  | ò         | ' සි   | òO             | 7 음  | Qy  | qq  | ΟŊ   | ΩΩ    | δδ d  | 3  |

| 110   SGIUSETERSEGENACESTEGENATGENATGENACESCENTCTTCCTTCGGCCCCTCA   9507     110   SGIUSETESSEGENACESTEGENATGENATGENATGENATGENESIS   9507     110   SGIUSETESSEGENATEGENATGENATGENATGENATGENATGEN   9117     111   TITLELGENITGENATGENATGENATGENATGENATGENATGENATGEN   9118     112   TITLELGENITGENATGENATGENATGENATGENATGENATGENATGENA  | ### ### ############################## | , | ### ### ############################## |   | 1553      81631   GGTAAGGTCCCTCCTTTTCTCCTAGCTCCCACCTATCCAATCCCTCCC  |
|--|--|---|--|---|---|
| 1107   ScinserAbacoacotrochartechartegramsococotrocotrochartegramspass validates   1127   1110   1 |  |   |  | 4 d d d d d d d d d d d d d d d d d d d                           |   |
|  |  | 1165                                    | ### ### ############################## | 1271 eulysArgleuGlnMetGlnMetAspAsnLeuGluSerArgValAlaleuGluCysLysG | 2769 ATGAACTGACAACCACATGGTGTCCCAGATCCCCTTCTTGGACTACCGGTUVAL- 1321 hrmetargValLeuPheProGlyIleGluaspHisProValLeuArgAspLeuGluVal- 1340 1341 proGlyTytArgGlnGlu |

| ٥y       |   | Qy         | 1699.IlePheSerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysTyrMetPheAsp 1718 :::1 |
|----------|---|------------|---|
| g. č     | 81451 ATCCTCCAAGATGAGGACATCACTACAAAGATTGAGTGTGACTGGAAGAGGGTCAACTCA 81392<br>1584 LeualahisTyr1587 | oy i       | 9 PheLeuAspGluGlnAlaAspLysHisGlyIleHisAspProHisValArgHisThrTrp 173          |
| qa       | #11991 TTGGCCCACTACCAGGTGAGGAACTTTGAACCTATTCAGCTCCAGGGACACCTAGAAGTA #1332                         | <b>Q</b> . | 3 ITCCTGGATGAACAGGCTGACCAGGCCCAGATCAGTGACCCTGATGTGCGTCACACCTGG 80           |
| · OY     | 15  | දු දි      | 1939 LYSSELASH<br>  |
| අධි .    | GIGGCCAGGICICCICTCGICCCITAICCCIAIACICATGAGGGCIICICAIAGGGCCIT 81                                   | Qy         | 11  |
| δδ<br>Op | 1587  | qa         | 80193 GGAAGAGGCTAGTTACTTAGCCAAGCCTCCAGGCCAATGGAGACAGGTTGACTAGCAACT 80134    |
| Oy       | sGln 16   | . ко       | 41 1741   |
| qq       | 81211 TCTGTTTCTTTGGACCTCCAGGTGACTGATGGTTCTTTAGTAGCACTGGTGCCCAAACAA 81152                          | g å        | 80.33 GAATAGCCTTCCATGCAGGAGGGATGGACCAGTGGTATGGCCTGGAAGTGAATATGAGTA 80074    |
| Ολ       | ValThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThrSer 16<br>    :::                                    | Z 23       | 1 1/1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                     |
| qa .c    | 81151 GTGTCTGCCTATAACATGGCCAACTCGTTCACCCGGTC-ACTTAGTCGCTACGG 81093                                | ٥y         | ;   |
| ·<br>3   | TAGGTATCCATATGTGGTGGCTTTCCTGGTCCCGTGTGAATTAAAACGCTGAATTAAAAAAAA                                   | qq         | 80013 GACCATTTTCTCTAGGGTCCTGTGCAGGGTAGAGACACTGATGGCTTGGCATAGGTGGA 79954     |
| Qy       | 10  | Qy         | 1741  |
| qq       | 81032 AGGAATCCCCAAGTAGCTGTCTTGATCCATTTGGAAAGACTTTCATTATTTTGGGCCCCT 80973                          | qq         | 53 GACAĞTGGAAĞTTTCAGGGGTGGAĞGTTGAĞGACAĞAAAĞCCATCTATTCTTATTTCTCA 798         |
| δλ       | 1617 1617   | δλ         | 1 174   |
| QQ       | 80972 GGGTGGTCTTCAGTTGTATAGAGCCTAATAGGGAGGGGGGGCCAAGGATAGGTGGGTCCCA 80913                         | qq         | 93 TTGCCTGAGTGCAGCAGAAGGTTAAAGAAAAACCCATTTATCCAAAATAGTCTCTCTGT 798          |
| Qy       | 1617  | δλ.        | 41  |
| Dp       | 80912 CAAAGACTTCTAGAAGATAATGGAGCAAGGGTGGGTAATGGCCAGAGCCTGTAGGGCT 80853                            | qq         | 33 TACTTCAGGACAAGATATGACCTGGCCAAACAGGACAAGGTGTGAAGGAAG                      |
| QY       | 1618AlaSerLysTyrGluAsnMetlleArgTyrThrGlySerProAsp 1632  | Qy<br>Ph   | 1742CysLeuPr 1744   |
| QQ       | 80852 TAAGAGTCACATCTGTCCTCTGCCCTAGAGAGCTTGCTCCGTGCTGCCAGCAGCCCGGAT 80793                          | 3 3        | 10   10   10   10   10   10   10   10                                       |
| δ d      | 1633 SerLeuargSerargThrProMetIleThrProAspLeuGluSerGlyValLysMetTrp 1652                            | Å q        | 1/44 OLGURIGFRETTERFYGAISMETLEELYSASNETGGIDNEVALTREASPLEHISLYSAS 1/04 11    |
| λō       | HistourallysAsnHisGluHisGlyAspGlnLysGluGlyAspArgGlySerLysMet 167                                  | Qy         | 1764 nSerIleThrAspAlaCysLeuSerValValAlaGlnThrPheMetAspSerCysSerTh 1784<br>  |
| qq       | CACCTGGTGAGGAACCACGACCACACTGATCACCGAGAAGGAGCCGCGGCGGCAGCAGATG 806                                 | Qy         | 4 rSerGluHisArgLeuGlyLysAspSerProSerAsnLysLeuLeuTyrAlaLysAspIl 1804         |
| oy<br>Ob | 1673 ValSerGlulleTyrLeuThrArgLeuLeuAlaThrLys  | qq         |   |
| Oy       |   | , Qy       | 804 eProSerTyrLysAsnTrpValGlu   |
| Dp       | 80613 CACCTICTAGCCCAGICTTAAACATGAGATGAGCTGCTTTCTTAGGGCCTTGGCACTAGG 80554                          | g 8        | /9533 TCCCAATTACAAGACTGGGTGGGCCCTGGGATACTGCTGTGTGTG                         |
| ογ       | 168   | qa<br>Dp   | 473 GGCAGGCAGGAACTGCCTAAACAGCCTGTCTGAGGCTGGCCAGATACAAGAAAAAGCCTC 794        |
| g :      | 04  | Qy         | 1812 1812   |
| g<br>S   | TTTTTTTTACTGAGCTATTCTGCCCCCTGTCTGTCAGATTTTGGGAACTTCCTGACA   | qa         | 79413 AGAGGCTGGCCAAACACTGATGGCATGAGTTTTGGCATTATGACCTGTGCATGATTCAC 79354     |
| ογ       | uThr 169  | oy<br>G    | 813ArgTyrTyrSerAspileGlyLysMetProAlaileSerAspG 1827                         |
| q<br>q   | 80433 TTCCTTTACCATCACACATGGGCACGTTGCAGAAGTTTGTAGATGACTTGTTTGAAACT 80374                           | 0 V        | 27  |

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   HUMFLNG6PD 219447 bp DNA linear PRI 17-MAY-1999 Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's.
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1A gene; 2_19 gene; ABP-280 gene; DNL1L gene; DNase I-like protein gene; EMD gene; FLN gene; G4.8 gene; G4.8 gene; G5PD gene; GDT gene; GA gene; GA gene; GA gene; MAP-1 gene; MAP-2 gene; MAP-4 gene; MAP-7 gene; AAP-7 gene; AAP-7 gene; AAP-7 gene; AAP-7 gene; ACP-6 gene; AAP-7 gene; ACP-6 gene; AAP-7 gene; ACP-6 gene; AAP-7 gene; ACP-6 gene; AAP-7 gene; ACP-6 gene; AAP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; ACP-7 gene; AC
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Chen, E.Y., Zollo, M., Mazzarella, R.A., Ciccodicola, A., Chen, C.-N., Zuo, L., Heiner, C., Burough, F.W., Ripetto, M., Schlessinger, D. and
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Note: Gene predictions were accomplished with runs of Grail
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PUBMED
COMMENT
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SOURCE

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130601 CTGCCGGCCATGCCC----TCTGTCTGCCTCCTCCTG---CTGCTCTTCCTTGCCGTG 130651
                                                                                                                                                     130588 GTGGTG------ACAGACACCACGCTTACCCACGCTGTGCACGGGTGACT 130735
                                                                                                                                                                                                                                                                                                                                                                                                                                                         131096 AGCAAGCTGTTTGTGGGCACTGCTGTCGACGCAAGTCGGAGTACTTCCCCACCTTGAGC 131155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131.276 TGAGAGGGGACTTTCGGCTCCTCAGTGTCTGGGATGCAGACAGGTTGCGGAGGGTGGGAT 131335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131336 GACAGCCTGAACCCCAGGTTGCGGGGGTCCCCTGTGTGCAGGGAGGCTGGTCACCCTGCCC 131395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131396 TCTGCAGCCTTTCTGGCCTGGGCCTCTGTGATCATCCAGGCGGGAGGGGGATGCAGAGGG 131455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AspTyrLysGluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeu 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 SerGlyValAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAsp 180
                            MetLysAlaMetProTrpAsnTrpThrCysLeuLeuSerHisLeuLeuMetValGlyMet 20
                                                                                                                                                                                                                                                                                                                                                                                                                       LeuValThrHisGluThrGlyProAspGluAspAsnProLysCysTyrProProArg1le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ValThrPheArgGlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ValGlnThrCysAsnGluProLeuThrThrAsnAsnValAsnLysMetLeuLeuIle
                                                                                                                         GlySerSerThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKLNPKKARAYGPGIEPTGNMVKKRAEFTVETRSAGGGEVLVYVEDPAGHQEEAKVTA
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PSGNIANKTTYFEIFTAGAGTGEVEVVIQDPMGQKGTVEPQLEARGDSTYRCSYQPTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKGDAVRDVDI IDHHDNTYTVKYTPVQQGPVGVNVTYGGDP IPKSPFSVAVSPSLDLS
KIKVSGLGEKVDVGKDQEFTVKSKGAGGQGKVASKI VGPSGAAVPCKVEPGLGADNSV
VRFLPREEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSKVKAFGPGLQGGSAGSPARF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKTGVAVNKPAEFTVDAKHGGKAPLRVQVQDNEGCPVEALVKDNGNGTYSCSYVPRKP
VKHTAMVSWGGVSIPNSPFRVNVGAGSHPNKVKVYGPGVAKTGLKAHEPTYFTVDCAE
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YTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSRVRVHGPGIQSGTTNKPNKFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGVHTVHVTFAGVPIPRSPYTVTVGQACNPSACRAVGRGLQPKGVRVKETADFKVYTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKGDGSCDVRYWPQEAGEYAVHVLCNSEDIRLSPFMADIRDAPQDFHPDRVKARGPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGQGDVSIGIKCAPGVVGPAEADIDFDIIRNDNDTFTVKYTPRGAGSYTIMVLFADOA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPTSPIRVKVEPSHDASKVKAEGPGLSRTGVELGKPTHFTVNAKAAGKGKLDVQFSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIDTKGAGTGGLGLTVEGPCEAQLECLDNGDGTCSVSYVPTEPGDYNINILFADTHIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPFKAHVVPCFDASKVKCSGPGLERATAGEVGQFQVDCSSAGSAELTIEICSEAGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEVY IQDHGDGTHTITY IPLCPGAYTVTIKYGGQPVPNFPSKLQVEPAVDTSGVQCYG
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                                                                   /rpt_family=^Alu-Sb0 or Alu-Sb1"
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219447 1127 297 423 2023 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 4394.00 36.84% 29.16% 43.98% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Pred. No.: .. Q Score:

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US-09-964-956-13 (1-1896) x HUMFLNG6PD (1-219447)

|                                       | _          | 451 LysSerGlyLysLeuLysLys 457  | Qy             |
|---------------------------------------|------------|--|----------------|
| 458                                   | oy o       | 132656 GGCATGGCCAGCGTAGCCGTACCCTACCGCCAGCACTCTGTGGCTCTTCATTGGCACG 1                                | qa             |
|                                       | Z          | 431 ArgMetThrSerVallle   | QY             |
| 133676 TGGCCTCCGGGCTGTGGGTGTGAGTGCTGA | qa .       | 132596 CAGCCTGGGAGGCCTGCATGTGATCGAGGGGCTGCCCTGCTGGCGGACAGCAGCACAA.13                               | q <sub>Q</sub> |
| 457                                   | Oy         | 13239 CICCICIONITICACONOCCINICACONITICACONITICACONITICATOR AND AND AND AND AND AND AND AND AND AND | a è            |
| 133616 GAATCACTCCGTCCTTCTGTTTGCTGAGGG | qq         | 400  | Qy<br>4d       |
| 457                                   | ٥٧         | 132476 CTGGGACTCAGGAACTGCCGGCCTCCATCTTGCGCCTGGGAGCTTTGACTCTCACGGGTT                                | qa             |
| 133556 CTAATCAATGCCATCTTCTAGCTCTTCCCC | qa         | 399  | δ              |
| 457                                   | QY         | 132416 ACCCTAGGGCGAGCAGTCAGTCCTGGCTGGAGGGGACCGGGTTCTAGATCCCGCTCTTT 1324/                           | ga             |
| 133496 AGTTCAGTGGGTTTCTGTGGATCTGCAGAG | qa         | 995  | δλ<br>Oλ       |
| 457                                   | QY         | 132356 GCTCCTCGCTGCTGTCTCTCTGTCTCCTCCGCAGCCACCACTTTCCTGGAGC  | qa             |
| 133436 TITCCITIGIAGCAGCITIGIIGAACGCGI | අි         | 368  | δλ             |
| 457                                   | Qy         | 132296 GCTCCGTCTCCCGGTTGCCCCTTGTCTTGAGCCAACAAGAGTCTTGTGGGCCCAGGCTTC                                | qa             |
| 133376 GGTTTGTGGAGAAGGATGATGAACTCTCCT | qa         | 399. Thr 399   | Qγ             |
| 457                                   | Qy         | 132236 CTCTCTGGGCTGCCCAGTGCCCCACTTCTGCTTCCGTTCCCAGCTCGTTCCTTCTT 13                                 | <b>q</b> a     |
| 133316 CCTCGTAGATGCAGTGCCATCCCCCAGGAG | qq         | 394SerSalaLeuLeu 398   | , 0y           |
| 457                                   | ^O         | 132176 TGGCACCTTTGCCCTCCCACCTGTTTCTCCCTCCCAGGGGTCCCTGCCCTCTCCTTGCCT 132235                         | qa             |
| 133256 CACTCAGGTACGTGTTGAATAGGTAGGAGT | - qa       | 393  | QY             |
| 457                                   | ò          | 132116 ATGCCCAGCGTGGGCTCACGGCCAGTCATCCTGTCCCAGGCTTTGCCATGGCCCTGGGAG 132175                         | qq             |
| 133196 AGCTGCTTCCATTGGGGATCTGGGGGTAGC | qū         | 393 393  | Qy             |
| 457                                   | Oy         | 132056 ATCAACACCGTGAGCCCCTCATCACCCCACACTGGTCCTTGCCCTGTCCCAGGTCTACC 132115                          | qa             |
| 133136 CCCTCTCCTTGGCTCACTTCCCATCCT    | qa         | 393 393  | Οy             |
| 457                                   | δλ         | 131996 TGCTATCGTGGGGAGGGC  | qα             |
| 133076 GGGAGCAAATGCCTTGCCCCTCAAGCCTCC | qa         | 374 CysTyrArgGlyGluGlyThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCys 393                               | Qy             |
| 1 C                                   | G :        | 131936 ATCCTCTGCCTCTCACCTCAGCAACATCAATGCCCACATCCGGGGGCGCGCATCCAGTCC 131995                         | qa             |
| X                                     | δία        | 354  | Qy             |
| 132956 CTGAATTGCCAGCTTCGTATGGCTCTGGGG | අ <u>ධ</u> | :::  | qa             |
| 457                                   | Qy         | 1314 IniterPheThrValPheSerIvsGlvGlnIvsArdLvsNetLvsSerIeuAspGluSer 353                              | 8 8            |
| 132896 CCTGCTCCTCGGGTCGCCCCTTGGCCGCCC | qa         | 314 Tyricuserlysalasiyalavalleuslyarginrieuslyvalhiskroaspaspasp 333<br>                           | Q              |
| 457                                   | . 09       | 131/56 GTGGAATTCCCCATCGGCTGCTCTGGCGCGCGTGGAGTACCGCTTGGTGCAGAGCGCC .13181                           | qq             |
| 132836 GGAGAGGACACGGCTGGTGCAGGGAGGAGG | qa         | •  | QY.            |
| 457                                   | Qy         | 131696 AAATTTTCACGTCCAAGAICGTGCGCATGTGCGGGGGGGGCTCAGAGTTCTACTCATAC 13                              | qa             |
| 1                                     | 7 Q        | 274 GlnValTyrThrSerLysLeuValArgLeuCysLysGluAspThrAlaPheAsnSerTyr 293                               | Qy             |
| 32/16                                 | gg G       |  | qa             |
| :::                                   | <u>-</u>   | 254 ValTyrPheLeuThrLeuGlnProGluMetValSerProProGlySerThrThrLysGlu 273                               | Qy             |
|                                       |            |  |                |

| Db | 132716 | :::   |
|----|--------|---|
| Οy | 457    | 457   |
| Db | 132776 | TCTCAGATATGGGACAAGGCTGGTGGGGAACACACGGGAGAGCTCTGAGGACAGGACA 132835   |
| Qγ | 457    | 457   |
| qq | 132836 | GGAGAGGACACGGCTGGTGCAGGGAGGAGATTTCCCTGGCTGG                         |
| Qy | 457    | 457   |
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| ω, | 457    | 457   |
| qq | 133196 | AGCTGCTTCCATTGGGGATCTGGGGGTAGCTTGGCATGAAGGGGGAGATGAACTTCTGGG 133255 |
| QY | 457    | 457   |
| Db | 133256 | CACTCAGGTACGTGTTGAATAGGTAGGAGTCGGGGGACTGCAGTGCTCTCATCCTGCTTG 133315 |
| Qγ | 457    | 457   |
| Dp | 133316 | CCTCGTAGATGCAGTGCCATCCCCCAGGAGGGCAAGTGTTGGTCTGGGGGCGCAGGGAAG 133375 |
| Qy | 457    | 457   |
| qq | 133376 | GGTTTGTGGAGAAGGATGATGAACTCTCCTGGCCCACCTGCTCTTTCCTGGGACCCTCT 133435  |
| ٥y | 457    | 457   |
| QQ | 133436 | TTTCCTTTGTAGCAGCTTTGTTGAACGCGTACTATCCAATTCACCCATTTTAAAGTGCAC 133495 |
| Qγ | 457    | 457   |
| Dp | 133496 | AGTICAGTGGGTTTCTGTGGATCTGCAGAGTGGCACAACCATCGCCACTACCTCATTCTC 133555 |
| Qy | 457    | 457   |
| Db | 133556 | CTAATCAATGCCATCTTCTAGCTCTTCCCCTCCCTGCATCCCCTGACCTTGGGCAACAC 133615  |
| Οy | 457    | 457   |
| qq | 133616 | GAATCACTCCGTCCTTCTGTTTGCTGAGGGCATTTTCTGGCGTCTGCACCCTCCTTTTT 133675  |
| Qy | 457    | 457   |
| qq | 133676 | TGGCCTCCGGGCTGTGGGTGTGAGTGCTGAACCCCACCAGGTCCTGACGTCAGCTCAGCC 133735 |
| Qy | 457    | 457   |
| qq | 133736 | ACAACCTCCAAAGTCTTTGGCTGGAGAAGACAGTGTCCCAGGTGCAGGAGGCTGTGGTGG 133795 |
| Qy | 458    |   |

| £61  | Db | 134992 GACACCTTCAGGGCAGCTGTTTCTGGGGCATCAGGGGGTAACTGTCAGGCCCTGATAGCC | ду         661 | 661   | 135112 TGTGTCCTATTGGGGAGCAGTGAGGGCCAGTGCAGCCTCCTGTTATTTCTGAAGCCAC | <pre>Qy 662CysLeuSerCysValGluSerProTyrArgCysHisTrpCysLysTyr 677</pre> | 678   | 135232 GGCGAGGGGGCGCCCCCACGAGTGCTTCCAGGAGGGCAGGGTCCACAGC                 | Oy 698 ProGluAsp 700  Db 135292 CTGAGGT-GAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | 700   | Db 135351 CCGGCTTCTATGCGTTCTCGGTTTCTTTGAGCCTTCTCCAGGTTGGGCCTGGAGAGGGT 135410 | Qy 701   | 135411   | <pre>Qy 708 AspLysIleLeuValProValGluValIleLysProIleThrLeuLysAlaLysAsnLeu 727  :::   :::                             </pre> | Oy 728 ProGlnProGlnSerGlyGlnArgGlyTyrGluCysIleLeuAsnIleGlnGlySerGlu 747 | Oy 748 GlnArgValProAlaLeuArgPheAsnSerSerValGlnCysGlnAsnThrSer 766 | 99L 166  | 135651 AGTCCCACCCGCTGCCTTCGGGGTCTGGGCTGTGGCGTGGTGGATCGTTCTTG   | OY 766766  Db 135711 TCTATGCCCAGCTCTCGGCAGGGAACTGTCTGAGTCTCCTGCTAGGGATTCCTGTACCT 135770   | Qy         766   | 767TyrSerTyrGluGlyMetGluIleAsnAsnLeuProVa                             | Db 135831 CCCATGGGTTCCTTTCCTCCAGTACTCCTATGAAGGTGATGAGCATGGTGACACCGAGCT 135890 Ov 779 1GluLeuThrValValTrDASnGlvHisPheAsnIleAspasnProAlaGln-AsnLvsV 799 | 135891 GGACTTCCGTGGTCTGGGATGGAGACTTCCCCATAGACAAGCCTCCCCAGGCTTCCGAGG |  | DD 135951 YGAAGGCAYGGGCCAGGGAGCYYCCCYCCYAAGGCAAYYGGCACYGCYGGGGYCGGGYCY 138010 |
|--|----|---|----------------|---|---|---|-------|--|--|---|--|--|--|--|---|---|--|--|---|--|---|---|---|--|---|
| 133796 CATCAGGCTGGTCTTGTGGCTCAGGTGGGTCGATGCCTTCCAGGATGCCCACCTG 133852 470 TyrGluThrValGlnValValAspProGlyProValLeuArgAspMetAlaPheSerLys 489 |    | 490 AsplisGluGlnLeuTyrlloMetSerGluArg                               |                | 133973 GCTGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | GGTGGAGACCTGTGAGCAGTACCAGAGCTGCGCAGCCTGCTGCTGCGGGGCCCGCA          |   |       | 134152 AGGGCCCCACTGGCCAGGGGGAGCCAGCCACCCAGCCGTGCCCTTGCGGCCTCCCCCC 134211 | 535 535  | GCCCTCCTCCACTTTCTCCAGCTAATGAGTGGAACCTCCACCCCGAGTGACGTCCCTCGG 13 | 134.77. GCCCCABCGCBCCCCABACCCGCCABACCGGCCAACCGCCAACCGCAACAACAACAACAACAACAA   | VICENTAGE OF THE PROPERTY OF T | GCCCTCCCGGGGCAGGGGGACCGGCTCTGGCCCGAACCCCGTGCAGGTGCTGCCGCGA | 539 sGluArgCysGluArgSerLysGluProArgArgPheAlaSerGluMetLysGlnCysVa 559<br>   | ArgLeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeuLeu 577<br>  III     |   | 134512 CTTGGGGGTGCCCGGCTGGGTGTGCACATGTGTGCTGGGAGTCCGCCCTGCCCTGAGCCC 134571 | 2 TCTGCTTCCCCCAGCTGACCGTCACCCTGCACAACGTGCCAGACCTCAGTGCGGGGGGGG | 592 snCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIleG 611 :::    :::::: 134632 GCTGCCCTTCGGGGGGGGGAACAACAAGAGGGGGGTCCTCCCCTCAACTGC 134691 | lnCysTyrSerProAlaAlaLysGluValProArgIlelleThrGluAsnGlyAsp | 134692 TCTGCCCCTCACCCTCCAGGAGCTCCGAGCTCTTACCAGGGGCATGGTCAGTGGG 134751 | 134752 TTGGGGCTGCCCAGGATGGGGCAGAGTGGGGCCTCTCCCTACCCCCAGCGAGTTCACGGC 134811  | 630yseruyselu 641   | ThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerValHisAsnSer | 134872 ACAGGGGGGGTGTGGGGGGGGGGGGGGGGGGGGGGGGGG                                |
| ob<br>Qy   | qq | Qy<br>Dp  | Qy             | <b>a</b> è                                    | qq  | Qy<br>Pr  | OV OV | qq   | Qy   | අ <sub>ධ</sub> :  | Š 2  | 3 6  | <del>,</del> අ   | Qy   | Oy<br>Oh  | S 65  | g è  | G Q  | Qy  | 0 A  | d Q   | qa  | oy<br>D   | Oy   | qa  |

| Qy          | 008  | î               |           |
|-------------|--|-----------------|-----------|
| ପ୍ର         | 136011 GGGGGCCCTAGTGCTCCCCACTTTCTGCCACTGCCTGCTCCGTCAGCAGTGC 136070   | g               |           |
| δy          | 801  | λo 1            |           |
| qq          | 136071 CTTCTGTGCCTGCAGCCCTCCTGTACAAGTGCTGGGGGCGCAGCGGCCCAGCTGTGGGCCTT 136130   | a :             |           |
| ΟŸ          | 814 ysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGlnGlyProGlyGlnCysThrL 834   | λ ά             |           |
| QQ          | 136131 GCCTCAAGGCTGATCCCCGCTTCAACTGTGGCTGGTGCATCTCAGAGCACAGGTGCCAGC 136190   | 3 8             | 1057204   |
| Οy          | 834 euArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGluLeuSerGlyAlaLysSerL 854   | ζ, <del>έ</del> | 2601      |
| QΩ          | 136191 TGCGGACCCACTGCCCGGCCCCGAAGACCAACTGGATGCACCTGAGCCAGAAGGGCACCC 136250   | G 6             | 107/204   |
| ΟŊ          | 854 ysCysThrAsnProArglleThr  | Š Š             |           |
| qq          | ::   :::::   | a à             | 13/324 AD |
| οy          | 862Gluilellep 865  | χ . 4 <u>.</u>  |           |
| qq          | 136311 CAGGGCCCCTGGGGAGTCTGAGCCAACTCTCACTGCCCATCCTGCTCCACAGATCCAC 136370   | a i             | 1000      |
| δλ          | 865 roValThrGlyProArgGluGlyGlyThrLysValThrIleArgGlyGluAsnLeuGlyL 885   | δλ              |           |
| qq          |  | qq              |           |
| ٥٨          | 885 euglupheArqAspIleAlaSerHisValLysValAlaGlyValGluCysSerProLeuV 905   | δλ              |           |
| · 60        |  | qq              | 137504 G  |
| ٥           | 905 albanglyTvrTleProblaglii   | Oy .            | 1080 Ly   |
| 7 8         | CGGCCGAGTACATCAGAGGTGAGAGGTGCGGCTCTGTGGGGTGCCGGGCCGTATGT   | . qa            | 137564 A  |
| ì à         |  | Qy              | 1086      |
| 3 6         |  | QQ              | 137624 C  |
| 3 3         |  | . Оу            | 1093 G    |
| Š i         | Lyspiosefeinhisalaciyrhevalciulilecysvalatavalcysargriociur  | q <sub>0</sub>  | 137684 G  |
| QQ          | TGGTGCCCAGCCCGCGGGGCCCGTGGAGCTGTGTGTGTGT   | Qy              | 1113 G    |
| οy          | 941 heMetAlaArgSerSerGInLeuTyrTyrPheMet  | qa              | 137744 G  |
| QQ          | 136665 TCCGCACGCAGTCGGAGCAGGTCTACAGCTTTGTGGTGCGTGGCTGCCGGCCCTACCCCT 136724   | . ^0            | 1133 L    |
| Οy          | 952 952  | Ş               |           |
| qq          | 136725 TCCTGTCCCTTCTCTCCCGCAAGGGGCGTGTGGAGCAGCCCGGCCCGGCTCCTCCCCT 136784   | G :             |           |
| Qy          | 953ThrLeuThrLeuSerAspLeuLysProSerArgGlyProM 966  | δ               |           |
| qq          | 136785 CAGGGCAGCTTCTCCCGCAGACCCAAGTTGACCAAGTGAGTCCCAGCCGTGGCCCGG 136844  | qa              | 137864 C  |
| ,<br>,<br>, | 966 etSerGlvClvThrGlnValThrIleThrGlvThrAsnLeuAsnAlaGlvSerAsnValV 986   | Qy              | 1165      |
| 7 E         | CONTROL OF THE CONTRO | qq              | 137924 G  |
| 3 8         | 5 1 Va 1 Wat 1 bh x 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1  | Qy              | 1168 u    |
| S 2         | ALVALMENTING 1 TO SOCIETION SOCIETIO | QQ              | 137984 G  |
| a d         | CAGTGACTGTGAGGGAACAGCGAGGGCCAGTTTGTAAGGTGGGCCCGGGGCCCCTGCCAGCTT  | δy              | 1188 s    |
| 5           | CO. C. C. C. C. C. C. C. C. C. C. C. C. C.   | qa              | 138041 G  |
| QQ          | TGGGTTGGGCATCGTGGGGGGCCGTGGGGACGGGTGGCTGAGGGCCCTGGGGCCACCC   | Qγ              | 1208 y    |
| δ i         | erProSerTyrIleValCysAsnThrThrSerSerAspGLuValLeu  | qq              | 138101 C  |
| o<br>D      | CICCAAGCACCCTGCT -TGCCAATGTAGGAGAGATGCCAAGGCGATCGTGTGCATCTCAC  | Qy              | 1214      |
| Qy          | 1016   |                 |           |

| CCCCAGCCAGCCCCCATCACATTGCCATTGACCGGGCTAACA 137143 | uvalpheGlnTyrValGluAspProThrileValArgileGlup 1047   :::   :::   :::    :: | A1C1ACACC1ACACCCACCACCACCACCACCACCATACACCACATACACCAC | TOTAL | 1052 | GGTCTCTGAGCTCCGGTGGGGCCCTCCTGGAGCCTAGGCCCTC 137323 | 1052          | GAGCTGTCCTGGCTGCACAGTACCCGGCACCCACTAGGCGATCC 137383 | 1052                                    | TGGCTGCCATGCCAGCCTTGATCGCTCTCCAGGGCTGGGTTGGT 137443 | 1059 | GCCCTGTCCCTAGTGGAAGCACTGCCAT   | LeuaspLeulleGlnAsnProGlnIleArgalaLysHisGlyGly 1079 |                  | ::<br>HGAGTACCAGCTGCCCCGCCCACCCGACCCTGCAGCCCATGG 137623 | 092                             | CTTTGTCCCCACAGACATGCCAAGTGATCAACGAC | OAlaLeuAlaLeuGlyPrOAspHisGlnSerAspLeuThr 1112<br>  ::: | CGGCATCTTTCTT          | PheGlyPheIleLeuAspAsnValGlnSerLeuLeuIeLleLeuAsn 1132<br>           :::      :::       :::<br> rrgGcTrccTgCrgGAcCacGTGCAAACGGCCCGCTCCCTCAAC 137803 | nProValPheGluAlaPheGlyProSerGlyIl | :::   | 31yThrProlleleLeuLys1164 | CGTGG                    | GlybysAsnLe 1168 | CCT                           | ### ### ############################## | cccgcctcaactacactgtgttgtaaggagg | ValSerAspValGlnLeuLeuCysGluSerProAsnLeuIleGl 1208 | stricedacacacacteristicescricacecage | 1213 | GGTAGGTGGGGATGGGGAGACCCCCTGGGCAGCCCAGGGTGGGCG 138160 | AlaArgValGlyGlyMetGluTyrSe 1222 |
|---|---|--|---|------|--|---------------|---|---|---|------|--------------------------------|--|------------------|---|---------------------------------|-------------------------------------|--|------------------------|---|-----------------------------------|-------|--------------------------|--------------------------|------------------|-------------------------------|--|---------------------------------|---|--------------------------------------|------|--|---------------------------------|
| CICICICCACCCIGGGCCCCAGCCAG                        | leHisGlnAspLeuValPheGlnTy   | 101000000000000000000000000000000000000              | roGluTrpSerIleVal   | i i  | STCTCT   | 1 1 1 1 1 1 1 | rgrccr  | 1 | STGCCAT   |      | 4 GCACTGGAGGAGGGAGCCTGAGGCCCCT | pLeuIle<br>:::<br>3ACGGTC                          | sGluHisIleAsnIle | CCAG  | 1<br>1<br>1<br>1<br>1<br>1<br>1 | 4 CTTCACGTGCCTGGCTGTCCACCTTTG1      | etThrCysGlnAlaProAlaLe                                 | TGCTGTGTAAGGCCCCCGGCAI | (I) ·· (T)  | sThrAsnPheThrTyrTyrProAsn         |       | LysproglyThrProlle       | SACGICAAACCGGGCICCCACGIG |                  | 4 GCGCCGGAAAGTGGAGAGTCCTGGGCT |  | CCGCGGCAGCCGCAGCTCC             | erAspVa   | cceretrecereacterecedacac            | lMet | cescaeccrercarecraecre                               | †                               |
| 137084  | 1028  | 7 / 7  | 1047  | 1052 | 137264   | 1052          | 137324  | 1052                                    | 38  | 1053 | 13744                          | 106(   | 108              | 137564  | 1086                            | 13762                               | 109  | 13768                  | 111.  | 113                               | 13780 | 115                      | 13786                    | 116              | 13792                         | 116                                    | 13798                           | 118   | 13804                                | 120  | 13810  | 121                             |
| qa .  | ογ<br>γ   | 3  | Oy<br>Dp  | QY   | Db   | QY            | QQ  | δÿ                                      | qq  | ΟŊ   | QQ                             | Qy   | ογ.              | qa  | Qy                              | QΩ                                  | Οy   | qq                     | QQ<br>Dp  | ολ                                | qq    | Qy                       | qa                       | QY               | qq                            | Qy                                     | QQ                              | Οy  | QQ                                   | δy   | qq   | Qy                              |

| qq     | 138161 TGGTGGTCAGCTCACCTCAGGCCTGTCCCCACAGGTGCTGGTGGGTG   |          | rade Tordy (Savin(Stewn) 1468       |
|--------|--|----------|-------------------------------------|
| Qy     | 1222 rProGlymetValTyrIleAlaProAspSerProLeuSerLeuProAlaIleValSerIl 1242   | qq       | Ö                                   |
| qq     | 138221 GCTGGGCACCTGCACATCTCGGCAGAGCGGGCGCTGACCCTACCGGCCATGATGGGGCT 138280  | 3 6      |                                     |
| Oy     | 1242 eAlaValAlaGlyGlyLeuLeuIleIlePheIleValAlaValLeuIleAlaTyrLysAr 1262   | λ 6      | 1488 spLysLeulleArgGlnGlnll6<br>    |
| QQ     | 138281 GCCGCCGCGCGCTCCTCCTCCTCCTCCCATCACACCCTCCTCGTCGTCTACAACCC 138340   | 3 8      |                                     |
| ٥y     | 1262 gLysSerArgGluSerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeuG1 1282   | Š        |                                     |
| qu     | 138341 CAAGACTCAGGACGGGACCGTACCCTCAAGCGTCTGCAGCTGCAGCTGCAGATGGACACAGCTGGA 138400   | gn i     |                                     |
| Οy     | 1282 uSerArgValAlaLeuGluCysLysGluAla1292   | Oy .     | 1502LeuSerCysValSer                 |
| QQ     | 138401 GTCCCGTGTGGCCCTGGAGTGCAAGGAAGG-TGCCTGAGGCGGGGGGGGGATGTGGTGG 138459  | <u>a</u> | 480                                 |
| δy     | 1293PheAlaGl 1295  | δλ       | 1519                                |
| Db     | 138460 AAGCTGGGGACCTCCTCCCCCCACTCATCCCTCTCTCCACCCCCCAGCTTTGCAGA 138519   | qQ<br>—— | 539                                 |
| Qy     | 1295 uLeuGlnThrAspIleHisGluLeuThrSerAspLeuAspGlyAlaGlyIleProPheLe 1315   | 0y       | 1539 snValProCysSerHisArgPrc<br>::: |
| QQ     |  | අු       | 139599 GCATTCCGTACTCCCAGCGTCCC      |
| Oy     | 1315 uAspTyrArgThrTyrThrMetArqValLeuPheProGlyIleGluAspHisProValLe 1335   | ογ       | 1553                                |
| qq     |  | qa       | 139659 TCTCCTCCTGCTCCCACTCATA       |
| òO     | 1343   | Qy       | 1553                                |
| 7 8    |  | qa       | 139719 TCCCCACCTGAACCCTGTTTCCT      |
| l è    | 1262   | Qy       | 1554                                |
| Z E    | n a  | qa       | 139779 AATCTTAAGGGCTGTCTGTGGCC      |
| ł      | 7007   | Oy       | 1565 LeuGlnAspGluAspIleThrTP        |
| රි සි  | 1555 SteuknehlatuleasnasnysvalPheLeuLeasserPhelleargThrLeuGl 13/3<br>1787 (CHTCHTGGGARCTHGGHGCARGCGGGGGGHGARANASAGGHGARA) 15610  | qa       |                                     |
| ò      | iiSprijnardserpheserWetarraenardijuaenValalasearteuri ewatmine 1202  | δλ       | 1585 AlaHisTyr                      |
| Z qq   | GECCCAGAGCAGCTTTTTCCATCCGCGGCACCGCGGCACCTGGCTTCACCATGGCTTTTTTCACCATGGCTTTTTTTT   | qq       | 139899 GCCCACTACCAGGTGAGGGGTTG      |
| ò      | Lengin Sprive Length Wave lambra en Valloni vecloi en Lengin Length en Lengin Length en Length | ογ       | 1587                                |
| 7 E    |  | ф        | 139959 CCCTGCCTTGAGCTGCAGCAGGA      |
| 3 8    |  | . Oy     | 1587                                |
| 7 A    | CGAGAAGAACTCGAGAAGAACACCCCCAAGCTACTTACTT   | qu       | 140019 CCTGGGCTCGTGGGCTCCCCTCC      |
|        |  | QY       | 1588                                |
| r da   | CTCTATCCAGGCCACACCTTTGTCCTGGGCCTGCCCCCTGTCCAAGCCCCACCCT  | qa       | 140079 TICCTGCACTGCCCCCCTCTGTC      |
| ò      |  | Qy       | 1596 aLeuValSerLysGlnValThr         |
| 1 6    | GCCAGGCCCGAGCCCCTTTGCCCTTAGGAAAGAAAAAAAGAAAAAAAA   | qa       | 140139 ATTGGTGCCCAAACAAGTGTCTC      |
| 8 8    | hrAsnTropheThropheTent.ent.vrphet.ent.vs1441   |          | 1616 rSerAlaSerLysTyr               |
| a<br>a |  | qa       | 140197 -TCCTCAGCCGCTACGGTAGGT       |
| Ò      | 1451   | δλ       | 1621                                |
| qa     | AGGGAGGTGGTGGCAGACCGGCCAGTGGTCAGGCAGGCAG   | qq       | 140256 CCCCACTTCCAAGTGCCATCGAT      |
| ΛO     | 1468   | δō       | 1621                                |
| QQ     | CTGGCTGCAGGAGTGTGCTGGGGAGCCTCTCTTCTTACTGTGCCATCAAGCAGC 13  | qQ       | 140316 AGATGGGTCCCCACATGCTGCTG      |
|        |  |          |                                     |

| λ<br>S   | 1468   | InMetGluLysGlyProlleAspAlaileThrGlyGluAlaArgTyrSerLeuSerGluA<br> | 1488   |
|----------|--------|--|--------|
| Qy       | 148    | .euIleArgGlnGlnIleAspTyrLysThrLeuVal                             | 501    |
| og q     | 36     |  | 39     |
| ٥y       | 1501   |  | 1501   |
| qq       | 139420 | CAGAGGTAGGGGCGCAGAGAGAGGCCTCGCCCCAGACTGACACTGGAGTCCGCTTTCCCC     | 139479 |
| Qy       | 150    | LeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLysI             | 1519   |
| QQ       | 139480 | STGTCTCCGGAGACGAGGGCAGCGCCCAGGTCCCAGT                            | 139538 |
| Oy .     | 1519   | eLeuAsnCysAspThrIleThrGlnValLysGluLysIleLeuAspAlaIlePheLysA:     | 1539   |
| QQ<br>Q  | 139539 | ctcaactgracagcatcacccaagccaaagataagctgcracactgracaa              | 139598 |
| Qy<br>Dh | 1539   | snValProCysSerHisArgProLysAlaAlaAspMetAspLeu                     | 1553   |
| Oy       | 155    |  | 553    |
| QQ       | 139659 | TCTCCTCCTGGGCTCCCACTCATACCCTCTGTGCCGTGTGACCTCCGTGGGGTTCTCCCGC    | 139718 |
| Οy       | 1553   |  | 1553   |
| qq       | 139719 | TCCCCACCTGAACCCTGTTTCCTAAGAGGAGTGGGCCAGGCACTTGGGGGGCTGCCAGCAT    | 139778 |
| Qy       | 1554   | GluTrpArgGlnGlySerGlyAlaArgMetIle                                | 1564   |
| QQ       | 139779 | ATGACTCGCATCAT   | 139838 |
| ٥y       | 1565   | LeuGlnAspGluAspIleThrThrLysIleGluAsnAspTrpLysArgLeuAsnThrLeu     | 1584   |
| qq       | 139839 |  | 139898 |
| ٥y       | 1585   | AlaHisTyr  | 1587   |
| qq       | 139899 | CCAGGTGAGGGTTGGGGCCCATTCCTCCCCAGGGCCACCTGGGAGCCAGGA              | 139958 |
| Οy       | 1587   |  | 1587   |
| QQ       | 139959 | CCCTGCCTTGAGCTGCAGCAGGACAGGGAGCAGTGGCCCTGGCTCCCCTCGCCTTCTC       | 140018 |
| ٥y       | 1587   |  | 1587   |
| QQ       | 140019 | CCTGGGCTCGTGGGCTCCCCTCCTGGGTGGGTGGGTGGG                          | 140078 |
| Qy       | 1588   | InvalProAspGlyServalvalAl  | 1596   |
| qq       | 140079 | GGTTCCTTG  | 140138 |
| Οy       | 1596   | erArgTh  | 1616   |
| qq       | 140139 | regreccaaacaagrererecraraacareeccaacrecrrcaccrrc                 | 140196 |
| ٥y       | 1616   | 3Tyr   | 1621   |
| qq       | 140197 | CCTCAGCCGCTACGGTAGGTGTCCTCAGTGTGGTGGCCATGTGCCCTTCGAGGGAAC        | 140255 |
| οy       | 1621   |  | 1621   |
| Db       | 140256 | CCCCACTTCCAAGTGCCATCGATTCTGTAGAGTGTAGACGGAGGGTCGGCCAGCGAGGGC     | 140315 |
| ΟÝ       | 1621   |  | 1621   |
| QQ       | 140316 | ATGGGTCCCCACATGCTGCTGAGCTCCCGGGAGAGTGGGGCCAGGGGCCAGGTGGTGGC      | 140375 |
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                                                            Insert size: 159556; sum-of-contigs
Insert size: 142754; agarose-fp
Quality coverage: 6.25x in 020 bases; sum-of-contigs Quality
coverage: 7.30x in 020 bases; agarose-fp
                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7280: gap of 100 bp in length 100 bp 70963: contig of 13683 bp in length 11063: gap of 100 bp 100 bp 100 pp 100 pp 100 pp 100 pp 100 pp 100 pp 100 pp 100 pp 100 pp 100 pp 100 pp 100 pp 100 pp 100 pp 100 pp 100 pp 100 pp
                                                                                                                                                                                                                                                                    17742: contig of 17742 bp in length
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                                                                                                                                                                                                                                                                                                               53: gap of 100 bp 29396: contig of 3843 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                         78142: contig of 7079 bp in length 42: gap of 100 bp 84646: contig of 6404 bp in length
                                                                                                                                                                                                                                                                                17743 17842: gap of 100 bp
17843 25453: contig of 7611 bp in length
                                                                                                                                                                                                                                                                                                                                               p of 100 bp contig of 7494 bp in length
Dye-terminator Big Dye; 73% of reads
Consensus quality: 156400 bases at least Q40
Consensus quality: 158019 bases at least Q30
Consensus quality: 158870 bases at least Q20
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78243 8464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 SerGlyValAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAsp 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetLysA.LaMetProTrpAsnTrpThrCysLeuLeuSerHisLeuLeuMetValGlyMet
                                                                                                                                                                                                                                                                                                                                                                                              21 GlySerSerThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyHisIleTyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 ValGlnThrCysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspTyrLysGluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 LeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 ValThrPheArgGlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55279 GTGGTG-----ACAGACACCACGCTTACCCACCTGGCTGTGCACCGGGTGACT
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425
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Matches:
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43.82%
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| \$4511 GACAGCTGAACCAGGTTGCGGGGGTCCCTGTGTGCAGGGGGGGTCCCTGCCC 54572  \$4511 ACCTGCAGCTTTCTGGCCCTGGTCCTGTGTGCGGGGGAGGGTCCCTGCCCC 54572  \$4511 ACCTGCAGCTTTCTGGCCCTGGTCCTGTGCCAGGGGGATCCCTGCTCCTCTCTCCTCCTCCTCTCTCT |   | Db 53551 ACCCTAGGGCAGCAGTCAGTCCTGGCTGGAGGGACCGGGTTCTAGATCCCGCTCTT 53494 | 53491 CTGGGACTCAGGAAPTGCCGGCCTCCATCTTGCGCCTGGGAGCTTTGACTCTCACGGGTT 53 | 400 | 53431 CCTCCTCTGTTCACCAGCCCATGCAGATCAACGGCAACTTCTGTGGGCTGGTGTGAAC | Oy 411 AlaProLeuGlyValSerAspMetValArgGlyIleProValPheThrGluAspArgAsp 430 | 53371 CAGCTCTGGGAGGCCTGCATGTGATCGAGGGGCTGCCCTGCTGGCCGACAGCACCGCC | QY 431 ArgMetThISSEYALLIEALBHYFVALHYFLYSAShHISSEFLEUALBFNEVALGITHT 450<br> | Qy 451 LysSerGlyLysLeuLysLys | Qy 457 457 | 53191 TCTCAGATATGGGACAAGGCTGGTGGTGGGAACACACGGGAGAGCTCTGAGGACAGGACA S | 0y 457 | 457 | 53 | 43/<br>53011 CIGAAITGCCAGCITCGTATGGCTCTGGGGACAGAGAACAGACCTAITGTGGAGTCTCCC | Qy 457 | Oy 457 457  Db 52891 GGGAGCAAATGCCTTGCCCTCAAGCCTCCCTATGCCTGGGACACACAC | 457 457 | Db 52831 CCCTCTCCTTGGCTCACTTCCCATCCTTCCCTCCTACCATGGGCCCGGGGGCTGA 52772 | Qy 457 457 | Db 52771 AGCTGCTTCCATTGGGGATCTGGGGGTAGCTTGGCATGAAGGGGGAGATGAACTTCTGGG 52712 | 457 | 52/11 CACTCAGGIACGIGITGAATAGGIAGGGGGGGGGGGGGGG | 51 CCTCGTAGATGCAGTGCCATCCCCCAGGAGGCAAGTGTTGGTCTGGGGGCGCAGGAAG 5 | 457 | 52591 GGTTTGTGGAGGATGATGAACTCTCCTGGCCCACCTGCTCTGTTCCTGGGACCCTCT | 457 | Db 52531 TTTCCTTTGTAGCAGCTTTGTTGAACGCGTACTATCCAATTCACCCATTTTAAAGTGCAC 52472 | ογ 457 457 |
|--|---|---|---|-----|--|---|--|--|------------------------------|------------|--|--------|-----|----|---|--------|---|---------|--|------------|---|-----|--|---|-----|---|-----|---|------------|
|  | _ | .2  |   |     |  |   |  |  |                              |            |  | -      |     |    |   |        |   |         |  |            |   |     |  |   |     |   |     |   |            |

| 592 snCysThrPheGluAspLeuSerCluMetAspGlyLeuValValGlyAsnGlnIleG 611 | TTGGGGCTGCCCAGGATGGGCAGAGTCGGGCCTCTCCCTACCCCCAGCGAGTTCACGGC    | 661                                   | 50795 TTCCCCCCAGGTGCATCTCTTTTTGCAGCCCTTACCCCTGGTGTAAGTAC 50736  678 ArghisValCySThrHisAspProLySThrCysSerPheGInGLUGIJyArgValLySLeu 697  11111111111111111111111111111111111 | 701   |
|---|--|---------------------------------------|--|---|
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| 52471 AGTTCAGTGGGTTTCTGTGGAGTGGCACAACCATGGCCACTACCTCATTCTC 52412  | 52291 TGGCCTCCGGGCTGTGAGTGCTGAACCCCACCAGGTCCTGACGTCCAGCC   457 | 490 AspHisGluGlnLeuTyrIleMetSerGluArg | 11   | 536   |
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| 100   | · £      |  | qa *C    |  |
|---|----------|--|----------|--|
| 10.56   20.00   20.0  | ז        | TCTATGCCCAGCTCTCTGGCAGGGAACTGTCTGAGTCTCCTGCTAGGGGATTCCTGTACCT 501      | - ^4     |  |
| \$0195 GGAGGAGGGGGCANGATGGGATAGGGTTCGCACATCTANCTGGGGT 5017 07 99 91 91 91 91 91 91 91 91 91 91 91 91  | οy       |  | ה ל      |  |
| 767   10   10   10   10   10   10   10   1  | qq       | GGAGGAGGGGGCAGCTG  | ad g     |  |
| \$0116 CCCAPTGGGTTCCTTTCCTCCAPTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  | ٥y       | TyrSerTyrGluGlyMetGluIleAsnAsnLeuProVa                                 | λα<br>qq |  |
| 779 IGAIL GAUTH THE TEMPORATE LIGAS AND ACCUPACION TO THE THE THE THE THE THE THE THE THE THE   | Op       | CCCATGGGTTCCTTCCTCCAGTACTCCTATGAAGGTGATGAGCATGGTGACACCGAGCT            | ΛO       |  |
| 1999 al His   1900     | Qy<br>Db | IGluLeuThrValValTrpAsnGlyHisPheAsnIleAspAsnProAlaGln-AsnLysV           | qq       |  |
| \$0016 FANGGGCTAGGGCCAGGGAGCTTCCCTCTAAGGCAATTGCCACTGCTGGGCTCGGTCT 49957   | οy       | alHis  | δλ       |  |
| 9956   0000000CCTAGTOCTCCCACTTTCCCACTTCCCCCACTCCCCCCCCCC  | QQ       | <br>  FGAAGGCATGGGCCAGGGAGCTTCCCTCCTAAGGCAATTGGCACTGCTGGGGTCGGGTCT     | g .      |  |
| 49956   GGGGGCCCTAGTGCCTCCTCCCCCCCCCCCCCCCCCCCC   | Qy       |  | Z =      | CTCTCTCCACCCTGGGCCCCAG                 |
| 801   | Dp       | GGGGGCCCTAGTGCTCCCCCACTTTCTGCCACTGCCTGCTCCGTCAGCAGTGC                  | à Å      |  |
| 49996 CTTOTOTOTOTOTOTOTOTACAGGGCCAGCGGCCAGCGGCTCCTC 49877  49996 CTTOTOTOTOTOTOTOTACAGCCCCTCCTGAGCGCCAGCGGTCCCTCCTC 49877  49916 GCTCCCCCCCCCCCCCCCTCCTGAGCGCCCCAGCTGCCCCCCCC   | οy       |  | qa<br>·  | <br>  TCTCCAGCC                        |
| ### ### ##############################  | qq       | CITCTGTGCCTGCAGCCCTCTGTACAAGTGCTGGGGGGCGCAGCGGCCCAGCTGTGGCCCTCT        | Oy       |  |
| ### ### ##############################  | ۵۷<br>ور | 814 ysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGlnGLyProGLyGlnCySThrE       | qq       | CCACC                                  |
| 10.000   1  | 3 8      | 834 enArd(lnHisCvsProAlad)nGluSerGlnTrbLeuGluLeuSerGlvAlaLvsSerL       | Qy       | 1052                                   |
| ### 955 ### 959 ### 95 | G        |  | qa       | · 48704 GGGCTCAGGGACTGGGTGGTCTCTGAGCTC |
| 49716 GGTGCACCCCCGCAACCCCCCCCCCCCCCCCCCCCCCCC   | QY       | ysCysThrAsnProArglleThr  | oy 4     |  |
| ### ### ##############################  | qq       | GGTGCAGCCCCCCCCCCAGCTCAGCCTCCCTCACCCCCCTGCCCAA                         | 8, 8     |  |
| 49656 CAGGGCCCTGGGAGTCTCTCACTGCCCACCACATCTCCCCCACAGATCCACC 49597  865 rovalThrCdlyproArgGluGlyGlyThrLysValThrIleargGlyGluAsnLeuGlyL 885  1  | QY       | delialinia.  | 7 A      |  |
| 865 rovalThrGlyProArgGluGlyGlyThrLysValThrIleArgGlyGluAsnLeuGlyL       885         49596 CTCTCGCGCCACGGGGGCCACCTCGGGGGCCACCTGGCCC       49537         885 cuGluPheArgAspIleAlaScHisValLySValAlaGluCySSerProLeuV       905         885 cuGluPheArgAspIleAlaScHisValLySValAlaGluCySSerProLeuV       905         905 alAspGlyTyrIleProAlaGlu   | qq       | CAGGGCCCCTGGGAGTCTGAGCCAACTCTCTCACTGCCCATCCTGCTCCACGAGTCCACC           | 3 8      |  |
| 49596 CTCTCGTGGGGCCCAAGGAGGGGCCCGGGTCAACCTGGGCC 49537  885 euGluPheArgAspIleAlaSerHisValLysValAlaGluCysSerProLeuV 905  885 euGluPheArgAspIleAlaSerHisValLysValAlaGluCysSerProLeuV 905  11   11   11   11   11   11   11   11  | Oy.      | roValThrGlyProArgGluGlyGlyThrLysValThrIleArgGlyGluAsnLeuGlyL           | g da     | 48524 GTGCACTGGAGGAGGGAGCCTGAGGCCCCT   |
| ### 885 euGlupheArgAspIleAlaSerHisValLysValAlaClyValGluCysSerProLeuv 905  ### 49536 TCTTGTCCGAGAGGTGGCT   | Db       | CTCTCGTGGGGCCCAAGGAAGGAGGCACCCGGGTCACCATCGTGGGTGACAACCTGGGCC           | -        |  |
| 49536 TCTTGTCCCGAGAGGTGGCCCTGCGGCTGCCTGCATTC 49483 905 alAspGlyTyTleProAlaGlu   | Οý       | euGluPheArgAspIleAlaSerHisValLysValAlaGlyValGluCysSerProLeuV           | Z qq     |  |
| 905 alAspGlyTyrIleProAlaGlu   | qa       | TCTTGTCCCGAGAGGTGGGCCTGCGGGTGGCTGGCGTGCGTTGCAACTCCATTC                 | 2        |  |
| 49482 CGGCCGAGTACATCAGTGCAGTGCGGCTCTGTGGGTGCCCGGCCGTATGT 49423  913   | Οy       | alAspGlyTyrileProAlaGlu  | S &      |  |
| 913   | Db       | CGGCCGAGTACATCAGTGCTGAGAGGTGAGTGCGGCTCTGTGGGGGGCCCGGGCCGTATGT          | à ò      |  |
| 49422 GGCCTGGCCGGCCCTGACGCTCTCTGAGCTGTGTGAGATGGAGGAGTCGC 49363  922LysproSerGlnHisalaGlyPheValGluIleCysValAlaValCysArgProGluP 941  49362 TGGTGCCCAGCCGCGCGCGCGGGCCCGTGGAGTGTGTGTG   | QY       | GlnIleValCysGluMetGlyGluAla-   | qa<br>qa | 48344 GGCTTCACGTGCCTGGCTGTCCACCTTTG1   |
| 922LysproSerGInHisAlaGlyPheValGluIleCysValAlaValCysArgProGlup 941  49362 TGGTGCCGGGGCCGTGGGGCTGTGTGTGTGTGTGCGGGTT 49303  941 heMetAlaArgSerSerGlnLeuTyTTyrPheMet  | QQ       | 9422 GGCCTGGCCGGCCCTGACGCTCTCTGAGCCCTAGGATCGTGTGTGAGATGGAGGAGTCGC      | ۵C       |  |
| 49362 TGGTGCCCAGCCCGGGGCCCGTGGAGCTGTGTGTGTGTGT  | οy       | LysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgProGluP             | 7 A      |  |
| 941 hemetalaArgSerSerGlnLeuTyTTyrPhemet   | Dp       | TGGTGCCCAGCCCGCCGCGGGCCCGTGGAGCTGTGTGTGGGTGACTGTTCAGCCGACT             | δλ       |  |
| 49302 TCCGCACGCAGGCAGCAGCAGCTTTGTGGTGCGTGGCTGCCGGCCCTACCCCT 49243  952  | οy       | hemetAlaArgSerSerGlnLeuTyrTyrPheMet                                    | qq       |  |
| 49242 TCCTGTCCTTCTCTCTCCCGCAAGGGCGTGTGCAGCCGCCCGGCCCCGCTCCTCCCT 49183  OY 1152  | Dþ       | 9302 rccgcacgcagtcggagcagtctacagctttgtggtgcgtggctgccggccctaccct        | Qy       |  |
| 49242 TCCTGTCCCTTCTCTCCCGCAAGGGGCGTGTGGAGCAGCCCGGCTCCTCCCCT 49183  Qy 1152  | δλ       | 952 952  | qq       |  |
| 440 MCS 131 CS CS CS CS CS CS CS CS CS CS CS CS CS  | qo (     | 9242 TCCTGTCCCTTCTCTCTCTCCCGCAAGGGCCGTGTGGAGCAGCCGGCCCGGCTCCTCCCT 4918 | Qy       | 1152 leLeuGluLeuLysProGlyThrProIle     |

eGInAsnProGlnIleArgAlaLysHisGlyG 1079 :||| |||::::::|||||||||||: | ccaGGAGCCCGGGTCCGTGCCAAGTACCGG 48405 CTGCCCCGCCCCGACCCTGCAGCCCAT 48345 GCTGCACAGTACCCGGCACCCACTAGGCGATC 48585 CTGCCCTGTCCCTAGTGGAAGCACTGCCATCA 48465 STITGIAAGGIGGGCCGGGGCCCTGCCAGCTT 49003 CTGGGGGACTGGGGAGCCTGGCAGTGTCCAGA 48705 TCCGGTGGGGCCCCTCCTGGAGCCTAGGCCCT 48645 GGCAGCCTTGATCGCTCTCCAGGGCTGGGTGG 48525 STTTGACCAAGTGAGTCCCAGCCGTGGCCCGG 49123 3GGACGGGTGGCTGAGGGCCCTGGGCCACCCG 48943 CCCCATCACACTTGACCGGGCTAACA 48824 SAGAGATGCCAAGGCGATCGTGTGCATCTCAC 48884 tLysValSerValGlnValAspArgAlaLysI 1028 -----SerGlyAsnThrProlleA 1059 uAlaLeuGlyProAspHisGlnSerAspLeuT 1112 elleLeuLys-----1164 ...-Args 1000 ----- 1052 866 ----rSerSerAspGluValLeu----uPheHisArg-----

| 1428   | 1451               | 46508 GGAAAGCTCCTCCAGCAGATCCACTACAGACACTGGTAGGCCCAGGCCGGCGGG 46549 1501   | 1538 SASNValProCysSerHisArgProLysAlaAlaAspMetAspLeu  | 46189 ATAATCTTAAGGGCTGTCTGTGGCCCACAGGGCGCCCATGACTCGCATCA 46130 1564 leleuGlnAsplleThrThrLysIleGluAspTrpLysArgLeuAsnThrL 1584 11111111111111111111111111111111111 |
|--|--------------------|---|--|--|
| 48104 TGCTGGACGTCCAAACCGGGTGCTGAAGGTGGGGGGGGGG | GlyArgHisLysValMet | 1262 ArglysSerArgGluSerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeu 1281 1262 ArglysSerArgGluSerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeu 1281 1262 ArglysSerArgGluSerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeu 1281 1262 ArglysSerArgGluSerAspLeuThrLeuLysArgLeuGlnMetGlnMetGlnMetAspAsnLeu 1281 1262 GCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | GluLeuGlnThrAspileHisGluLeuThrSerAspLeuAspGlyAlaGlyIleProPhe 1314 [4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 1344   |

| Db         44812         GCCTGGCCTGGGGTTGACACTGACGGTGCCATCAA           Oy         1741 | Db         44572 CCGTTCACCCTAAATGTGTTGCTCTCACCACCTCT           Qy         1741 | 1796<br>44272<br>1812<br>44213<br>1812<br>44153<br>44093 | Oy 1819 lyLysMetProAlaileSerAspGlnAspMetAsi Db 44033 CAAAGATGCCATCCATCAGGACCAGGACATGGAC OY 1839 etHisMetAsnGluPheAsnThrMetSerAlaLea Cy 1839 etHisMetAsnGluPheAsnThrMetSerAlaLea Cill ::::   :::   ::: |
|--|--|--|---|
| 1588   | 1621   | 4535:<br>1685<br>4529:<br>4523<br>1685<br>1685<br>1685   | 45172 CTGCCTCCATCTGCTGCTGGGGACATCCCGACCTGGCTCCCTCATAGCCTGGACC 45113  1686   |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0  | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6  | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                    | 60 00 00 00 00 00 00 00 00 00 00 00 00 0  |

| qo   | 44812 (            | GCCTGGCCTGGGGTTGACACTGACGGTGCCATCAAGCCAAGGGGCCTGTTGCGTCCAGTT 4475                            | 53  |
|--|--------------------|--|-----|
| Οy   | 1741               | 1741   |     |
| qo   | 44752 (            | CTGGAGCTGGACTGCCTGGGTGGGTGGTGGTGGTGAGGCCTTTGCCCTCTGGGGT 4469                                 | 93  |
| oy   | 1741               | 1741   |     |
| qq   | 44692              | CTTGCACCAGGTAGAGATGCTGGTGGTCGCAGGTGGTGAGAGCGGTGACAGGAGAA 4463                                | 33  |
| QY   | 1741               | 1741   |     |
| qa   | 44632              | GCTGCGGAGGGGGTTGAGCCCTATTGAGAACAGAAGTTCAGCAGAGACTTAGAGGAAAGG 4457                            | 73  |
| QY   | 1741               | 1741   | 7   |
| qq   | 44572              | CCGTTCACCCTAAATGTGTTGCTCTCACCACCTCTGGACAAGATGTGAGCCGGCCG                                     | 13  |
| λō.  | 1741               | 1741   | 1   |
| QQ   | 44512              | GGAAAGAAGATGTGCACATGGGAGGGGCCCCTTGGGGCTAACTAGGGAGCCTCAGGCGCAC 4445                           | 53  |
| QY   | 1742               |  | 9   |
| Db   | 44452              | 443  | 93  |
| . ко                                       | ū                  | 77   | 9   |
| Ωp   | 44392              | 443  |     |
| Qy   | 1776               | InthrpheMetAspSerCysSerThrSerGluHisArgLeuGlyLysAspSerProSerA 1796                            | 9   |
| Dβ   | 44332              | 442  | :73 |
| QY   | 1796               | snLysLeuLeuTyrAlaLysAspIleProSerTyrLysAsnTrpValGlu 1812                                      | 2   |
| qq   | 44272              | CAAACTGCTCTACGCCAAGGACATCCCCAACTACAAGAGCTGGGTGGA-GAGGTGGGCT 442                              | 14  |
| Qy   | 1812               | 1813   | . 2 |
| qa   | 44213              | CCGCCCTGCTGTGGGTGGCAGGAGGGCAGGACCTGCCCTCCCT  | 54  |
| Qy   | 1812               | 1813   | 2   |
| qq   | 44153              | CAGGCCAGCTACAGGCAGGAAGCCCGGGGGGTGGCTGGGCAGTGAGGGCAGGGGTTCTAG 4405                            | 94  |
| QY   | 1813               |  | 67  |
| qq   | 44093              | G 440  | 34  |
| δy   | 1819               | 1yLysmetProAlaileSerAspGlnAspMetAsnAlaTyrLeuAlaGluGlnSerArgM 1839                            | 68  |
| Db   | 44033              | C 439  | 374 |
| Οy   | 1839               | rvalGlyL 185   | 69  |
| Db   | 43973              | CCACGCCAGCGACTICAGCGTCCTGAGTGCTCTCAACGAGCTGTATTTCTATGTCACCA 439                              | 914 |
| ο λ.                                       | 1859               | GlyPr  |     |
| QQ   | 43913              | GTCATCCCCACAGACTCCCAGTTACTTGGT   |     |
| RESULT<br>AC02576<br>LOCUS<br>DEFINIT      | 15<br>84/c<br>FION | 193961 bp DNA linear HTG 04-MAY-20<br>us clone RP23-142E5, *** SEQUENCING IN PROGRESS ***, 6 | 01  |
| ACCESSION<br>VERSION<br>KEYWORDS<br>SOURCE |                    | GI:<br>HASE<br>S.  |     |
| ORGANI                                     | SM                 | ıs musculus  |     |

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Elicable J. (Dassa 1 to 1939b).

Sanderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boushgalter, B., Brown, A., Burkett, G., Collymore, A., Cooke, P., Denerallano, K., Dowar, K., Daz, J.S., Collymore, A., Cooke, P., Denerallano, K., Dowar, K., Daz, J.S., Collymore, A., Gondo, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Grand-Pierre, N., Grand, G., Heaford, A., Horton, L., Grand-Pierre, N., Grann, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., Mihova, T., Mihova, T., Miranda, C., Manga, V., Morrow, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Norman, C.H., O'Connor, T., O'Connell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rochman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Travers, M., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Vong, C., Zainoun, J., Zimmer, A. and Zody, M., Sander, 320 Charles Street, Cambridge, MA 02141, USA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              All repeats were identified using RepeatMasker:
Smit, A.F.A. 6 Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50357 50456: gap of 100 bp
50457 92748: contig of 42292 bp in length
92749 92848: gap of 100 bp
92849 94975: contig of 2127 bp in length
94976 95075: gap of 100 bp
95076 144036: contig of 48961 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144037 144136: gap of 100 bp
144137 170034: contig of 25898 bp in length
170035 170134: gap of 100 bp
170135 193961: contig of 23827 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50356: contig of 50356 bp in length
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45525 c .43881 g 51443 t 604 ot
                                                                                                   Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-142E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: 142_E_5
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                                                                       (bases 1 to 193961)
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ORIGIN
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Alignment Scores:

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-----AGGCCATTT 117748
                                                                                                                                                                                                                                                                                                                                       117690 GGGAGGTGTTTGTAGGTGCCGTGAATCGAGTTTTCAAGCTGGCTCCAAACCTAACTGAG 117631
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                                                                                                                                                                                                                                                                                      117?47 CGTACCTTTGTGGTAACAGATACCACT---CTGACTCACCTGGCTGTGCACCGAGTGACT 117691
                                                                                                                                                                                                                                                                                                                                                                                                 117390 TCAGGGGCCCAGGACCCTGATTCCATGGCTGGCGTCATTGTTGAACAGGTCCAGGGGCCT 117331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117210 GTTGCTTTTGTCTTTCTTTCCCCTGGTTCTTATGAGCCCAGGTCTTATTCACTCCTTTCTC 117151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117090 ACTGTCACATAGATGTAGACCAGCTGTTGAGGACAGGAAGATGGGCAGAGTTTACCTGTG 117031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117030 GAAAGTCTGTCTATAGAGAGGCTAAGGTCACCTTGCACTCTGTGGCATGGAATCCAGTAA 116971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116970 TTGTCCAGGTGGGGCAGATGGGAGATCACTGGGGAAGCCTTTAGAAAACCGCATTGTTGG 116911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerGlyValAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAsp 180
                                                                                                                                                                                                                                                                                                                                                                               81 LeuValThrHisGluThrGlyProAspGluAspAsnProLysCysTyrProProArgIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                          ValGlnThrCysAsnGluProLeuThrThrAsnAsnValAsnLysMetLeuLeuIle 120
                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                    GlyHisIleTyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysVal 80
                                                                                                                                       --MetValGly-----Met
                                                                                                                                                                                              21 GlySerSerThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPhe
                                                                                                                                                                                                                                                          41 ValThrPheArgGlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AspLysLeuPheIleAlaThrAlaValAspGlyLysProGluTyrPheProThrIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerArgLysLeuThrLysAsnSerGluAlaAspGlyMetPhe-------
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                                 Conservative:
Mismatches:
                  Matches:
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                                                           Indels:
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| Qy      | 215Ala 215   |   | 1111                                    |
|---------|--|---|---|
| qa      | 116910 AACAGGGTTGGGAAGTGAAGGTGGGCCTTCACCCTGCTCTCATACTTTGTTCTAATCTCC 116851   | 1 10 4  | ) # 4 # C                               |
| Qy      | 216 TyrValPheHisAspGluPheValAlaSerMetlleLyslleProSerAspThrPheThr 235   | 12  | THIE                                    |
| QD      | 116850 AG-GTGTACCAGGATGAGTTGTCTCTTCTCAGATCAAGATCCCTTCAGACACATTGTCC 116792  | 2//011  |   |
| Qy      | 236 IleIleProAspPheAsplieTyrTyrValTyrClyPheSerSerGlyAsnPheValTyr 255   | QY 441 SASINISSELLEUALAI<br>                ::  <br>DA 115712 CORGCARREGERY | SUALA<br>::<br>GGTT                     |
| qa      | 116791 TTGTACCCTGCCTTTGACATCTACTACATATATGCCTTTGTCAGTGCCTTCGTGTAC 116732  | 457   |   |
| Qy      | 256 PheLeuThrLeuGlnProGluMetValSerProProGlySerThrThrLysGluGlnVal 275   | 1. A. A. A. A. A. A. A. A. A. A. A. A. A.                                   | )<br>Д.П.С.П.С.                         |
| qa      | 116731 TTCTTAACGTTGCACTGGACACCCAGCAGACGCTGTTGGATACAGCAGGCGAGAAATTC 116672  | 200011  | 10101                                   |
| ΟŸ      | 276 TyrThrSerLysLeuValArgLeuCysLysGluAspThrAlaPheAsnSerTyrValGlu 295   | י הירו  | ) TO WOLLY                              |
| qa      | 116671 TTCACATCCAAGATCGTGCGCATGTGTGTGGGGACTCAGAGTTCTACTCTTATGTAGAG 116612  | 767011  | 04011                                   |
| Oy      | 296 ValProlleGlyCysGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeu 315   | 1155  | AATCC!                                  |
| QΩ      | 116611 TICCCIATIGGCIGCICCTGGCGIGGIGIGGAGIACCGCITGGIGCAGAGIGCCCAICIG 116552   |   | 1                                       |
| δŏ .    | 316 SerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeu 335   | 1154  | CATTT                                   |
| q<br>O  | 11   | Qy 457  | 1                                       |
| ογ<br>ά | 336 PheThrValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeu 355   | Db 115412 CTGAATACAGACTCAA  | CTCAA                                   |
| 2       | 1077   | Δλ 457  |   |
| ò á     | 356 CysilePheileLeuLysGln1leAsnAspArgIleLysGluArgLeuGlnSerCysTyr 375   | Db 115352 GGCCGAAGAGCGTGCT  | STGCT                                   |
| 3 8     |  | Qy 458  |   |
| Š f     | 3/0 AIGGLY GIGGLYITTLEUASPLEUALAITPLEULSSVALLYSAAPILEETO 392<br>   | Db 115292 TCTCTGTCCTGGTCTT  | STCTT                                   |
| 3 8     |  | Qy 469 nTyrGluThrValGln   | a1G1n                                   |
| ž ć     | 上書 かいかい かんかい かんかい かんかい かんかい かんかん かんかい かんかい かんかい かんかい かんかい かん かん | Db 115235 ATATGAAACGGTCTCT  | rcrcr                                   |
| 8 0     | 392  | Oy 489 sAspHisGluGlnLeu'  | lnLeu                                   |
| ; g     | 116251 TCTGCCTTTCTGCTGAGTGGCTGTCTGTCCAGTCCTAGGCTTGGCATGATCATGGGATTG 116192   | Db 115175 TGACCACCGACACATC  | ACATC                                   |
| λÓ      |  | Qy 505  |   |
| g<br>G  | 116191 GCAACTTAGTTTTGACACCCACACTACCTTGAGAGCCTTACTCTTTTTTCTCTTTCT 116132  | Db 115115 GTGTGGGGCAAGG   | CAAGG                                   |
| ٥٨      | 392 392  | 50  | CysG1                                   |
| QQ      | 116131 TTTCTCTTGGCCAGTGTCCTGTTTGTATACTGCCATTTTCCTTTTCTGCCTCTATATTCA 116072   | 115055  | rgrga                                   |
| Qy      | 392 392  | 76  | - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 |
| đ       | 116071 TICCCACCITICICCTIGCICTAICICAAGICTAACAGGGICAGGCTICICCICCTIGCC 116012   | 114995  | rgrgr                                   |
| δλ      | 392 392  | 534   | <br>                                    |
| qq      | 116011 CCGACTȚICCATCCCCAGICCCATTICCCAIGGGGICCTAGGGGAAACAAACIGICAAG 115952  | 1149  | reese                                   |
| QY      | 392 392  | 534   |   |
| qq      | 115951 CATGTCTGGAGGCCAGTGGCTTCCAGGTTCTGCTCTTTACAGAATGTGAAATCTGATAG 115892  | 114   | AGCCA                                   |
| Qy      | 393CysSerSerAlaLeuThrIleAs 401   | 0.000 114915 COMMONDOCOMMONOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO                |   |
| qQ      | 115891 CATCTGTTTAGCTTGAACTCTCACTCACCCCTCCTGTGTCACCAGCCT-CTGCAGATCAA 115833   | 534   | י ניני                                  |
| Qy      | 401 paspasnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValArgGl 421   |   |   |

| QQ         | :<br>115832 T |   | 115773  |
|------------|---------------|---|---------|
| Qy         | 421 y         | 11  | 441     |
| qq         | 1<br>115772 G | :: ₺  | 115713  |
| Qγ         | 441 S         | AsnHisSerLeuAlaPheValClyThrLysSerGlyLysLeuLysLys.             | 457     |
| QQ         | 115712 C      | CCAGCATTCTGTGGTTTTCATCGGTACACGCGGTAATTTGAAGAAGGTTGGTCCTAG     | 1.15653 |
| Οy         | 457 -         |   | 457     |
| QQ         | 115652 A      | AACCCTTGTCTTATGTGATTGGGGATGTTTTTCACACTATGGGAAGAAGGGCTGAGGAAC  | 115593  |
| Qy         | 457 -         |   | 457     |
| Db         | 115592 A      | AGAATGTGAACATGAGCCTGGATAACCCTGAATAGGGTGTAATAACTTCCCAGGTTAGGC  | 115533  |
| Qy         | 457 -         |   | 457     |
| qq         | 115532 T      | CCAAGAACTGAATCCTGTTCCTTTGGTGGCTCCTCTGCCATCTACCTTCGCCAGCATTG   | 115473  |
| Qy         | 457 -         |   | 457     |
| qq         | 115472 T      | TTCGAAGGTAGCATTTGTCTTAGTCTAAGGCTATGGCTGTTGGAACTATAAGCCTACAAA  | 115413  |
| Qy         | 457 -         |   | 457     |
| qq         | 115412 C      | CTGAATACAGACTCAAGGAGGCCATATCTGACCAGCTCAAACTGTAATCTAGAAAGTCCCT | 115353  |
| Qy         | 457 -         |   | 457     |
| qq         | 115352 0      | GGCCGAAGAGCGTGCTCTGGGTGCAGGGAGCTATGGTAGCATGAAGCTGGCTTGTCATTT  | 115293  |
| Οy         | 458 -         | IleArgValAspGlyProArgGlyAsnAlaLeuGl                           | 469     |
| qq         | 115292 T      | TCTCTGTCCTGGTCTTGTGGCTCAGGTGCGGTCGATGGCTCTCAGGATGCCCAGCT      | 115236  |
| Qy         | 469 r         | TyrGluThrValGlnValValAspProGlyProValLeuArgAspMetAlaPheSerLy   | 489     |
| <b>q</b> 0 | 115235 #      |   | 115176  |
| ΟŊ         | 6             | AspHisGluGlnLeuTyrIleMetSerGluArgGlnLeu-ThrArg                | 504     |
| Db         | 115175 1      | TCACCACCACCACATCTACCTCCTCAGTGAGAAGCAGGTGGGCCCCGTGGTGGGTG      | 115116  |
| δy         | 505           | qlanvalp  | 909     |
| Ob         | 115115        | GTGTGGTGGGCCAAGGGTGGGCTGTGTGTGTGTGCCTGTCCCCAGGTGAGCCAACTCC    | 115056  |
| Qy         | 506 r         | ovalGluSerCysGlyGlnTyrGlnSerCysGlyGluCysLeuGlySerGlyAspProH   | 526     |
| QQ         | 115055        |   | 114996  |
| Oy         | 526 j         | /sGlyTrpCysValLeuH  | 534     |
| qq         | 114995 #      |   | 114936  |
| δλ         | 534           |   | 534     |
| qq         | 114935 #      | AGTGGGCTCCCTGGGGCCATTATCTTGGGAGACAGAGGATTTAGGAGGACCTTGCCAGCT  | 114876  |
| 0y         | 534           |   | 534     |
| QQ         | 114875 0      | GGACAGGAGCCAGCCACACTTGCTATACTTTCCTTCACCCACC                   | 114816  |
| Qχ         | 534           |   | 534     |
| qq         | 114815 (      | CCTTGAGCCTTCCCCCTCCCTTCCTCCACTTTCTCCAGCTAATGAGCGGAACTTCTA     | 114756  |
| . ,        | í             |   | 733     |

| Ę        | 111466 | 1111<br>1111  | 111407  |
|----------|--------|---|---------|
| 3        | )<br>  |   |         |
| Qy<br>G  | 1054   | JASnThrProileAlaValTrpGlyThrHisLeuAspLeuTleGinAsnProGinileA<br> | 1074    |
| 3 .      |        |   | 1 0     |
| ζλ<br>Dp | 111346 | GTAGTGGGTTTCTACCCCTGTTC   | 111287  |
| δy       | 980    | S Å C · · · · · · · · · · · · · · · · · ·                       | 1087    |
| qa       | 7      | CATTGCTACTCATGGGTTCATGCGGTGAGATGATTGCTGTTGTCTTCACAGACA          | 111227  |
| оу .     | 1087   | luValLeuAsnAlaThrGluMetThrCysGlnAlaProAlaLeuAlaLeuGlyProAspH    | 1107    |
| qq       | 111226 | GGTGATCAACGACACTGCAATGTAAGGCCCCTGGCA                            | 1111167 |
| Qy       | 1107   | isGlnSerAspLeuThrGluArgProGluGluPheGlyPheIleLeuAspAsnValGlnS    | 1127    |
| QQ       | 111166 | AGCCTCGGGCCCAAGGCGAGCACCCTGACGACTTTGGCTTCTTGCTGGACCACGTGCAGG    | 1111107 |
| Qy       | 1127   | erLeuLeulleLeuAsnLysThrAsnPheThrTyrTyrProAsnProValPheGluAlaP    | 1147    |
| qq       | 111106 | CAGCCCGCTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT                      | 111047  |
| Qγ       | 1147   | heGlyProSerGlyIleLeuGluLeuLysProGlyThrProIleIleLeuLys           | 1164    |
| QQ       | 111046 | TIGGGCCCTCTGGTGTGTAGATGTCAAACCTGGTTCACATGTTGTATTGAAGGTGCTGG     | 110987  |
| Qy       | 1164   |   | 1164    |
| QQ       | 110986 | GGATAAGGATAGGGAGTAGAAAGGAGGGGAAGAACCGAGAGCTGGAGTGCTTGACTGTTT    | 110927  |
| Qy       | 1165   | GlyLysAsnLeulleProProValAlaGlyGlyAsnV                           | 1177    |
| qa       | 110926 | CTGTGTGGGTTATCCACTACTAGGCCAAGAACCTGATCCCTGCTGCTGCAGCTGCAGCTCC   | 110868  |
| QΥ       | 1177   | alLysLeuAsnTyrThrValLeuValGlyGluLysProCysThrValThrValSerAspV    | 1197    |
| qq       | 110867 | CTCAACTACACAGTGTTGATTGGAGGACGACCATGTGCACTAACTGTCT               | 110810  |
| Qy       | 1197   | alGlnLeuLeuCysGluSerProAsnLeuIleGlyArgHisLysValMet              | 1213    |
| qq       | 110809 | CCCAAGCCAGACAGGCCGGCAG  | 110750  |
| Οy       | 1213   |   | 1213    |
| ρp       | 110749 | GCTCAAGAGGCCACCAGGCCAGCCCTGGCTGCCATGGGAGTTGGTTCACCTCAAGCTTG     | 110690  |
| Qy       | 1214   | AlaArg-ValGlyGlyMetGluTyrSerProGlyMetValTyrIleAlaPro            | 1230    |
| qq       | 110689 | CCCTTACAGGTGCTGGTGGCTGGCCTGGATTGGGTTGGG                         | 110630  |
| Qy       | 1231   | AspSerProLeuSerLeuProAlaIleValSerIleAlaValAlaGlyGlyLeuLeuIle    | 1250    |
| QQ       | 110629 | GATCGGGCACTTACCAGCTATGGTGGGGGCTAGCAGGGGGGGG                     | 110570  |
| Qy       | 1251   | IlePheIleValAlaValLeuIleAlaTyrLySArgLysSerArgGluSerAspLeuThr    | 1270    |
| qq       | 110569 | CTGGCCATCACTGTTGTGTGCTGCCTACAAGCGTAAGACTCAGGATGCAGAGCGCACA      | 110510  |
| Qy       | 1271   | LeuLysargLeuGlnMetGlnMetAspAsnLeuGluSerArgValAlaLeuGluCysLys    | 1290    |
| qq       | 110509 | TTCAGCTACAAATGG   | 110450  |
| Qγ       | 1291   | Glu   | 1291    |
| QΩ       | 110449 | GAAGGTGCCTAAAAGCAGGGGGTGTACCACATTGTGTGAGAAGCTGAGGGACTTTCCTGCTT  | 110390  |
| δλ       | 1292   | AlapheAlaGluLeuGlnThrAspIle                                     | 1300    |
|          |        |   |         |

| ,<br>Oy        | 1685 1685  |   |
|----------------|--|---|
| qq             | 108173 TAGACACCTTCTAGCCCAGTCTTAAACATGAGATGAGCTGCTTTCTTAGGGCCTTGGCAC 108114 | 107093  |
| Ωy             | 1685 1685  | 1812  |
| qq             | 108113 TAGGACCTCTACGCCTGAGGTCAAGGTCTATTTTAGGAATGTTGGCCCTTCAGAG 108054      | ĭ   |
| QY             | 1685 1685  | 2181  |
| qq             | 108053 AAGTTTTTTTTTACTGAGCTAITCTGCCCCTGTCTGTCAGAITTTGGGAACTTCCTGAC 107994  | 7.6901  |
| Οy             | 1686   | Qy 1813   |
| Dp             | 107993 ATGGTTCCTTTACCATCACTCATAGGGCACGTTGCAGAAGTTTGTAGATGACTTGTTGT 107934  | 1826  |
| Oy<br>Dp       | 1697 uThrilePheSerThralaHisArgGlySerAlaLeuProLeuAlaileLysTyrMetPh 1717<br> | 106853  |
| Oy<br>Op       | 1717 eAspPheLeuAspGluGlnAlaAspLysHisGlyIleHisAspProHisValArgHisTh 1737<br> | Qy 1846 ThrMetSer<br>Db 106793 GTCCTAAGT        |
| Qy             | rTrpLysSerAsn  | Search completed: June<br>Job time : 13967 secs |
| g Z            | 107813 CTGGAAGAGCAACTGGTACTTACTGGTTCCTGACTGCTGCTGCTCTTCTGAGGGTGGGT         |   |
| q <sub>0</sub> | 107753 GGGAGGAAGGCTAGTTACTTAGCCAAGCCTCCAGGCCAATGGAGACAGGTTGACTAGC 107694   |   |
| ΟŊ             | 1741 1741  |   |
| ОĎ             | 107693 AACTGAATAGCCTTCCATGCAGGAGGGATGGACCAGTGGTATGGCCTGGAAGTGAATATG 107634 |   |
| Qγ             | 1741 1741  |   |
| qq             | 107633 AGTATATAGAAGGTGGGTGCTGCTGGGTTGTGCAGATGGGAAGTGCTAGTTAGCACTGG 107574  |   |
| Qy             | 1741 1741  |   |
| qq             | 107573 GATTGACCATTTTTCTCTAGGGTCCTGTGCAGGGTAGACACACTGATGGCTTGGCATAGG 107514 |   |
| Qy             | 1741   |   |
| ф              | 107513 IGGAGACAGIGGAAGTITCAGGGGIGGAGGIIGAGGACAGAAAGCCAICIATITI 107454      |   |
| Qy             | 1741 1741  |   |
| QQ             | 107453 CTCATTGCCTGAGTGCAGCAGAAGGTTAAAGAAAACCCATTTATCCAAAATAGTCTCTC 107394  |   |
| ογ             | 1741 1741  |   |
| QQ             | 107393 CIGITACTICAGGACAAGAIAIGACCIGGCCAAACAGGACAAGGIGIGAAGGAAG             |   |
| 6y             | 1742CysL 1743  | · .   |
| qa             | 107333 GGGGGAAGGGGCCACATAGGGCCATTAGGGAGTCTCAAGTGTATGTCCCTCTGTTCAGCT 107274 |   |
| Qy             | 1743 euProLeuargPheTrpValasnMetIleLysasnProGlnPheValPheAspIleHisL 1763<br> |   |
| Qy             | 1763 ysasnSerIleThraspalaCysLeuSerValValalaGlnThrPheMetaspSerCyss 1783<br> |   |
| Oy.            | 1783 erThrSerGluHisArgLeuGlyLysAspSerProSerAsnLysLeuLeuTyrAlaLysA 1803     |   |
| 67 67          |  |   |
|                |  |   |

| qa | 107093 |  | 107034 |
|----|--------|--|--------|
| Οy | 1812   |  | 1812   |
| qq | 107033 | 107033 TGGTGGCAGGCAGGAACTGCCTAAACAGCCTGTCTGAGGCTGGCCAGATACAAGAAAAAG 106974 | 106974 |
| Qy | 1812   | 1812   | 1812   |
| Dp | 106973 | 106973 CCTCAGAGGCTGGCCAAACACTGATGGCATGAGTTTTGGCATTTATGACCTGTGCATGAT 106914 | 106914 |
| Qy | 1813   |  | 1825   |
| qq | 106913 | TCACTCACCCAAGGTCTCTATAGGTACTATCGAGATATCGCAAAAGATGGCATCCATC                 | 106854 |
| Qy | 1826   | 1826 AspGlnAspMetAsnAlaTyrLeuAlaGluGlnSerArgMetHisMetAsnGluPheAsn 1845     | 1845   |
| qq | 106853 | GACCAGGACATGCACGCTACTAGTGGAGCAGTCCCGCCTCCATGCTAATGACTTCAAT 106794          | 106794 |
| Οy | 1846   | Thr  | 54     |
| qq | 106793 | 106793 GTCCTAAGTGCACTCAGCGAGCTCTACTTCTATGTCACCAAGTACCGTCAGGAGGTA 106737    | 5737   |

28, 2003, 15:21:45

Human cDNA encodin Thyroid cancer rel Human plexin-B1/SE Human EST-derived

Human plexin-B1/SE Human cDNA encodin

Drosophila melanog Human cDNA encodin Human differential

Novel human coding

DNA encoding novel Human CDNA encodin Human NOV/Plexin-A Human CDNA, SEQ ID Human full-length

Human PRO235 prote Human PRO235 cDNA Human cDNA sequenc Human PRO235 cDNA.

cDNA encoding huma Protein PR0235 cDN

Viral-encoded sema Human VESPR cDNA.

Perfect score:

Title:

Sequence:

OM protein

Run on:

Scoring table:

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Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
neuroprotective; antiparkinsonian; protein therapy; EST;
expressed sequence tag; gene; ss.
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       SUMMARIES
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Database :

Viral encoded sema viral encoded sema Human VESPR cDNA.

Nucleotide sequenc Human cDNA encodin Human prostate exp Human prostate exp Human brain expres Human brain expres Probe #1141 used Drosophila melanog

Human brain expres

Drosophila melanog

Human cDNA

Probe #24492 used

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                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of 444 movel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopolesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple solarosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
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Matches:
Conservative:
                                                                                                                          Asundi V, Zhang J,
J, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1762 G; 1298
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Indels:
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                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 310; 509pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 1416 A; 1911 C;
                                                                                                                        Liu C, Zhou P, As
Yang Y, Wehrman T,
                                       10-SEP-2001; 2001WO-US26015
                                                                    11-SEP-2000; 2000US-0659671
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6794.00
80.23$
67.47$
68.01$
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                                                                                                HYSE-) HYSEQ INC
                                                                                                                                                                                  P-PSDB; ABB97486
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6387
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             21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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uGluAspLeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeuSerGlyVa 163

143

1652 1352 1232 1292 1592 1353 CCGGGCCATCAACTTGCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAA 1412 499 360 420 460 516 320 340 400 440 479 ----ACCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCAT uLysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyTh rLeuAspLeuAlaTrpLeuLysVallysAspIleProCysSerSerAlaLeuLeuThrIl sLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheVa GCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACCAGCGATTTTGT lAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAspIleTy tValSerProProGly-----SerThrThrLysGluGlnValTyrThrSerLysLe 320 aValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPheSe 340 rLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLe eAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValAr 460 lAspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValVal---AspProGl  $y \verb|ProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrIleMetSerGlugInLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspMetAlaPheSerLysAspHisGluGlnLeuArgAspMetAlaPheSerLysAspMetAla$ uArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCy lAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAspAspLysLe 360 380 440 1593 479 400 499 223 263 1057 759 819 879 939 669 163 183 203 qq qq q qq Op δ qq οy QY q δy qq ΩD QΥ g δ q Q 원 à δ a 9 qq Qg οy qq Q δy QY δ g QΥ δy

| 379 9<br>2910 1<br>899 1<br>2970 0   | 3030 CCATGC<br>939 OG1uPh<br>939 OG1uPh<br>3090 AGAGTT<br>959 ULYSPK<br>11111<br>3150 CAACCC | 3210 TGGGGG<br>999 GSETPL<br>1111<br>3270 GTCAAT<br>1018 SVALSE<br>11111<br>3330 TGTTTC<br>1038 UASPPL<br>11111<br>3390 TGACCC | 1058 ealavalrrpG : :::   3450 GACCATCACAG  1078 yGlyLySGlUH   111111111111111111111111111111111111 | 1138 rTyrProAsnP 1590 CTACCCCAACC 1158 yThrProlleI 1158 yThrProlleI 1178 sLeuAsnTyrT 1178 sLeuAsnTyrT 1198 nLeuLeuCysG 1198 nLeuLeuCysG 1198 nLeuLeuCysG 1198 nLeuLeuCysG 1198 nLeuLeuCysG 1198 nLeuLeuCysG 1198 nLeuLeuCysG 1198 nLeuLeuCysG 1198 nLeuLeuCysG 1198 nLeuLeuCysG 1198 nLeuLeuCysG 1198 nLeuLeuCysG 1198 nLeuLeuCysG 1198 nLeuLeuCysG |
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| 2 2 2 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6  | 2 2 2 2 2 2 4 4 5 5 5 5 5 5 5 5 5 5 5 5  |  |  |   |
| GAGACAGGTCACCAGGGAGTCATGTGAGCAGTATACGACTTGTGGGGAGTG 18 sLeuGlySerGlyAspProHiscysGlyTrpCysValLeuHisAsnThrCysThrArgly 53 [ | 559 lArgLeuthrvalHisProAsnAsnIleSerValSerGinTyrAsnValLeuLeuValLe 579                         |  | UASPCYSProGInLeuLeuArgValAspLysIleLeuValProValGluValIleLysPr 7                                     | IGLULEUT IGLULEUT IGLULEUT IHISTEUT CCATCTCT COASPPRA OASPPRA OASPRING III GAACTTTG OALAGING III GAACTTTG OALAGING III GAACTTTG OALAGING III GAACTTTG AATCACCG  |
| 90 OX  | 6 6 6 6 6 6  | 4 6 6 6 6 6  | 6 6 6 6 6 6 6  |   |

TyrlleValCys---AsnThrThrSerSerAspGluValLeuGluMetLy 1018 1198 AlaLeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPh 1118 LeuAspAsnValGlnSerLeuLeuIleLeuAsnLysThrAsnPheThrTy 1138 GTGGGAACCACCTCCGGGCCAGTACGCCTGTGTATTGGCGAGTGTAAGCC 3089 666 ProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgPr 939 Proval PheGluAlaPheGlyProSerGlyIleLeuGluLeuLysProGl HislleAsnIleCysGluValLeuAsnAlaThrGluMetThrCysGlnAl GluSerProAsnLeuIleGlyArgHisLysValMetAlaArgValGlyGl LeuGlyLeuGluPheArgAspIleAlaSerHisValLysValAlaGlyVa SerAsnValValValMetPheGlyLysGlnProCysLeuPheHisArgAr GlyThrHisLeuAspLeuIleGlnAsnProGlnIleArgAlaLysHisGl ProLeuValAspGlyTyrIleProAlaGluGlnIleValCysGluMetGl AlaArgSerSinLeuTyrTyrPheMetThrLeuThrLeuSerAspLe

| qa .   | 0y 1  | , vo   | ag ag   | Oy da  | Qy   | oy do  | ĀĀ QQ (  | λλ qq (  | ζζ,<br>QO  | oy<br>do   | Z qq ;   | A G  | λλ dd ·  | δο da   |  | RESULT Z AB199504 ID AB19 XX   |  | XX XX MOUS KW MOUS KW VASO   | XX OS Mus |
|--|---|--|---|--|--|--|--|--|--|--|--|--|--|---|--|--|--|--|-----------|
| 8 allevalSerlleAlaValAlaGlyGlyLeuLeullellePhellevalAlaValLeull 125 | CGTCAGCATCGCGGCCGGCGGCAGCCTCCTCCTCATCATCGTCATCATCATCATCATCATCATCATCATCATCATCATCAT | 4047 TGCCTACAAGCGCAAGTCTCGAGAAAATGACCTCACTCTCAAGCGGCTGCAAATGCAGAT 4106 | 1278 tAspasnLeuGluSerArgValAlaLeuGluCysLysGluAlaPheAlaGluLeuGlnTh 1298 • 4107 GGACAATCTGGAGTCCCGTGTGGCCTTGGAGGAAGGAAGCTTTTGCTGAGCTCCAGAC 4166 | 1298 rAspileHisGluLeuThrSerAspLeuAspGlyAlaGlyIleProPheLeuAspTyrAr 1318<br> | 1318 gThrTyrThrMetargValLeuPheProGlyIleGluAspHisProValLeuArgAspLe 1338<br> | 1338 uGluValProGlyTyrArgGlnGluArgValGluLysGlyLeuLysLeuPheAlaGlnLe 1358<br> | 1358 ulleasnasnLyšValPheLeuLeuSerPhelleargThrLeuGluSerGlnArgSerPh 1378<br> | 1378 eSerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLe 1398<br> | 1398 uGlutyralathraspValLeuLysGlnLeuLeualaaspLeutleaspLysasnLeuGl 1418<br> | 1418 uSerLysAsnHisProLysLeuLeuLeuArgArgThrGluSerValAlaGluLysMetLe 1438<br> | 1438 uThrasnTrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGluProLe 1458<br> | 1458 upheSerteuPheCysalaileLysGlnGlnMetGluLysGlyProileAspAlaileTh 1478<br> | 1478 rGlygluAlaArgTyrSerLeuSerGluAspLysLeuIleArgGlnGlnIleAspTyrLy 1498<br> | 1498 SThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLy 1518<br>        ::: | 1518 sileLeuasnCysAspThrileThrGlnValLysGluLysIleLeuaspAlailePheLy 1538<br> | 1538 sASNValProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGl 1558<br> | 1558 ySerGlýalaargMetIleLeuGlnaspGluaspIleThrThrLysIleGluasnaspTr 1578<br> | 1578 pLysArgLeuAsnThrLeuAlaHisTyrGlnValProAspGlySerValValAlaLeuVa 1598<br> | 598       |
| δλ   | oy<br>Oy  | QQ   | Qy<br>Db  | Qy   | Qy   | oy<br>og   | Qy<br>Dp   | OY<br>Db   | Qy   | Oy<br>Dp   | Qy   | Oy<br>Dp   | QY   | Oy<br>Db  | QY<br>Dp   | Qy<br>Db   | Qy   | Qy   | Qy        |

1738 5486 1758 5546 1778 9099 1798 5666 1818 5726 1838 5786 gMetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSerTyrValGl 1858 1858 yLysTyrSerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysGlyLysGlnLy 1878 1718 5426 5306 1698 aSerLysTyrGluAsnMetIleArgTyrThrGlySerProAspSerLeuArgSerArgTh pLysSerAsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnProGlnPheVa SS. se; ischaemia; compressive ischaemia; occlusive ischaemia; ospastic ischaemia; ischaemic condition; ischaemic disease; se ischaemic condition related cDNA sequence SEQ ID NO:479 BP 99504 standard; cDNA; 6730 (first entry) musculus MAR-2002 1838 1738 2067 1618

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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes are used as an indicator when screening for ischaemic condition-improving represent PCR primers for a mouse ischaemic condition improving represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                    Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                            Ishii Y;
                                                                                                                                                                                                            Nagata T,
                                                                                                                                                                    (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 1319-1331; 2690pp; English.
                                                                                                                                                                                                            Takahashi Y,
                                                                                          18-MAY-2001; 2001WO-JP04192
                                                                                                                              18-MAY-2000; 2000JP-0145977
                                                                                                                                                                                                          Ishikawa K, Asai S,
                                                                                                                                                                                                                                              WPI; 2002-034733/04
P-PSDB; ABB57196.
                WO200188188-A2
                                                      22-NOV-2001
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Sequence 6730 BP; 1656 A; 1850 C; 1740 G; 1482 T; 2 other;

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|  |   | 44  | 675  | 63   | 735  | 83   | 795  | 103  | 855  | 123  | 915  | 143  | 975   |
|--|---|---|--|--|--|--|--|--|--|--|--|--|---|
| 6730<br>21268<br>239<br>357<br>14  |   | 25 LeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPheValThrPheArg | CTGCTAGCTCGTGGGACCACAGGTATGCCTCAGTACAGCACTTTCCAC | 45 GlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThrGlyHisIle | 676 TCTGAGAATCGTGACTTTCAACCATTTGACTGTACACGGAAGAGAGGGGGTGTG | TyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysValLeuValThr | TATGTGGGGGCTATCAATGGTGTCTACAAGTTGACTGGGAACCTCACCATCCAGGTGGCT | HisGluThrGlyProAspGluAspAsnProLysCysTyrProProArgIleValGlnThr | CACAAGACGCCAGAAGAGGACAACAAGGCTTGCTACCCACCC | CysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuIleAspTyrLys | TGCAGTGAAGTGCTTACACTCACCAACAATGTCAACAACTACTGATCATTGACTACTTTACT | 124 GluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeu | 916 GAGAATCGCCTGCTGCTGCGCGAAGCCTCTACCAGGGTGTTTGCAAGCTCCTGCGACTA |
| Length: Matches: Conservative: Mismatches: Indels: Gaps:                                   | 04 (1-6730)                                   | ProLeuSerGlnLysGlr  | :::<br>AGGTATGCCTCAG                             | PheAsnHisLeuValVal   |  | JIleTyrLysLeuSerSer  |  | ASPASnProLysCysTyr   | SGACAACAAGGCTTGCTAC                        | rThrAsnAsnValAsnLys  | CACCAACAATGTCAACAAA  | sGlySerLeuTyrGlnGly  | GGAAGCCTCTACCAGGGT  |
| 0<br>6765.00<br>80.24%<br>7: 67.52%<br>24.72%  | JS-09-964-956-13 (1-1896) x ABI99504 (1-6730) | hrArgGlnProAla  | CTCGTGGGACCAC                                    | roAlaGluGl   | ATCGTGACTGGAC  | lyAlaValAsnAr  | GGGCTATCAATCG  | hrGlyProAspGl  | CAGGGCCAGAAGA                              | luProLeuThrTh  | SAAGTGCTTACACT   | rgLeuIleAlaCy  | GCCTGCTGGCCTG   |
| es:<br>rity:<br>ilarity  | 13 (1-1                                       | LeuLeul   | CTGCTAC  | SlyGluE  | TCTGAG   | TyrLeuC  | ratgig   | HisGlu]  | CACAAG                                     | CysAsn(  | rgcagic  | 3luAsn2  | SAGAATO   |
| Alignment Scores: Pred. No.: Score: Scoret Similarity: Best Local Similarity: Duery Match: | -09-964-956-                                  | 25 1  | 628 (  | 45 (   | 929 .  | 64 7   | 736 7  | 84   | 967  | 104 (  | 856  | 124 (  |   |
| Ali  | S   | $\stackrel{\sim}{\lambda}$                                      | g  | ζ  | g  | ≿  | g  | $\overset{\sim}{\Delta}$                                     | g  | Š  | ď  | ζ.   | g   |

| . 144        | GluaspleuPheLysLeuGlyGluPrOTyrHisLysLysGluHisTyrLeuSerGlyVal 163<br>:::  |   |
|--------------|--|---|
| 164<br>1036  | euAspAspLysLeu 18<br>              <br>AAGATGGCAAGCTT 10   |   |
| 184          | 11.<br>  |   |
| 204<br>1156  | LeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheVal 223   |   |
| 224          | <pre>fleProAspPheAspIleTyr 2 f:: free                                   free CACTTCGACATCTTC 1</pre>                 |   |
| 244<br>1276  | PheValTyrPheLeuThrLeuGlnProGluMet 26   |   |
| 264          | SerThrThrLysGluGlnValTyrThrSerLysLeu 2: ::::::::::::::::::::::::::::::::::   | _ |
| 281<br>1390  | PheAsnSerT<br>   :::    <br> TTCCACTCCT  | _ |
| 301          | GluargSerGlyValGluTyrargLeuLeuGlnalaalaTyrLeuSerLy<br>    :::  | _ |
| 321<br>1510  | ValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPh<br>     :::  | _ |
| 341          | LysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysI<br>               <br>  AGGGGCAGAAGCAGCACCCCCCTGATGACTCTGCCCTCTGTG | _ |
| 361          | ysGluargLeuGlnSerCysTyrargGlyGluGlyThr 38<br>  | _ |
| 381.<br>1690 | LeudspLeudlaTrpLeuLysValLysAspIleProCysSerSerAlaLeuLeuThrIle   | _ |
| 401          | AspaspasnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValArg 4   | _ |
| 421          | GlyileProvalPheThrGluAspArgAspArgMetThrSerVallleAlaTyrValTyr 440<br>   :::::::                                       |   |
| 441          | eualaPheValGlyThrLysSerGlyLysLeuLysLysIleArgV<br>::  |   |
| 461<br>1930  | valGlnvalva<br>    <br>GTCTCTGTGTT   |   |
| 1990         | luGlnLeuTyrIleMetSerGlu 4<br>       ::   |   |

Mon

3546 1138 1218 1013 3906 4083 MetGluTyrSerProGlyMetValTyrIleAlaProAspSerProLeuSerLeuProAla SerProSerTyrIleValCys---AsnThrThrSerSerAspGluValLeuGluMetLys ValSerValGlnValAspArgAlaLysIleHisGlnAspLeuValPheGlnTyrValGlu AspProThr11eValArg11eGluProGluTrpSer11eValSerGlyAsnThrProI1e GACCCACGGGTCCAACGTATTGAGCCAGAGTGGAGTATCACTAGTGGGCACACACCCTA ProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPhe ThrProllelleLeuLysGlyLysAsnLeulleProProValAlaGlyGlyAsnValLys LeuAsnTyrThrValLeuValGlyGluLysPròCysThrValThrValSerAspValGln LeuLeuCysGluSerProAsnLeuIleGlyArgHisLysValMetAlaArgValGlyGly GlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMetThrCysGlnAla GluCysSerProLeuValAspGlyTyrIleProAlaGluGlnIleValCysGluMetGly GlualaLysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgPro LysProSerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeu AsnAlaGlySerAsnValValValMetPheGlyLysGlnProCysLeuPheHisArgArg GluPheMetAlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeu GlyGluAsnLeuGlyLeuGluPheArgAspIleAlaSerHisValLysValAlaGlyVal

90 AQ

0y 0y 0b

Qy Db

Db Oy Db

| Qy 1599 SerLysGloValThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThrSerAla 1618  | Oy 1619 SerLysTyrGluAsnMetIleArgTyrThrGlySerProAspSerLeuArgSerArgThr 1638 | Qy 1639 ProMetileThrProAspLeuGluSerGlyValLySMetTrpHisLeuValLySAsnHis 1658 | Qy 1659 GluHisGlyaspGlnLysGluGlyaspargGlySerLysMetValSerGluIleTyrLeu 1678  ?::  | Oy 1679 ThrargLeuLeualaThrLysGlyThrLeuGlnLysPheValaspAspLeuPheGluThr 1698 |              | PheLeudspGluGlnAlaAspLysHisGlyIleHisAspProHisValArgHisThrTrp<br>           | Qy 1739 LysSerAsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnProGlnPheVal 1758  | 9 PheaspileHisLysasnSerileThraspalaCysLeuSerValValalaGlnThrPhe 177 [11] | Oy 1779 MetAspSerCysSerThrSerGluHisArgLeuGlyLysAspSerProSerAsnLysLeu 1798  1111111111111111111111111111111111 | Qy 1799 LeutyralaLysaspileProSerTyrLysasnTrpValGluArgTyrTyrSerAspile 1818 11 | Oy 1819 GlyLysMetProAlaileSerAspGlnAspMetAsnAlaTyrLeuAlaGluGlnSerArg 1838                               | Qy 1839 MetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSerTyrValGly 1858 ::: | Qy 1859 LysTyrSerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysGlyLysGlnLys 1878 | Qy 1879 LeuAlaTyrLysLeuGluGlnVallleThrLeuMetSerLeuAspSerAsnLys 1896 | SULT 3<br>117265<br>ABL172   | 7.003;<br>AR-2002 (first entry)  | DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3268.<br>XX<br>KW Drosophila; developmental biology; cell signalling; insecticide;<br>KW pharmaceutical; gene; ds. |
|--|---|---|---|---|--------------|--|--|---|---|--|---|---|---|---|--|--|--|
| 4204 AIGGRETTCTCACCTGGCTCCTGGAGCGTCATCTCCGGACGCTGTTGACCCTGCCAGCC 4263 1239 IleValSerIleAlaValAlaGlyGlyLeuLeuIleIlePheIleValAlaValLeuIle 1258 | AlaTyrLysArgLysSerArgGluSerAspLeuThrLeuLysArgLogInMetGluMet               | 279 ASPASNLE<br>  | AspileHisGluLeuThrSerAspLeuAspGlyAlaGlyIleProPheLeuAspTyrArg 131<br>        ::: | ThrTyrThrMetArgValLeuPheProGly11eGluAspHisProValLeuArgAspLeu 1            | SlnLeu 1<br> | 1359 IleAsnAsnLysValPheLeuLeuSerPheIleArgThrLeuGluSerGlnArgSerPhe 1378<br> | 1379 SerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLeu 1398<br> | 1418  | LLeu 1<br>    <br> CTG 4  | oleu<br>   | 459 PheserLeuPhecysAlaileLysGlnGlnMetGluLysGlyFroileAspAlaileThr 1   111:::1111111111111111111111111111 | rLys 1<br>    <br> AAG 5  | ThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLys 151<br>      | eLys<br>:   <br>TAAG  | 1539 ASNVAlProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGly 1558<br> | 1559 SerGlyalaargMetIleLeuGlnAspGluAspIleThrThrLysIleGluAsnAspTrp 1578 | 1579 LysargLeuasnThrLeualaHisTyrGlnValProAspGlySerValValAlaLeuVal 1598<br>   |

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                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGIT6-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
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            Drosophila melanogaster.
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Best Local Similarity:
                                 WO200171042-A2.
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                                                                                                         --GCTGTTGTGGCTAATGATGCCAACTCCTCAACC
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122 TyrLysGluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeuLeu 141

CGTGCAACTTCAAGACTTATTGCGTGTGGATCACTATTTCAAGGTACATGCACAGTTCGT

ArgLeuGluAspLeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeuSer 161

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| YATTTGATT YATTTGATT YATTTGATT YATTTGATT YATTTGATT YATTTGATT  |
| SGTTAAGT<br>SGTTAAGT<br>PProHisCy<br>IIII::II  |
| LeuTyrileMetSerGluArgGlnLeuThrArgvalProvalGluSerCysGlyGlnTyr :::   :::      ::  ATATATGTTATGCCAAAAGTATCCAAGGTTTGATTGATTG |
| CAAAAGTU<br>CAAAAGTU<br>CUGLYSE1<br>I H I I I : : : : TAGGTGCT   |
| CCAAAAC<br>luCysLe:<br>::     <br>ATTGCTT  |
| GTTATGTC CysGlyGl  |
| F 7.15   |
| GlnSe  |
| 1657 ATATA<br>514 GlnSe<br>1717 AAGAC  |

HisargargserProSerTyrIleValCysAsnThrThrSerSerAspGluValLeuGlu 1016 :::::||| ::::||| ::::||| CTAAGCACAGTTCTTCTCAAGCAATATGTCGCACTTCTGCTTCTGCTATGTAA 3261 GGGAAAACTGATTGGTTAAATCGAAGT-----GAAATTTGCCCAAACCTGAAATT 2799 MetLysValSerValGlnValAspArgAla---LysIleHisGlnAspLeuValPheGln 1035 GGAAGACTAAAAATGTCTTTTGATAATGGGCCCCGAGAGTTTAATGACTACAATTTTAAA 3321 ||||||| || |||||||||:: |TATGTACTGGATCCTACAGTTGAACACGTTAGTTCTGGACCAAGCGGGCAAATAAAAGTT 3381 ValLeuAsnAlaThrGluMetThrCysGlnAlaProAlaLeuAlaLeuGlyProAspHis 1107 ||| :: ||||||||| ||| :::||| GTGCAATGGGAAATGGGAAATGTGCATCTCAGTTGTTGATGTG-----GACAGC 3555 ValPheGluAlaPheGlyProSerGlyIleLeuGluLeuLysProGlyThrProIleIle 1162 CATACATTCCAACCAAAAACAGGTCCCTGGGAAGGAGGAACAAATATAACAATACGAGGA 2859 TyrvalGluAspProThrIleVal----------ArgIleGluPro 1047 GluTrpSerIleValSerGlyAsnThrProIleAlaValTrpGlyThrHisLeuAspLeu 1067 IleGlnAsnProGlnIleArgAlaLysHisGlyGlyLysGluHisIleAsnIleCysGlu 1087 GAGTATTTTATATTCGAAGAAAGA-----GTTAAGTACTTTAAGAGTGAATACTTAACC 3729 GlnSerAspLeuThrGluArgPro-----GluGluPheGlyPheIleLeuAspAsn--- 1124 ---GluSerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnProArgIle 860 ThrGlullelleProValThrGlyProArgGluGlyGlyThrLysValThrIleArgGly 880 GluAsnLeuGlyLeuGluPheArgAspIleAlaSerHisValLysValAlaGlyValGlu 900 --- GlyGluAlaLysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCys 937 AspLeuLysProSerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThr 977 AsnLeuAsnAlaGlySerAsnValValValMetPheGlyLysGln---ProCysLeuPhe 996 ArgProGluPheMetAlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSer 957 GlyTrpCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCysProAlaGln----- 841 CysSerProLeuValAspG1yTyrIleProAlaG1uG1nIleValCysG1uMet----CCTGGAGAACAGATGTATAGAAATGGCAAAATAGTGGTACAAATT-------

| Qy<br>Db  | 1163 LeulysGlyLysAsnLeuIleProProValAlaGlyGlyBasnValLysLeuAsnTyrThr 1182 :::  | ਰ <u>ੂ</u>     | m  |
|-----------|--|----------------|--|
| oy<br>E   | 1183 ValLeuValGlyGluLysProCysThrValThrValSerAspValGlnLeuLeuCys 1201<br>  | da<br>da       | 1519 IIELEUASNOYSASPINTIIEINTGINVALLYSSUU<br>1::    ::   |
| i ko i    | 02 GluSerProAsn  | QV             | 1539 ASNVALProCysSerHisArgProLysAlaAlaAsp<br>  |
| Qy<br>Qy  | 838 AGACCICCTTCTGAAGCAACGAACGAAGGCATGAATGGACTGAAGTAATTGTTGTTGTT 38 216 ValGly-'GlyMetGluTyrSerProGlyMetValTyrIleAlaProAspSerPro 12 :::    :::                            | Qy             | 1559 SerGlyAlaArgMetlleLeuGlnAspGluAspIle :::  |
| oy<br>oy  | 898 ATTGGAACTTCGCTAGAGTATCGTATCGGTATACTTAGGTACGAATCGTCTAACATCTT 3 234 LeuSerLeuProAlaileValSerIleAlaValAlaGlyGlyLeuLeuIleIlePheIle 1 11111111111111111111111111111111111 | Q7             | 1579 LysArgLeuAsnThrLeuAlaHisTyrGlnValPro  |
| oy (      | 958 TTGGATTGGGGAGAAATGTAATTTTGCTGTAATAGCCACAATTGTTATCTTGCTGCTG 254ValAlaValLeuIleAlaTyrLysArgLysSerArgGluSerAspLeuThrLeu   | da<br>Dp       | 1599. SerLysGlnValThrAlaTyrAsnAlaValAsnAsn<br>              ::            <br>  5083 CCAAAGCAAGTTCCATTTATAACTTCAGTATTTA        |
| ga Ko     | 018 ATTITISTICCTITICCTICTICCTITATAAAAAGAAAAGTICGGAAATCGAGGCCGAGTTCTT 40 272 LysargLeuGlnMetGlnMetAspasnLeuGluSerArgValAlaLeuGluCysLysGlu 12 :::                          | QQ<br>Dp       | 1619 SerLysTyrGluAsnMetIleArgTyrThr<br>  |
| 9 6 6     | /8 CGAAACAIGCAGGAGGAGAGAGGACATICIGGAGCIACGAGTCGCAGTCGAATGTAAAGAG 4.1 92 AlaPheAlaGluLeuGlnThrAspIleHisGluLeuThrSerAspLeuAspGlyAlaGly 1.3                                 | , qq           | 1636 SerargThrProMetileThrProAspLeuGluSer::::::::::::::::::::::::::::::::::::  |
| ga Vo     | 38 GCCTTIGCCGAACICCAAACIGAAAIGACIGACIGCTCACAGGCGAAICITACITCIGGGAGGC 4<br>12 ilepropheleuAspTyrArgThrTyrThrMetArgYalLeuPheproGlylleGluAsp 1<br>                           | λ <sub>O</sub> | 1656 LysasnHisgluHisglyaspglnLysgluGlyasF<br>    :::    :::<br>  5260 AAACATCATGATAGTGATATGCAAAAAGAAGGGGAA                     |
| oy<br>Oy  | 198 ATTCCATTTTGGATTACCGGTCATATGCAATGAGATTCTATTTCCAACCATGAAGAC 4<br>332 HisprovalleuargaspleuGluValProGlyTyrargGlnGluArgValGlu 1<br>             ::                       | . QQ qq        | 1676 IleTyrLeuThrArgLeuLeualaThrLysGlyThr<br>  |
| oy<br>Oy  | 258 CACATTGTACTACAATGGGAACGTCCTGAGCTTCTTCGGAAGAA 4<br>350 LysGlyLeuLysLeuPheAlaGlnLeuIleAsnAsnLysValPheLeuLeuSerPheIle 1<br>   | QY<br>Dp       | 1696 PheGluThrIlePheSerThrAlaHisArgGlySer<br>  |
| d y q     | 4303 AAAGGCTTACGTATTTTGGCCAACTAATCATGAATAAACTTTCGTCCTTGTTTTATA 4362 1370 ArgThrLeuGluserGlnArgSerPheserMetArgAspArgGlyAsnValAlaSerLeu 1389 1310 All                      | QV             | 1716 MetPheAspPheLeuAspGluGlnAlaAspLysHis<br>  |
| g & 1     | <pre>0 IleMetThrValLeuGlnSerLysLeuGluTyrAlaThrAspValLeuLysGlnLeuLeu 14                                      </pre>   | Qy             | 1736 HisThrTrpLysSerAsnCysLeuProLeuArgPhe<br>  |
| oy<br>oy  | AIRAIGGICACICIGCAAICIAAACIAGAAIATIGCACAGAIAIAITAAAAACITITAIIG 448 AlaAspLeuIleAspLysAsnLeuGluSerLysAsnHisProLysLeuLeuLeuArgArg 142                                       | . dg           | 1756 GlnPheValPheAspIleHisLySAsnSerIleThr<br>  |
| oy o      | 30 ThrGluSerValalaGluLysMetLeuThrAsnTrpPheThrPheLeuLeuTyrLysPhe 144 11   | Qy             | 1776 GINThrPheMetAspSerCysSerThrSerGluHis<br>  |
| oy<br>Oy  | 450 LeuLysGluCysAlaGlyGluProLeuPheSerLeuPheCysAlaIleLysGluGlinet   | QY             | 1796 AsnLysLeuLeuTyrAlaLysAspIleProSerTyr<br>:::   |
| Oy<br>Dp  | 470 GluLysGlyProlleAspAlalleThrGlyGluAlaArgTyrSerLeuSerGluAspLys 1<br>:::          ::      ::  | δγ<br>Oγ       | 1816 SeraspileGlyLysMetProalaileSeraspGln<br>        <br> 5740 AGAGACATTCGGGATATGTCCCCCATTTCAGATCAC                            |
| Qy and Dp | 490 LeuileargGinGinileaspTyrLysThrLeu  | d do           | 1836 GINSErArgMetHisMetasnGluPheasnThrMet :::       :::    5800 GAGTCAAGGCTGCACACAACAGAATTTAATACGAAT 1856 TVFVAIGIVIASSTVESPER |
| οy        | 1501 ValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLys 1518   | <del>-</del>   | )  |

etSerAlaLeuSerGluIlePheSer 1855 ||||||| ATTGTGCTTTACATGAGCTATACACA 5859 roLeuAspHisAspAspGlnCysGly 1875 spArgGlySerLysMetValSerGlu 1675
::|||, :::|||:::|||||||||||
aAcGGGTTAACAATTAGTGTCAGAG 5319 herrpValasnMetileLysAsnPro 1755 ||||||||||||||| TTTGGGTGAACTTAATTAAAAATCCA 5559 YrlysAsnTrpValGluArgTyrTyr 1815 ||::: ||||||:::||||||||| ATCGAAAATGGGTAGATCGCTATTAT 5739 snSerThrValSerArgThrSerAla 1618 FATCGGACAAAATGAAAAATCG--- 5139 nr---GlySerProAspSerLeuArg 1635 CICACACCGAAAATGTATCTGTTAAA 4842 luLysIleLeuAspAlaIlePheLys 1538 coAspGlySerValValAlaLeuVal 1593 

Conservative: Mismatches: Indels: Gaps:

(1-6408)

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AspGluAspAsnProLysCysTyrProProArgIleValGlnThrCysAsnGluProLeu 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrThrThrAsnAsnValAsnLysMetLeuLeulleAspTyrLysGluAsnArgLeuIle 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11111111 | 111:::::::111111:::
274 CAGCCTACCAACAACCCGAATCAGCTGCTGCTGGTG-----AGCCCAGGGGCCCTGGTG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 Leu-------GlyGluProTyrHisLysClyGluHisTyrLeuSer 161
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                                                                                                                      LeuSerHisLeuLeuMetValGlyMetGlySerSerThrLeuLeuThrArgGlnProAla 31
                                                                                                                                                                                                                                                                                            -----CTGCAGCACCTGGCAAGGGACCCCACCTCAGGCACCCTCTACCTGGGGGGCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaCysGlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAspLeuPheLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        517 ACCAGCAGGGGTGTGGGGGTGGCATTCCACCCATCACAACCCGGGCCCTGTGGCCG---
                                                                                                                                                                                                                                                      GluGlyPheAsnHisLeuValValAspGluArgThrGlyHisIleTyrLeuGlyAlaVal
                                                                                                                                                                                                                                                                                                                                                           AACTTCCTGTTCCAGCTGAGCCTGGGCTGCAGGCCACAGTGTCCACCGGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCTAGACAGCAGGGACTGCCTGCCACCTGTGATGCCTGATGAGTGCCCCCAG---GCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574 CCCGACCCCCAAGCTGCCTTCTCCTAT-----GAGGAGACAGCCAAGCTG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----CAGGCTCAGTCTAGAGCTTTTCGTGCCTATGTATCTCGAGTGTGTCTCCGGGAC
                                                                                                                                                     ProLeuSerGlnLysGlnArgSerPheVal------ThrPheArgGlyGluProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysIleProSerAspThrPheThrIleIleProAspPheAspIleTyrTyrValTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 PheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGluAsp
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   46.31%
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5860 TACGCTGTGAAGTACAATGAACAACTAACTGTTACACTTGAAGAGGATGAATTTTCGCAA 5919
                                                                                                                                                                                                                                                                     Human; Plexin; semaphorin domain; hyperplasia; neoplasia; cancer;
neurodegenerative disease; autoimmune disease; lupus; multiple sclerosis;
inflammatory bowel disease; diabetes type I; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence encodes a Human Plexin. Plexins are large transmembrane proteins whose extracellular domain shares homology with Scatter factor receptors and contain an approximately 500 amino acid Semaphorin domain. The plexin polynucleotides and polypeptides, and plexin-specific binding agents are useful in diagnosis, therapy and in the biopharmaceutical industry. In particular, the plexin polynucleotides and polypeptides are useful for generating compounds (e.g. plaxin-specific binding agents or antibodies) for treating or diagnosing a disease or disorder involving aberrant cell growth (e.g. hyperplasia, neoplasia, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegenerative disease), or diseases or disorders involving aberrant fimune regulation (e.g. autoimmune diseases such as lupus, inflammatory bowel disease or Diabetes Type I), or immunosuppressive diseases such as multiple sclerosas or rheumatoria arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in polynucleotides and polypeptides, useful in diagnosis, and in producing compounds for treating diseases involving cell growth (e.g. cancer) or immune regulation (e.g.
                                                 LysGlnLysLeuAlaTyrLysLeuGluGlnValIleThrLeuMetSer 1891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tesier-Lavigne M;
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1..6408
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                                                                                                                                                                                                                                       Human cDNA encoding a Plexin
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Tamagnone L;
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196

207 573 618 247 765

307

ArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGly 327

308

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6408 689

Length: Matches:

4.66e-213 2707.00

Alignment Scores: Pred. No.: Score:

267 711 287

| 659<br>1900<br>675<br>1960<br>689<br>2020          | Db 2080 CCACCCACAGCCCCAAAGCCCTGGCCAC  Qy 692  Db 2140 GGGCTCCTCCACAGCCACAGCTTCGGA  Qy 692  Db 2200 AGCCCTGGGGGCCATGGCAGCTTCTGG  Ov 692 | 226<br>69<br>232<br>69<br>63  | Qy         693           Db         2440         GTGCCCTGGACTGCCCCTGCCACTGT           Qy         694         ArgValLys  | Oy 700AspCysProGlnLeuLeuArgVi Oy 700AspCysProGlnLeuLeuArgVi Db 2680 CAGTATGACCCCCGGGCTCTGGGAGC Oy 710  |
|--|--|---|---|--|
| 820 GGGCTGATCCAGGCTGCACCTCCAGGGAGGTG               | 3/6AGGLYQLUGIYINILEHASPLENTALIPSARINIENTOCISCO OF 11   | 431 ArgMetThrSerVallleAlaTyrValTyrLysAsnHisSerLeuAlaPheValGlyThr 450 :::::   :::   :::    1210 CAGCTAACAGCTGGCAGTCACCATGGAAGATGGACACCATCGCTTTCCTGGGTGAT 1269 451 LysSerGlyLysLeuLysLyslleArgValAspGlyProArgGlyAsnAlaLeuGlnTyr 470 | HisGluGlnLeuTyrIleMetSerGluArgGlnLeuThrArgYalProValGluSerCys   HisGluGlnLeuTyrIleMetSerGluArgGlnLeuThrArgYalProValGluSerCys   Hill   Hill     Hill | 551PheAlaSerGluMetLySGlnCysValArgLeuThrValHisPro 565 1567 TGGCTATGGAGCTTCCAGCCTGAGCTGGGCTGTCTGCAAGTGGCAGCCATGAGTCT 1623 566 AsnAsnileSerValSerGlnTyrAsnValLeuLeuValLeuGluThrTyrAsnValPro 585 1624 GCCAACATCAGCGAGGAGGAGGAGGAGGTTTCCTATCAGTGCCA 1671 586 GluLeu |
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| λy   | 629   | 4  |
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| qc   | 1900  | GAACTCCGCCCATCTGCGCAGTGCCAGGCCTGTGTGAGCAGCCGCTGGGGGTGTAACTGG 1959  |
| λλ   | 675 ( | AspProLysThrCys 688  |
| qc   | 1960  | TGTCTGGCAGCACCTGTGCACCCACAAGGCCTCGTGTGATGCTGGGCCCCATGGTTGCA 20   |
| ΣΥ   | 689   | 692  |
| qo   | 2020  | GCCATCAGAGCCCGCTTGTCTCCCCAGACCCTCCTGCAAGAGGTGGACCCAGCCCCTCC 20   |
| οy   | 692   | 693  |
| qq   | 2080  | CCACCCACAGCCCCCAAAGCCCTGGCCACCCTGCTCCTGACACCCTTCCCGTGGAGCCT 2139   |
| Qy   | 692   | 693  |
| qd   | 2140  | GGGGCTCCCTCCACAGCCACAGCTTCGGACATCTCACCTGGGGCTAGTCCTTCCCTGCTC 2199  |
| Qy   | 692   | 693  |
| Db   | 2200  | AGCCCCTGGGGGCCATGGGCAGGTTCTGGCTCCATATCTTCCCCTGGCTCCACAGGGTCG 2259  |
| Qy   | 692   | 692  |
| qq   | 2260  | CCTCTCCATGAGGAGCCCTCCCTCCCAGCCCCCAAAATGGACCTGGAACCGCTGTCCCT 2319   |
| Qy   | 692   | 693  |
| qq   | 2320  | GCCCCCACTGACTTCAGACCCTCAGCCACCTGAGGACCTCTTGGCCTCCCGCTGTCA 2379   |
| Qy   | 692   | 692  |
| Db   | 2380  | CCGTCAGAGGTAGCAGCAGTGCCCCCTGCAGACCCTGGCCCCGAGGCTCTTCATCCCACA 2439  |
| QY   | 663   |  |
| Db   | 2440  | GTGCCCCTGGACCTGCCCCTGCCACTGTTCCTGCCACCTTTCCCAGGGGCCCATGGGC 2499  |
| QY   | 694   | ArgValLys  |
| qq   | 2500  | AGAGAAGGCGGC   |
| Qy   | 669   | 669  |
| qq   | 2560  | GAGIGGACGGGGGGTGACGCACCCGCCTTCTCCACCTTCCACCTCCTCAGGTGAIGGA 2619  |
| Qy   | 669   | 669  |
| qq   | 2620  | GACTCAGCAGAGCTTGAGGGCCCTCCGCCCCCTCATCCTCCGGTCCAGCCTCGACTAC 2679  |
| QY . | 700   | AspCysProGlnLeuLeuArgValAspLys709  |
| Db   | 2680  | CAGTATGACACCCCCGGGCTCTGGGAGCTGGAAGAGGCGACCTTGGGGGCAAGCTCCTGC 2739  |
| Qy   | 710   | 110.000 110.00 |
| Db   | 2740  | CCCTGTGTGGAGGGCTTCAGGGCTCCACGTTGATGCCGGTCCATGTGGAGCGGGAAATC 2799   |
| QY   | 721   | ThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyGlnArgGlyTyrGluCysIle 740   |
| Db   | 2800  |  |
| QY   | 741   | snileGlnGlySerGluGlnArgValProAlaLeuArg 754   |
| qq   | 2860  | ATGGAGCTGGAGGCCTCGAGGTGGTGGTTGAGGCCCGGGTCGAGTGTGAGCCACCTCCA 2919   |
| Qy   | 755   | le 7   |
| qq   | 2920  |  |

| ### ### ##############################                                  | GlyGluLysProcysThrValThrValSerAspValGlnLeuLeuCoGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | 4501 GCTCTGGGTGTCATCATTGTCATGTACAGGAGGAAGAGCAGCACCTGAGG 4560 1270 ThrLeuLysargLeuGlnMetGlnMetAspasnLeuGluSerArgValAlaleuGluCys 1289 1130 ThrLeuLysargLeuGlnMetGlnMetAspasnLeuGluSerArgValAlalaLeuGluCys 1289 11310 ThrLeuLysargLeuGlnMetGagaCTGTGGGGAGCGGGAGCGTGTGGGGAGCGTGTGGGGAGCGGAGCGGAGAGTATAAGAAGATCAGAGTGTGGGAAATTGGGGAAGTTGCGGGAGCGGGAGCGGGAGGAGGAGAGAATTGAGAAGGATGAGAGAATGAGAAGGAATTGACAGAGAGAG | 1330 GludsphisProValLeuArgAspleuGluValProGlyTyrArgGlnGludrgValGlu 1349  1351 IIII |
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| 8 8 8 8 8 8   |   | 9 6 9 6 6  | 8 8 8 8 8 8 8 8 8   |
| 775 AsnAsnLeuProValGluLeuThrValValTrpAsnGlyHisPheAsnIleAspAsnPro 794  1 | 3196 CAGTGCCCAGCGCCTCATCCACTCGGTGGAGCCACTGACTG                                      | 949 'YYTYPPDEMETTHILEUSERASPLEULYSPROSERAGGLYPCOMETSER[]  11   11   11   11   11   11   11   11  | 1022<br>3709<br>1039<br>3751<br>1059<br>3811<br>1076<br>3931                      |
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                                        GluLysGlyProlleAspAlaIleThrGlyGluAlaArgTyrSerLeuSerGluAspLys
                                                                                          .CysValSer
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                                                                                                                                                                         ProAspAsnAlaAsnScrProGluValProValLysIleLeuAsnCysAspThrIleThr
                                                                                                                                                                                         CCTGGGGCAGGAGAGGCCCAGGGCGTGAAGGTCCTAGACTGTGACACCATCTCC
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SerAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLysAsnTrpValGluArgTyr
           TyrSerAspIleGlyLysMetProAlaIleSerAspGlnAspMetAsnAlaTyrLeuAla
                                                      TATGCAGACATCAGACAGACTGTCCCAGCCAGCGACCAAGAGATGAACTCTGTCCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids differentially expressed between tumor and normal celuseful for diagnosis or therapy of tumors and for screening active
                                                                                                                                                                                                                                                                                         transcription; human; rat; tumour cell; cytostatic; c; Class II tumour suppressor gene; gene therapy; ss
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Sers C;
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Schmitz A,
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Grips M. Hellriegel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-483415/52.
                                                                                                                                                                                                              AAH81745 standard;
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This invention describes a nucleic acid (1) with differential expression between tumour and normal cells and which has cytostatic activity. (1) work as modulators of Ras activity by inducing expression of tumour suppressor genes. (1), and polypeptides encoded by them, are useful as targets for diagnosis or therapy and in screening to determine the effects of an active compound (potential pharmaceutical) on a cell line, particularly for diagnosis and treatment of tumors, especially by modulating expression of (1) (by gene therapy, antisense RNA or ribozyme methods) or by modulating the amount and/or location of (1)-encoded onlypeptides (by administration of the polypeptide or its activator, antibody (optionally as a conjugate) or inhibitor). The method allows identification of many class II tumour suppressor genes (i.e. genes that ARB1492-AARB2376 represent the human and rat derived nucleic acid fragments described in the method of the invention.

Disclosure; Page 403-404; 579pp; German.

| so seq                 | Sequence 6252 BP; 1255 A; 2022 C; 1915 G; 1060 T; 0 other;   |                   |  |
|------------------------|--|-------------------|--|
| Alignment<br>Pred. No. | Scores: 1.44e-202 , Length:  | δŏ                | GlyGlnLysArdLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLys                             |
| Score:<br>Percent      | Score: 2580.00 Matches: 654 Percent Similarity: 50.63% Conservative: 344 Rest Local Similarity: 33.18% Mismarches: 713 | <sup>-</sup> qа . |  |
| Query Ma               | 25.83% Indels:<br>22 Gaps:   | Oy.               | Gln1leAsnAspArg1leLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThrLeu 381                         |
| US-09-964              | 4-956-13 (1-1896) x AAH81745 (1-6252)  | ad .              | AAGGTGCACGCCAAGGTGGAGGCCAACGCCAACGCCTGTTACACAGGCACCCGG                                   |
| Qy                     | 24 ThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPheValThrPhe 43   | do do             | 382 ASpleuklaTrpLeuLysvalLysAspliekrocysserSerAlaLeu 397<br>:::                          |
| Qy<br>Db               |  | δδ<br>QQ          | 398 LeuThrileAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyVal 415 :::                          |
| Oy<br>Db               | TyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysValLeuValThr<br>   | da<br>Oy          | 416 SerAspMetValArgGlyIJ.eProValPheThrGluAspArgAspArgMetThrSerVal 435   1   :::      ::: |
| . VO                   |  | VQ QD             | 436 IlealaTyrValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeu 455<br>                 |
| Oy<br>Db               | CysasnGluProLeuThrThrThrAsnasnValasnLysMetLeuLeuIleAspTyrLys   | Qy<br>Dp          | 456 LysLysIleargValAspGlyProArgGlyAsnalaLeuGlnTyrGluThrValGlnVal 475                     |
| Qy                     | 124 GluasnargLeullealaCysGlySerLeuTyrGlnGlyIleCysLysLeuLeuargLeu 143<br>   | Qy<br>Dp          | 476 ValaspProGlyProValLeuArgaspMetAlaPheSerLysAspHisGluGlnLeuTyr 495                     |
| Oy<br>D                | GluAspLeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeuSer AGAACATCTCCTCGCCTGTTCTTTTTTTTTTTTTTTTTT                         | δ dα              | 496 IleMetSerGluArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSer 515                     |
| oy<br>D                | GlyValAsnGluSerGlySerValPheGlyVallleValSerTyrSerAsnLeuAspAsp  ::   | oy da             | 516 CysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsnThr 535<br>    :::          |
| 7                      | LysLeuPhelleAlaThrAlaValAspGlyLysProGluTyrPheProThrIleSerSer<br>::::::::::::::::::::::::::::::::::::                   | oy<br>Db          | 536 CysThrArgLysGluArgCysGluArgSerLysGluProArgArgPheAlaSerGlu 554                        |
| Qy<br>Db               |  | ζζ<br>Dp          | 555 MetLysGlnCysValArgLeuThrValHisProAsnAsnIleSerValSerGln 572                           |
| oy<br>Oy               | PheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAsp<br>TACAAGGCGGCTACCTGTCCACCAACACACAGAGTTC                  | Qy<br>Dp          | 573 TyrAsnValLeuLeuValLeuGluThrTyrAsnValProGluLeuSerAlaGly 590                           |
| Qy                     | TyrPheLeuThrLeuGlnPro<br>:::   :::<br>TTCTTTGACCAGCAG  | λ<br>O            | 591 ValasnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIle 610 :::                 |
| Oy de                  | GluMetValSerProProGlySerThrThrLysGluGlnValTyrThrSerLysLeuVal   | S G               | 611 GlnCysTyrSerProAlaAlaLysGluValProArglleIleThrGluAsnGlyAsp 629                        |
| 3 6 8                  | ArgLeuCysLysGluÅspThrAlaPheAsnSerTyrValGluValProIleGlyCysGlu<br>   :::   :::   :::                                     | Qy                | 630 HisHisValValGlnLeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThr 649<br>                 |
| 3 6 2                  | ArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAlaVal   | % qa              | 650 SerPheValPheTyrAsnCysSerValHisAsnSer   |
| Oy<br>Oy               | B12 GACCCCGACATCCACGCCGCTGCCTTTGGCACCTGC 847<br>322 LeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPheSerLys 341   | oy .              | 664 SerCysValGluSerProTyrArgCysHisTrpCysLysTyrArgHisValCysThrHis 683                     |

| AGTGCCGGGAG 1954   |  | 700   |  |  | yrGluCysIle 740 Di   | 758   | <br> TCATGGAGCCG 2146 | o vsnAsn 776  | 2206  | Asn 793 |                                       | 2311                  | 831  | 2371   | ceuSerGlyAla 851 .   | AACACC 2398           | 871  |   | ArgAspileala 891<br>       <br>3GGGACATC 2515                    | TyrileProAla 911                                 | I     ::: I | 3lyPheValGlu 931   |   | Ser 946<br>CCTCCCAATGTC 2674   | ArgGlyProMet 966                                 | CAGGGACCGCAG 2731  | SerAsnValVal 986   | rccaggaggac 2791                             | TyrIleValCys 1006  | GGCGTCCCGTGT 2821           |
|--|--|---|--|--|--|---|-----------------------|---|---|---------|---------------------------------------|-----------------------|--|--|--|-----------------------|--|---|--|--|-------------|--|---|--------------------------------|--|--|--|--|--|-----------------------------|
| A PARTICIO P | ICC I GCG ; GAGCAACCGC I GGACC I GCCAG I GGGACC I GCGC I ACCAC | AspProLysThrCysSerPheGlnGluGlyArgValLysLeuProGluAsp | CysproGlnLeuLeuArgValAspLysIleLeuValProValGluValIleLysProIle | IGTCCCCAGTTCCTGGGACCCAGCCCCTGGTGATCCCCATGAACCAC( | ThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyGlnArgGlyTyrGluCysIl :: | LeuAsnileGinGlySerGluGinArqValProAlaLeuArgF | SACTT                 | SerValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIleAsnAsn- | GTGACCATGCAGGAATCTGGGACCTTCGCCTTTCGGACCCCAAAGCTGTCCCAACGATGCC |         | AACGAGGTGCCCCTGCACCTCTAAGTCTTACGGCAAG | PIOAIAGIAASHUASYAIHIS | GlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGlnGlyProGlyGln | <br>  AGCTGTGCCGGCCCCTAACCCCGACTACAGGTGTGCGTGC | CysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGluLeuSerGlyAla | TGCGTGTATGAGGCCCTGTGC | LysSerLysCysThrAsnProArgileThrGlulleIleProValThrGlyProArgGlu | ACCTCCGAGTGCCCGCCGCCGTCATCACCAGGATCCAGCCTGAGACGGGCCCCTTGGGT | GlyGlyThrLysValThrIleArgGlyGluAsnLeuGlyLeuGluPheArgAspIleAl.<br> | SerHisValLysValAlaGlyValGluCysSerProLeuValAspGly | :::         | GludinileValCysGluMetGlyGluAlaLysProSerGlnHisAlaGlyPheValGlu | ACCCGGAICGIGIGIGAICGAGGCIGCGGAGACGCCIIICACG | IleCysValAlaValCysArgProGluBhe | GlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSer | <br>  cagitcaccitccaacagcccaagccitcagigiggagccgcagcagcgaccgcag | SerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAlaGlySerAsnValVal | GCGGCGGCACCACTGACCATCCACGCCACCCACTGGACACGGGC | ValMetPheGlyLysGlnProCysLeuPheHisArgArgSerProSerTyrIleValCys | GTGCGGGTGACCCTCAACGGCGTCTGT |
| r,   | n  | 684 -   | 01   |  | 721 7  |   |                       | 759   | 2147  |         |                                       | 2261                  | 812 (  | 2312   | 832 (  | 2372                  |  |   | 872 (  |  | 2516        | 912  | .0  | 932                            |  | 2675   | 196  | 2732   | 987  | 2792                        |
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| Qy   | 1075 | sHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMet 109       | 94  |
| qq   | 3059 |   | 94  |
| Qy   | 1095 |   | 10  |
| . qa | 3095 | GCGGGAGGCTGAATCCCTGCAGCCCATGACGGTGGTGGTGCTACAGACTACGTGTTCCAC 315  | 4   |
| Οy   | 1108 | GInSerAspLeuThrGluArgProGluGluPheGly 1119                         | 19  |
| Db   | 3155 | SGTCGTCTTCCTGTCCCCGGCTGTGCCTGAGGAGCCAGAGGCCTACAAC 321             | 14  |
| Qy   | 1120 | -LeuAspAsnValGlnSerLeuLeulleLeuAsnLysThrAsn 113                   | 35  |
| Db   | 3215 | 327   | 74  |
| Qy   | 1136 | ProSerGlyIleLeuGluLeu 115   | 55  |
| Db   | 3275 | GTGCCTGACCCCACCTTTGAGAACTTC331                                    | 1.0 |
| QY   | 1156 | SProGlyThrProllelleLeuLySGlyLySasnLeulleProProValAlaGlyGly 117    | 7.5 |
| Db   | 3311 | SCACC 336   | 61  |
| QY   | 1176 | AsnValLysLeuAsnTyrThrValLeuValGlyGluLysProCys 1190                | 06  |
| Db   | 3362 | C 342   | 21  |
| ΟŸ   | 1191 | ThrValThrValSerAspValGInLeuLeuCysGluSerProAsnLeuIleGlyArg 1200    | 60  |
| Dp   | 3422 | AGACGCTGACGGAGACCGACCTGTACTGTGAGCCCCCGGAGGTGCAGCCCCCG 348         | 81  |
| QY   | 1210 | 121   | 16  |
| QQ   | 3482 | CGGCGGCAGAAACGAGACACACACACAAACCTGCCCGAGTTCATTGTGAAGTTC 354        | 4   |
| Οy   | 1217 | AlaProAspSerPro 123   | 3   |
| QQ   | 3542 | cgacacacggggagcgacgrgccg 360                                      |     |
| Qy   | 1234 | ly 124  | 46  |
| pp   | 3602 | 365   | 28  |
| QY   | 1247 | PhelleValAlaValLeulleAlaTyrLysArgLysSerArgGlu 126                 | 99  |
| Db   | 3659 | GTCTACTGCTACTGGAGGAGGCCAGCAG 368                                  | 88  |
| Qy   | 1267 | raspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeuGluSerArgValAla 128    |     |
| qa   | 3689 | 374   | 48  |
| Qy   | 1287 | LeuGluCysLysGluAlaPheAlaGluLeuGlnThrAspIleHisGluLeuThrSerAsp 1300 | 0   |
| qq   | 3749 | 380   |     |
| QY   | 1307 | 32  | 7   |
| qa   | 3809 | GTGCACGAGGCGGCATCCCCGTGCTGGACTACAAGACCTACACGGACCGCGTCTTCTTC 386   |     |

| 4868 ATCTACCTGACGCTCTCAGGCGCACACTGCAGCAGTTTGTCGACAACTTC 492 1696 PheGluThrIlePheSerThrAlaHisargGlySerAlaLeuProLeuAlaIleLySTyr 171 1696 PheGluThrIlePheSerThrAlaHisargGlySerAlaLeuProLeuAlaIleLySTyr 171 1716 MetPheAspPheLeuAspGluGlnAlaAspLySHisGlyIleHisAspProHisValArg 173 1716 MetPheAspPheLeuAspGluGlnAlaAspLySHisGlyIleHisAspProHisValArg 173 1716 MetPheAspPheLeuAspGluGlnAlaAspLySHisGlyIleHisAspProHisValArg 173 1736 HisTrTrpLySerAsnCysLeuProLeuArgPheTrpValAsnMetIleLySAsnPro 175 1736 HisTrTrpLySerAsnCysLeuProLeuArgPheTrpValAsnMetIleLySAsnPro 175 1736 GlnPheValPheAspPleCaGCCTCCGGTTCTGGGTGAACATCCTCAAGAACCC 509 1756 GlnPheValPheAspIleHisLySAsnSerIleThrAspAlaCysLeuSerValValAla 177 1716 Hilliliiii ::: | 5099<br>1776<br>5159<br>1796<br>5219<br>1816<br>5279 | 1836 GInSerArgMetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSer 1855  | RESULT 6 AASO0020 standard; cDNA; 6252 BP.  XX AC AASO0020; XX XX XX XX XX  Human cDNA encoding Plexin-B2.  XX XX XX XX XX XX XX XX XX XX XX XX X |   |
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The sequence encodes Human Plexin-B2. Plexins are large transmembrane proteins whose extracellular domain shares homology with Scatter factor receptors and contain an approximately 500 amino acid Semaphorin Gomain. The plexin polynuclectides and polypeptides, and plexin-specific binding agents are useful in diagnosis, therapy and in the biopharmaceutical industry. In particular, the plexin polynuclectides and polypeptides are useful for generating compounds (e.g. plexin-specific binding agents or antibodies) for treating or diagnosing a disease or disorder involving aberrant cell growth (e.g. hyperplasia, neoplasia, cancer or neurodegenerative disease), or diseases or disorders involving aberrant bowel disease or Diabetes Type I), or immunosuppressive diseases such as lupus, inflammatory bowel disease or Diabetes Type I), or immunosuppressive diseases such as multiple sclerosis or rheumatoid arthritis.
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AGCAACATCTCCCTCCGCCTGTTCTACGAGGACGGCAGCGGGGAGAAGTCTTTCGTGGCC
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| 116   CystilythicystoriclySkrOlyAspProHistyRellyTricysvalleuHistaenthr 535  |   | 852 LysSerLysCysThrAsnProArgIleThrGluIleIleProValThrGlyProArgGlu 871<br>   ::: | 872 GlyGlyThrLysValThrILeArgGlyGluAsnLeuGlyLeuGluPheArgAspIleAla 891 | 892 SerHisValLysValAlaGlyValGluCysSerProLeuValAspGlyTyrIleProAla 911 ::: | 912 GluGlnIleValCysGluMetGlyGluAlaLysProSerGlnHisAlaGlyPheValGlu 931 ::: | 932 IlecysvalalavalCysArgProGluPheMetAlaArgSerSer 946 :::            | 947 GlnLeuTyrTyrPheMetThrLeuThrLeuSeraspLeuLysProSerargGlyProMet 966 | 967 SerdiyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAladiySerAsnValVal 986 :::   | 987 ValMetPheGlyLysGlnProCysLeuPheHisArgArgSerProSerTyrIleValCys 1006   11 | 1007 ASNThrThrSerSerAspGluValLeuGluMetLysValSerValGhnValAspArgAla 1026<br> | 1027 Lysile  | 1035 GlnTyrValGluAspProThr1leValArgIleGluProGluTrpSerIleValSerGly 1054 | 1055 AsnThrProlleAlaValTrpGlyThrHisLeuaspLeulleGlnAsnProGlnIleArg 1074 | 1075 AlaLysHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMet 1094 :::             :: :: 3059GTGGTCATCGCGGAGCCCTGCAGTCCTGGCAGCCG 3094 | 1095 ThrCysGlnAla  | 1108    | 1120 PheIleLeuAspAsnValGlnSerLeuLeuIleLeuAsnLysThrAsn 1135 :::    ::::                          | 1136 PheThrTyrTyrProAsnProValPheGlualaPheGlyProSerGlyIleLeuGluLeu 1155<br> | 1156 LysProGlyThrProIleIleLeuLysGlyLysAsnLeuIleProProValAlaGlyGly 1175 | 1176 AsnValLysLeuAsnTyrThrValLeuValGlyGluLysProCys 1190 |
|---|---|--|--|--|--|--|--|--|--|--|--|--|--|---|--|---------|---|--|--|---|
| 516 CysGlyGluCysLeudlySerGlyAspProHisOysGlyTrpCysValleuHisAsmfhr  1433 TGCACCCAGTGCCCCACACCCAGACACCTATCGGTGGTGGTGGTGGTGGTGGGGGGGG | _ | yo<br>da   | QV<br>Db   | do<br>Oy   | Oy<br>Db   | . da   | da<br>-  | QQ Dbd   | QQ<br>Dp   | δδ<br>   | VO Db  | da<br>da   | QQ Dp  | da<br>da  |  | qa<br>— | Q   | da Db  | do do  | <br>  oy  |
|   |   | 516 CysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsnThr               | 536 CysthrArgLysGluArgCysGluArgSerLysGluProArgArgPheAlaSerGlu        | 555 MetLysGlnCysValArgLeuThr ValHisProAsnAsnIleSer ValSerGln             | 573 TyrAsnValLeuLeuValLeuGluThrTyrAsnValProGluLeuSerAlaGly               | 591 ValAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIle ::: | 611 GlnCysTyrSerProAlaAlaLysGluValProArglleIleThrGluAsnGlyAsp        | 630 HisHisValValGlnLeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThr   11   1775 CAGGTGGCGGTGACCACTCCTTAGACGAGGAAATCTTCCTCAGGTCA | 650 SerPheValPheTyrAsnCysSerValHisAsnSerCysLeu                             | 664 SerCysValGluSerProTyrArgCysHisTrpCysLysTyrArgHisValCysThrHis 1111111   | 684AspProLysThrCysSerPhedInGluclyArgValLysLeuProGluAsp   1   .::::1    .::::::1    .:::::::::: | 701 CysproGinLeuLeuArgValAspLysIleLeuValProValGluValIleLysProIle       | 721 ThrLeubysAlatysAsnLeubroGlnScrGlyGlnArgGlyTyrGluCysIle :::         | 741 LeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArgPheAsnSerSer 758  | 759 SerValGinCysGinAsnThrSerTyrGiuGlyMetGluIleAsnAsn 7147 GTGACCAGGAAGTGGAACTTTTGGACCAGGAAGTGGAAAGTGGAAATTTGGACGAAGTGGAAGTGGAAATTTGGAAGTGAAGAA | 777     | 794 ProalaginasniysValHisLeuTyrLysCysGlyalaMetargGluSerCys::::!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!! | ### ##################################                                     | 832 CysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGluLeuSerGlyAla       | 2372 TGGGTGTATGAGGCCCTGTGCAACACC                        |

snalaryrLeualaglu 1835 || :::!||||||||| |ACACACACTGGCAGAG 5338 isAspAspGlnCysGly 1875 AGGATCCTGCCGCCCAG 5458 snMetIleLysAsnPro 1755 ||::::::||||||||||| |ACATCCTCAGAACCCC 5098 ysLeuSerValvalAla 1775 ||||||||||||::|||| |CGCTGTCAGTCATCGCG 5158 rpValGluArgTyrTyr 1815 ||||||| |TGGTGGAGGATTACTAC 5278 euSerGluIlePheSer 1855 TCCACCAGCTCTACCAA 5398 ysPheValaspAspLeu 1695 ::||||||||||| AGTTTGTGGACAACTTC 4927 roLeualaileLysTyr 1715 || || || :::|||||| |CaccrGcaGTCaaGTAC 4978 isAspProHisValArg 1735 --LysMetValSerGlu 1675 ||| :::::||| CGAAGGCCATCACCGAG 4867 AGGATGAAGACACCATC 5038 teLysAsnValProCys 1542 :::: CCGTGGGCAGCCCTGC 4522 spTrpLysArgLeuAsn 1582 |||||||||||:::||| gGTGGAAGCGCGTCAAC 4639 snHisGluHisGlyAsp 1662 InGlySerGlyAlaArg 1562 |||||||| |GGCTCCACGCGCAG 4582 GGAGGACAGCCAGCAG 4726 gThrProMetileThr 1642 TGAAGGTCCTCAACTGT 4462 uValSerLysGlnVal 1602 G----- 4684 rAlaSerLysTyrGlu 1622 ----- 4753

Horrigan

Endress G,

Ebner R,

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326 AGGAAGCGCCTGGTGGAGTGCGGCACCTCTTCAAGGGCATCTGCGCTCTGCGCCCCTG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyValAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAspAsp 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 Gluasp-----LeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeuSer 161
                                                                                                                                                     The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene [1] of a signature gene set, where [1] comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL7010), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the
                                                                                                                                                                                                                                                                                                                              treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophagaal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysValLeuValThr 83
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TGCCATGAG---GCTGAGATGACTGACAATGTCAACCAGCTGCTGCTGCTCGACCCTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 GluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 AGCAACATCTCCCTCCGCCTGTTCTACGAGGACGCGGGGGGAGAAGTCTTTCGTGGCC
                                                                    Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6252 BP; 1255 A; 2022 C; 1915 G; 1060 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                           carcinoma, papillary carcinoma and Wilm's tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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                Weaver Z;
                                        WPI; 2002-188264/24.
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Best Local Similarity:
Query Match:
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Young PE, ,
Sopper DR,
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                                                                                                                                                                                                              Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                   Thyroid cancer related gene sequence SEQ ID NO:5616
             LysGlnLysLeuAlaTyrLysLeuGluGlnVal 1886
                            5459 AAGATGCAGCTTCCGCCTGCAGCAGATT 5491
                                                                                              ABL67279 standard; DNA; 6252
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| Qy       | 182 I | LysLeuPhelleAlaThrAlaValAspGlyLysProGluTyrPheProThrIleSerSer 201                     |
|----------|-------|--|
| Db       | 206   | GCGTGCTGTTTGTGGGCAAAGGCAATGGGCCACACGACAACGCCATCATCGTGAGCACT 565                      |
| ογ<br>γ  | 202 p | ArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGlu 221                     |
| à ô      |       | 24   |
| op<br>Op |       | TACAAGGCCGCTACCTGTCCACCACACACACAGAGTTC   |
| Qy       | 242   | IleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnPro 261                     |
| qq       | - 699 | GIGGGGGCCTTCGAGGACGGCCCCTACGTCTTTGTCTTCAACCAGCAG 715                                 |
| Qy       | 262 0 | LysG   |
| qq       | 716   | GACAAG CACCCGGCCCGGAACCGCACG   |
| Qy       | 7     | SerTyrValGluValProlleGlyCysGlu 30  |
| DP       | 752 ( | 8 81   |
| Qy       | 302 / | co   |
| qa       | 812 ( | SACCCCGACATCCAC  |
| Qy       | 322 1 | LeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPheSerLys 341                     |
| QQ       | 848 ( | creecceccrecreerecreecreecreereses   |
| Qy       | 342 ( | GlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLys 361                     |
| Db       | 908   | GACAGCGGAGCAGTGGGGGGCCCGGTGCGGCCTCTGTTCCCGCTGGAC 961                                 |
| Οy       | 362 ( | GlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThrLeu 381                     |
| qa       | 962   | AAGGIGCACGCCAAGAIGGAGGCCAACGCCAACGCCIGITACACAGGCACCCGG 1015                          |
| Qγ       | 382   | AspLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaLeu 397                                 |
| Db       | 1016  | SAGCCCGTGACATCTTCTACAAGCCCTTCCACGCGATATCCAGTGCGGCGGCCACGCG 1075                      |
| ٥y       | 398   | LeuThrIleAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyVal 415                           |
| qq       | 1076  | CCGGGCTCCAGCAAGAGCTTCCCATGTGGCTCGGAGCACCTGCCCTACCGGTGGGCAGC 1135                     |
| 0y       | 416   |  |
| QQ       | 1136  | ceccacegectcaeaegcacaecetectecaecetegaegeccteaaectcaeggecete 1195                    |
| Qy       | 436   | IlealaTyrValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeu 455                     |
| QQ       | 1196  | ACGGTCGCCGCGAGAACAACCACACTGTTGCTTTTTTTGGGCACCTCTGATGGCCGGATC 1255                    |
| Qy       | 456   | LysLysIleArgValAspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnVal 475                     |
| qa       | 1256  | CTCAAGGTGTACCTCACCCCAGATGGCACCTCCTCAGAGTACGACTCTATGTG 1312                           |
| Qy       | 476   | ValaspproGlyproValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyr 495                     |
| qa       | 1313  | GAGATAÀACAAGAGAGTCAAGGGGGGCGACCTGGTACTGTCTGGAGACCTGGGCAGCCTGTAC 1372                 |
| Οy       | 496   | IleMetSerGluArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSer 515                     |
| Dp       | 1373  | GCCATGACCCAGGACAAGGTGTTCCGGCTGCCGGTGCAGGAGTGCCTGAGCTACCCGACC 1432                    |
| Qy       | 516   | CysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsnThr 535                     |
| QQ       | 1433  | TecacccasTecescarcccassaccccTacTecescTecescGTesTesTesTesTesTesTesTesTesTesTesTesTesT |
| Qy       | 536   | CysThrargLysGluargCysGluargSerLysGluProArgArgPheAlaSerGlu 554                        |

| Db   |                                |   |
|------|--------------------------------|---|
| Qy   | 5 MetLysGlnC                   | HisProAsnAsnIleSerValS                                |
| Db   | -5                             | CGTCACCGCCCAGCCCAGAACATGAGCCGGCGGGCCCAG 1             |
| Qy   | 573 TyrAsnValLe                | TyrAsnValProGluLeuSerAlaGly 59                        |
| Db   | 1613 GGGGAGGTGCA               | GGGGAGGTGCAGCTGAGCCGTCAGCCCCCTCCCTGCCCTG              |
| Qy   | 91 Va                          | GlumetAspGlyLeuValValGlyAsnGlnIle 610                 |
| Db   | 1667 TIGCIGIGCT                | c 17  |
| δō : | 11 GlnCysTyr                   | SerProAlaAlaLysGluValProArgIleIleThrGluAsnGlyAsp 629  |
| QQ   | 27 ATCTGCAAC                   | CCCGICACACCCCAGGCCAGGAC I//                           |
| ολ   | 30 HisHisVal                   | SerLysGluThrGlyMetThrPheAlaSerThr 64<br>:::           |
| qq   | 5 CACGTGGCC                    | ACCATCCAGCTCCTCTTAGACGAGGCAACATCTTCCTCACGTCCTAC 18    |
| Qy   | 0 SerPhevalPh                  | ######################################                |
| qu · | ACCCCTT                        | TACGACTGCCGCCAGGCCATGAGCCTGGAGAAACCTGCCGTGCATC 18     |
| Qy   | 664 SerCysValG1                | SerProTyrArgCysHisTrpCysLysTyrArgHisValCysThrHis 6    |
| QQ   | CCTGCGTGAG                     | CAACCGCTGGACCTGCCAGTGGGACCTGCGCTACCACGAGTGCCGGGAG 13  |
| δλ   | 684AspProLys <sup>1</sup>      | hrCys   |
| qa   | 55 GCTTCGCCCAA                 | ctGaggacggcarccrccrgcccacarggagg                      |
| Qy   | 701 CysProGlnLeuI              | euArgValAs  |
| QQ   | 06 TGTCCCCA                    | TGGGACCCAGCCCCTGGTGATCCCCATGAACCACGAGACAGATGT         |
| QY   | vo -                           | aLysAsnLeuProGlnProGlnSerGlyGlnArgGlyTyrGluCysI       |
| qq   | ACTTCCAG                       | CAAGAACCTGGAC   |
| Qy   | AsnIleG                        | InArgValProAla  |
| Dp   | :522                           | crccrgcacgrggcagrgacrrgcrcaagrrcarggagc               |
| Qy   | rValG]                         | erTyrSerTyrGluG                                       |
| qq   | GACCAT                         | TGGGACCTTCGCCTTTCGGACCCCAAAGCTGTCCCA                  |
| Qy   | 777E                           | eAsnIleAspAs  |
| qq   | ~                              | GCACCTCTACGTCAAGTCTTACGGCAAGAATATCGAC 2               |
| Qy   |                                | HisLeuTyrLysCysGlyAlaMetArgGluSerCys 81               |
| qq   | 19                             | GCAGCGACTGC 23  |
| Qy   | 812 GlyLeuCysLe                | lyProGly  |
| Db   | 2312 AGCCTGTGCC                | GCCAGAGCAG  |
|      | 832 CysThrLeuAr                | euSerGly  |
| QO   | 72                             | AACAGC 23   |
| QY   | 852 LysSerLysCy                | 1yP   |
| da"  | σ                              | SCCCTGGGT 24  |
| Qy   | 872 GlyGlyThrLy:<br>        :: | svalThrIleArgGlyGluAsnLeuGlyLeuGluPheArgAspIleAla 891 |

|  | 3        |   | 40             | 1010  |
|--|----------|---|----------------|---|
| 110 CARAGGACTCTCTGTGGCCCCAACTCCTTTTCAGCCGGACCTTAATCCGTCCTCC 2575  111 CAGAGGACTCC  | Qy       | SerHisValLysValAlaGlyValGluCysSerProLeuValAspGlyTyrIleProAla  | Š i            |   |
| 11   Cluckin   Linker   Cluckin   Linker   Lin | qa       | CAGAGGATCTCTGTGGCCGGCCGGAACTCCTTTCAGCCGGAACGTTACTCGTGTCC 257  | an (           |   |
| 2976 ACCCGGATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG  | Qy       | GluGlnIleValCysGluMetGlyGluAlaLysProSerGlnHisAlaGlyPheValGlu  | Vo             | 1217 GLYGLYMetGluTyrSerProGL<br>  |
| 932 III-CysytalAlavalCysArgProGluphe   | Db       | ACCCGGATCGTGTGTGTGTCGAGGCTGCGGAGACGCCTTTCACGGGGGGTGTCGAG  | gg (           |   |
| 2533 GTGGAGCGTC  | Qy       | lleCysValAlaValCysArgProGluPheMetAlaArgSerSer   | Å å            | 1234 LeuSerLeu  |
| 947 GLIG-UTYFTYPPRACTATIONS TO THE THE THE THE THE THE THE THE THE THE   | Dp       | GTGGACGTCTTCGGGAAACTGGCCGTTCGCCTCCCAATGTC   | 20 20          |   |
| 2675 CAGTYCACCTTCCAAACCCCTAACCTTCAGT GTGGAGCCCCAGCAGCGACCCCC 2731  2772 GCGCCGCGCCACCTAACCTACCTTCAGT GTGGAGCCCCAGCAGCACCCCC 2791  2773 GCGCGCGCCACCACACTAACTACTACTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGT   | Qy       | GlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSerArgGlyProMet  | δο δ           | 124/ GlyLeuLeuIleIlePhelleVa  |
| 967 SerCigityThricityCharithristonical and year savalval 986 2722 GCGGGCGGCACCACACTGACCACTGACACCGGACCCC791 967 ValMetPheGlyLySGlaProcysteuPheHisharcharGacCCCTCCCGTGT 2821 97 ValMetPheGlyLySGlaProcysteuPheHisharcharGacCCCTCCGTGT 2821 97 ValMetPheGlyLySGlaProcysteuPheHisharcharGacCCCTCCGTGT 2821 97 ValMetPheGlyLySGlaProcysteuPheHisharcharGacCCCTCCGTGT 2821 97 ValMetPheGlyLySGlaProcysteuPheHisharcharGacCCCTCGTGT 2821 97 ValMetPheGlyLySGlaProcysteuPheHisharcharGacCCCTCGTGT 2821 97 ValMetPheGlyLySGlaProcysteuPheHisharcharGacCCCTCTCGTGT 2821 97 ValMetPheGlyLySGlaProcysteuPheHisharcharGacCCCTAGCGCGCCTCCGTGT 2821 97 ValMetPheGlyLyBGlaProcharGacCCCTAGCGCGCCTCCGTGT 2821 97 ValMetPheGlyLyBGlaProcharGacCCTCAGCCCCAGCGCGCCTTCTCTGT 2821 97 ValMetPheGlyLyBGlaProcharGacCCCTCAGCCCCCAGCGCGCCTTCTCTGT 2821 97 ValMetPheGlyLyBGlaProcharGacCCCTCAGCCCCCAGCGCCCTTCTCTGT 2821 97 ValMetPheGlyLyBGlaProcharGacCCTCAGCCCCCAGCGCCCTCCAGCGCCCTTCTCTGT 2821 97 ValMetPheGlyClyLyBGlaProcharGacCCTCAGCCCCCCCAGCGCCCCTCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCCAGCCCCAGCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCC  | Db       | CAGITCACCITCCAACAGCCCAAGCCICTCAGIGIGGAGCCGCAGCAGGGACCGCAG   | 3 6            |   |
| 2732 GCGGGGGGGCGCACCACACACACACACACACACACACAC   | Qy       | SerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAlaGlySerAsnValVal  | δō             | 126/ SerAspLeuThrLeuLysArgLeu   |
| 967 ValMetPheGlyLysGlnProCysteuPheHisArgArgSerProSerTyTileValCys 1006  2792 GTG  1007 AsmThrThYSerSerAspGluValLeuGluMetLysValSerPatGlnValAspArgAla 1025  2822 AAAGTGACGAAGTTTGGGGCGCGGCTCCCCGGCGCCCCCGGCGCCCCCGGCCCCCGGCCCCCGGCCCC   | qq       | GCGGCGCCACACTGACCACGCCACCCACCGCCTGGACACGGCCTCCCAGGAGGAC   | qa             |   |
| 2792 GTG  1007 ABRITHTHESETSETASPGLUVALLEUGLUMELLYSVALSETVALGINVALASPATGALA 1026  2822 AAAGTGAAGAGTTTGGGGGGGAGTTCCTAAGGGGGTCCCCTAGGGGGGCCAAGGGGG 2881  1027 Upg118   | Qy       | ValMetPheGlyLysGlnProCysLeuPheHisArgArgSerProSerTyrlleValCys  | λŏ<br>·        | 1287 LeuGluCysLysGluAlaPheAla<br>       ::                                |
| 1007 AsmThrThrSerSerAspCluValLeuGluWetLysValSerValClnValAspArgala 1026   | Db.      |   | QQ             | 3749 GACCGCTGCAAGAAGGAATTC  |
| 2822 AAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | Oy.      |   |                | 1307 LeuAspGlyAlaGlyIleProPho:::  |
| 1027 Lysile  | QQ       |   | qq             | 3809 GIGCACGAGGCCGGCATCCCC  |
| 2882 CAGATGCTTCTGGAGGTCTCCTACGGGGGGTCCCCGGTCCCCAACCCGGCATCTTTTC 2941  1035 GINTYTAIGLUASPPTOTHTIEVALATICGUAPCGUTTPSETILEVAISECTIC 1054  1035 GINTYTAIGLUASPPTOTHTIEVALATICGUAPCGUTTPSETILEVAISECTIC 1054  1055 ASHThPTOTICALAVATTCCGTACCCGTCCCCCGCGCTCCTACCAACCTTCCCATGCTTTTC 2941  1055 ASHTHPTOTICALAVATTCCTTACCCGTACCCCCCTACCAACCTTTCCCATGCTTTTCCTTTTC 1074  1056 ASHTHPTOTICALAVATTCCTTACCGTCACCCCTTACCCATGCTTTTCCTTTTCTTTTCTTTTTTTT   | <b>^</b> |   | δλ             | 1327ProGlyI.leGl  |
| 1035 GINTYPYVAIGHANSPPETTHILEVAIANTGHIGGUAPPOGUTTPSETTIEVAISEGES   1034   1035 GINTYPYVAIGHANSPPETTHILEVAIANTGHIGGUAPPOGUTTPSETTIEVAISEGES   1034   1034   1034   1034   1034   1035   1035   1035   1035   1036   | ; 음      | CAGATACTURAGE GATCHTCHTCHTCHTCHTCHTCHTCHTCHTCHTCHTCHTCHT  | qa             | 3869 CTGCCCTCCAAGGACGGCGACAA  |
| 2942 ACCTACCGGGAAACCCGTACTGGGCCCTACGAGGCTTTGCCGTGTGT 3001 1055 ASITHTPTOILEALING THE SEQUENCE CAGGCGCTACGAGGCTTTGCCGTGT 3001 1055 ASITHTPTOILEALING THE SEQUENCE CAGGCGCTACGAGGCTTTGCCGTGT 3001 1055 ASITHTPTOILEALING THE SEQUENCE CAGGCGTTGCCATGCTTGCCATGT 3001 1056 ASITHTPTOILEALING THE SEQUENCE CAGGCGTTGCCATGCTTGCCATGCTTGCCATGCTTGCCATGCTTGCCATGCTTGCCATGCTTGCCATGCTTGCCATGCTTGCCATGCTTGCT   | ò        | GInTvrValGluAcaptroThrIleValArdIleGluDroGluTrrcerIleValScarGlv  | Qy             | 1343 TyrArgGlnGluArgValGluLy  |
| 1055 ASDITHTPOILEALAVAITTPGILYTHTHISLEUASPLEUTIEGINASPPOGUITIEATG   1074   1075   1075   1074   1075   10 | ; 셤      | 2942 ACCTACCGCGAAACCCCGTACTACGAGCCGTTCGAGCGCTACGAAGCTTTGCAGCGTTACTAGCGTTTGCAAGCCGTTTGCAAGCGCTTTGCAAGCGTTTGCAAGCGTTTGCAAGCGGTTTGCAAGCGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGTTTGCAAGCGTTTGCAAGCGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGGTTTGCAAGCGTTTTGAAGCGTTTTGAAGCGTTTGAAGCGTTTTGAAGCGTTTTGAAGCGTTTTGAAGCGTTTTGAAGCGTTTTGAAGCGTTTTGAAGCGTTTTGAAGCGTTTTGAAGCGTTTTTGAAGCGTTTTTTTT | qa             | 3529 CCGCGGCGGCCGGTGGTGGAGCA  |
| 3002 GGCCGCAGCATCACGTCAGCCTACAGCTTCACCAGGCTTTCCATG 3058  1075 AlaLysHisGlyLyLySGluHisTleAsnIleDevanAlaThrCluwet 1094  1075 AlaLysHisGlyLyLySGluHisTleAsnIleDevanAlaThrCluwet 1094  1075 AlaLySHisGlyLyLySGluHisTleAsnIleCySGluValLeuAsnAlaThrCluwet 1094  1076 Size ThrCySGluAla   | δy       | 1055 AsnThrProlleAlaValTrpGlyThrHisLeuAspLeuIleGlnAsnProGln1leArq 1074  | ٥y             | 1363 ValPheLeuLeuSerPhelleAr  |
| 1075 AlaLysHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMet  | Ob       |   | qa             | . 3989 TCTTTCCTCATCAATTTCATC  |
| 3059   | δy       | 1075 AlaLysHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMet 1094  | ΟŊ             | 1383 ArgGlyAsnValAlaSerLeuIl  |
| 1095 ThrCysGlnAla  | qa       | :::             ::: ::: ::: ::: ::: :::   | qa             | 4049 AAGGTCTACTTCGCGTCCCTGCT  |
|  | ογ       | ThrCysGlnAlaProAlaLeuAlaLeuGlyProAspHis   | . ХО           | 1403 AspValLeuLysGlnLeuLeuAla   |
| 108  | Db       | :::   | qa             | 4109 GACATCATGCACACGCTCTT   |
| 1150   | ογ       |   | δλ             | 1423 ProLysLeuLeuLeuArgArgTh:   |
| 120 Phelle   | QQ       |   | qa             | 4166 CCCAAGCTGATGCTGCGCAGG  |
| 3215 CTCACGGTGCTGATCGAGACGGCCACGTGCCTGCTGAACAGAGGCCGGGCC 3274  1136 PherhrytyryrProAsnProValPhedluAlaPhedlyProSerGlyIleLeuGluLeu 1155  111   | Qy       | PhelleLeuAspAsnValGlnSerLeuLeulleLeuAsnLysThrAsn 113  | ολ             | 1443 ThrPheLeuLeuTyrLysPheLeu   |
| 1136 PherhrtyrtyrProAsnProValPheGluAlaPheGlyProSerGlyIleLeuGluLeu 1155   | qq       | :::    :::    :::    :::     ::::::   | අ <sub>ධ</sub> | 4226 ICCATCTGCCTGTACCAGTAC  |
|  | δy       | PheThrTyrTyrProAsnProValPheGluAlaPheGlyProSerGlyIleLeuGluLeu 115  | Ολ             | 1463 CysAlaIleLysGlnGlnMetGlu   |
| 1156 LysProGlyThrProllelleLeuLysGlyLysAsnieulleProProValAlaGlyGly 1175   | QQ       | ::  | qa             | 4286 AAGGCCATCAAACATCAGGTGGA  |
| 3311ACAGGTGGCGTCAAGAAGCAGGTCATCCACCCCGGGGCACC 3361 07 1176 AsnValLysLeuAsnTyrThrValLeuValGlyGluLysProCys 1190 07 1116 AsnValLysLeuAsnTyrThrVal   | οy       | LysProGlyThrProllelleLeuLysGlyLysAsniceulleProProValAlaGlyGly 117   | δλ d           | 1483 TyrSerLeuSerGluAspLysLer   |
| .1176 AsnValLysLeuAsnTyrThrValLeuValGlyGluLysProCys 1190 OY  | ДQ       | ACAGGTGGCGTCAAGAAGCAGGTCAACAAGCTCATCCACGCCCGGGGCACC   | 3 6            |   |
| 5552 MAILTOAMLANGGCGATGALGAGGAGGCCCGAGGCCTTCGTGGGTGCCGAGCGCTGC 3421 1191 ThrValThrValSerAspValGInLeuLeuCysGluSerProAsnLeuIleGlyArg 1209 0y   | oy<br>G  | AsnValLysLeuAsnTyrThrValLeuValGlyGluLysProCys   | à qa           | 1503 SercysvalserProAspAshAl<br>    :::    <br>4406 AGCGTGATCGTGCAGGACGAG |
| 1191 ThrValThrValSerAspValGInLeuLeuCysGluSerProAsnLeuIleGlyArg 1209  | a (      |   | Oy             | 1523 AspThrIleThrGlnValLys  |
| ::::::::   | λ<br>δ   |   | qa             | 4463 GACACCATCTCCCAGGTCAAGGA  |

| ~             | 1210         | ValMetAlaAr  |
|---------------|--------------|--|
| c             | 3482         | <br>  CCCAAGGGGGGGGAGAAGGAGACCACACACAGGCGGGGGTTCATTGTGAAGTTC 3541  |
|               | 1217<br>3542 | GlyGlyMetGluTyrSerProGlyMetValTyrIleAlaProAspSerPro 1233   |
| <b>5.</b> (   | 1234         |  |
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| 0             | 3659         | ::::::::::::::::::::::::::::::::::::::   |
| <b>&gt;</b> 0 | 1267<br>3689 |  |
| 5~. ·         | 8.2          | euGluCysLysGluAlaPheAlaGluLeuGlnThrAspIleHisGluLeuThrSerAsp 130  |
| 0 :           | - 1          | CCCCTSCAAGGAATTCACAGACCTGATGGATGGAGGAGCCAGACGACGACGACGACGACGACGACGACGAC  |
| , c           | 3809         | uasp<br>:<br>GCAC  |
| ,             |              | ProGlyIleGluAspHisProValLeuAr  |
| 0             | 3869         | 3GACGGCGACAAGGACGTGATGATCACCGGCAAGCTGGACATCC   |
| » c           | 1343<br>3529 | TyrargGlnGluArgValGluLysGlyLeuLysLeuPheAlaGlnLeuIleAsnAsnLys 1362  |
| <b>.</b>      | 1363         | ValPheLeuLeuSerPheIleArgThrLeuGluSerGlnArgSerPheSerMetArgAsp 1382  |
|               | 3989         | CCTCATCAATTTCATCCACACCTGGAGAACCAGGGGGGGTTCTCGGCCCG   |
| ~ 0           | 1383         | ArgGlyAsnValAlaSerLeuileMetThrValLeuGlnSerLysLeuGluTyrAlaThr 1402 :::  |
|               | 1403         | SPValLeuLysGlnLeuLeuAlaAspLeuIleAspLysAsnLeuGluSerLysAsn<br>   |
| c             | 4109         | SAGCTCCTGGAGCAGTACGTGGTG   |
| <b>5-</b> (   | 42           | TroLysLeuLeuLeuArgArgThrGluSerValAlaGluLysMetLeuThrAsnTrpPhe 144   |
| 0             | 9            | SAAGCTGATGCTGCGCAGGTCTGAGACTGTGGTGGAGGATGCTGTCCAACTGGATG 422   |
| <i>b</i> . c  | 1443         | ThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGluProLeuPheSerLeuPhe 1462 :::  |
| <i>.</i>      | 1463         | CysAlaileLysGlnGlnMetGluLysGlyProileAspAlaileThrGlyGluAlaArg 1482  |
| 0             | 4286         | TGGAAAAGGGCCCGGTGGTGCGGTACAGAAGAAGCCCAA  |
| <b>~</b>      | 1483         | yrSerLeuSerGluAspLysLeulleArgGlnGlnIleAspTyrLysThrLeuValLe   |
| 0             | 4346         | ACTCTCAACGAC   |
| >- C          | 1503         | SerCysValSerProAspAsnAlaAsnSerProGluValProValLysIleLeuAsnCys 1522  |
| _             | 1523         | s 154  |
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SerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGlySerGlyAlaArg 1562
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; attheroscies coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; cell culture; drug screening; infection; immune disorder; cell culture; drug screening; gene therapy; antihifammatory; antiathmatic; antiathritic; haemostatic; antiarteriosclerotic; antifungal; vulnerary; antiulcer; ss.
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                                                               plexin-B1/SEP receptor homologue cDNA, SEQ ID NO:838
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                                                                                                                                                                                                                                                                                                                                                03-FEB-2000;
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                                                                                                                                                                                                                                                                                                  09-AUG-2001
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Sequences ABBA08224 represent 1390 nover number polypepticus, and sequences ABBA08224 represent 1390 nover number of invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have arious activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth activity; haematopoiesis regulatory activity; tissue growth activity; haematopoiesis regulatory activity; tissue growth activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be compensed, cancer cell proliferation or metastasis.

Communomention are useful for preventing, treating or ameliorating medical involved in oncogenesis, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include concers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), cronicars haematopoletic disorders (e.g., myeloid or lymphoid cell cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell carterial ischaemia, bone disorders (e.g., myeloid or lymphoid cell carterial ischaemia, bone disorders (e.g., myeloid or promote wound createrial growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound

α RESULT

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides,

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cc healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.

CD Descerial and fungal infections in addition to immune disorders.

CC POLYPEPPIGES With growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness,

CC autoimmune disease or accidental damage. The polypeptides and nucleotides

CC autoimmune disease or accidental damage. The polypeptides and nucleotides

CC autoimmune disease. The present sequence represents a cDNA encoding a cover human polypeptide of the invention.
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261 oGluMetValSerProProGlySerThrThrLysGluGlnValTyrThrSerLysLeuVa 281

do yo

| 5516          | 301      | 5456                   | 321             | 5420         | 341                  | 5360               | 361        | 5306   | 381          | 5252                         | 397         | 5192   | 415                             | 5132                   | 435                       | 5072    | 455             | 5012   | 475           | 4955                             | 495                     | 4895   | 515   | 4835    | 535                           | 4775               | 554          | 4715              | 572            | 4655             | 590         | 4601       | 610       | 4541                                  | 629            |
|---------------|----------|------------------------|-----------------|--------------|----------------------|--------------------|------------|--|--------------|------------------------------|-------------|--|---------------------------------|------------------------|---------------------------|---------|-----------------|--|---------------|----------------------------------|-------------------------|--|---|---------|-------------------------------|--------------------|--------------|-------------------|----------------|------------------|-------------|------------|-----------|---------------------------------------|----------------|
| III<br>GCTGGC | ycysg1   | GTGCCG                 | yAlaVa<br>      | GGCACCTG     | eSerLy               | AGC                | eLeuLy     | GCTGGA   | yThrLe       | ACAGGCACCCG                  | rAlaLe      | CCACGC   | uGlyVa<br>                      | GGGCAG                 | rServa                    | GGCCGT  | GlyLysLe        | CCGGAT   | lGlnVa        | CCTTGT                           | nLeuTy                  | CCTGTA   | rGlnSe  | cccGAC  | sAsnTh                        | CGAGGGACG          | -SerGl       | gaggg             | 1Se            | GGCCCA           | G1          | GGACGA     | snGlnIl   | GAGGCCGT                              | yAs            |
| :-CI          | eG1      | CCTGCAGTG              | sAlaGly,        | G            | ValPh                | TGTCTT             | ePheI1     | GTTCCC   | yGluGlyThr   | - ACAGG                      | SSerSerAl   | ودودوه   | aProLe                          | cccccr                 | gMetThr                   | CCTCAC  | sserG1          | TGATGG   | uThrva        | CTCTAT                           | pHisGluGl               | GGGCAG   | yGlnTy  | GAGCTA  | uHi<br>:                      | CGTCGA             | PheAla       | GCTGTG            | Va             | 52952            | rAla        | GAGGA      | 1615      | AGGGCGA                               | uAsnGly<br>    |
|               | uValPr   | GATGGA                 | uSerLy          | 1            | uPheTh               | ATA                | uCysIl     | CTGCCT   | yrArgGl      | <br>                         | eProCy      | CCAGIG   | tAsnAl                          | GCCCTA                 | gAspAr                    | CCTGAA  | eValGlyThrLy    | CACCTC   | aLeuGlnTyrGl  | GTACGA                           | SASPHi                  | AGACCT   | rCysGl  | GTGCCT  | pcysva                        | GTCCCT             | gArgPh       | CCACTG            | roAsnAsnIleSer | CATGAG           |             | CCTGAG     | uValVa    | CGTGGA                                | leThrGl::      |
|               | TyrvalGl | ACCTGGP                | ~ ~             | CTTT         | preure               | scerce             | erAlaLeuCy | GGGCCT   | erCysTy      | CTGTTA                       | Aspil       | CCATAT   | 3pMe                            | GCACCT                 | uAspAr                    | STGGAGG | eValG1          | TCTGG  | aLeuGl        | CTCAG                            | eSerLy                  | GTCTGC   | 1GluSe  | rgcagg# | SGLYTI                        | CCCCTC             | luProAr      | AGGAGGCCAGCCACT   | OASDAS         | CACAGA           | alProGl     | rccrecc    | spGlyLeuV | ວວວວອວເ                               | IleI<br>:      |
| <br>3G        | snSerTy  | ACTCCTACCTGGAGATGGACCT | euGlnAlaAla<br> | ccccrccc     | spAspAspLeuLeuPheThr | CTGGCAGGGTGCT      | pGlus      | CCGGTGC  | euGlnSe      | :::IIIII<br>GCAACGCCTGTTAC-  |             | rccacgo  | LyteuAs                         | SCTCGG                 | roValPheThrGluAspArgAspAr | rgcagc  | erLeuAlaPh      | rgcrr'   | roArgGlyAsnAl | SCACCTO                          | pMetAlaPh               | rGGTAC   | alProva   | reccee  | roHisCy                       | CTACT              | erLysGl      | CCGAGG            | alHisPr        | CCAGC            | rAsnV       | . 5        | uMetA     | CACACCC                               | alProArg<br>:: |
| :::           | laPheA   | AACTACT                | enT             | )9           | HisProA              | CTGGCT             | erLeuAs    | 255555   | sGluArgLeuGl | CCAACC                       | Lys         | AGCCCT   | CysGlyLeuAspMetAsnAlaProLeuGly' | CATGTG                 | rovalP                    | CCGTGC  | isserL          | ACACTG   | roArgG        | CCAGATGGCACCTCCTCAGAGTACGACTCTTT | rgAspM                  | GCGACC   | hrargva   | TCCGGC  | GlyAspProHisCysGlyTrpCysValLe | AGGACC             | luArgSerLys  | ၁၅၅၁၁၁၁           | uThrVa         | GTCACCAGCGCCCAGC | LeµGluThrTy | rcagcccc-  | euSerGl   | ນອວວອວ                                | aLysGluVa<br>: |
| ອອວວວ         | spThrA   | ACCCCA                 | yrArg           |              | 1у Уа 1 н            | Crecerecerecerecer | letLyss    | cesageageageageageageageageargrapheageageageageageageageageageageageageage | эГл          | GAGGTGCACGCCAAGATGGAGGCCAACC | ysValL      | GACATCTTCTACAGCCCTTCCACGCGATATCCAGTGCGGCGGCCACGC | snPhe-                          | GCTTCC                 | gGlylleP                  |         | ysAsnHi         | GACGGTCGCCGCCGAGAACAACCACACTGTTGCTTTTCTGGGCACCTCTGATGGCCGG | AspGlyP       | 1                                | ValAspProGlyProValLeuAr | GAGATAAACAAGAGAGTCAAGCGCGACCTGGTACTGTCTGGAGACCTGGGCAGCCTGT | MetSerGluArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnS | AGGTGT  | lyserG                        | Acceaereceecacreee | gCys         | AGTGTC            | ArgLeuT        | CCGTCA           | =           | GACCGTCA   | luAspLeuS | cttitigggaagtcgccgccacaccccgcccgcgrgg | aA1            |
| CACCCGG       | LysGluA  | GTGCAGAGAGACCCC        | yValGluT        | ATCCAC-      | gThrLeuGlyVal        | rccgree            | ArgLysMet  | CGG  | pA           | SCCAAGA                      | FrpLeuLy    | SACATO   | eAspAspAsnPhe                   | GCCGGGCTCCAGCAAGAGCTTC | ValArgG                   | CTCAGAG | eAlaTyrValTyrLy | 3CCGAG?  | eArgVal       |                                  | 3lyProv                 | AAGAGAG  | 3luArgC   | CAGGACA | uCysLeuGly                    | recee              | LysGluAr<br> | AccedaaGecegagier | Cysval         | - ტ              | LeuLeuVa    | AGCT       | ThrPheG1  | CTTTTTC                               | SerProAl       |
|               | F. F.    | ATGTGC                 | gSerGly         | GGACCCCGACAT | lLeuGlyArg           | creeceec           | GlnLys     | AGC  |              | GTGCAC                       | uAspLeuAlaT | GAGGCCCGT  | uLeuThrIle                      | GGCTCC                 | AspMetVa                  | GACGGG  | AlaTyr          | GTCGCC   | Lysil         | AAGGTG                           | AspPro(                 | ATAAAC   | eMetSer(  | ATGACC  | sGlyGlu                       | ACCCAG             | SThrArg      | ACCCGG,           | LysGln         | AAGTCCT          | AsnValLe    | GGGGAGGTGC | AsnCys    | rrccrerec                             | CysTyr<br>     |
| GGACI         | lArg     | ACG                    | uArg            |              | lLeu<br>             | Ö                  | sGly       | AGACAGC  | ~            | Ö                            | uAsp        | GGAG   | uLeu                            | 9009                   |                           | ວອວວ    |                 | GACG   | uLys          | CCIC                             |                         | GGAG   | rI]   | 2252    | rCy                           | CTCC               | rCy          | ATGC              | uMet           | AAGC             | nTyr        | - 0        | yval      | 9                                     | eGln:          |
| 5551          | 281      | 5515                   | 301             | 5455         | 321                  | 5419               | 341        | 5359   | 361          | 5305                         | 381         | 5251   | 397                             | .5191                  | 415                       | 5131    | 4.35            | 5071   | 455           | 5011                             | 475                     | 4954   | 495   | 4894    | 515                           | 4834               | 535          | 4774              | 554            | 4714             | 572         | 4654       | 290       | 4600                                  | 610            |
|               |          |                        |                 |              |                      |                    |            |  |              |                              |             |  |                                 |                        |                           |         |                 |  |               |                                  |                         |  |   |         |                               |                    |              |                   |                |                  |             |            |           |                                       |                |
| qq            | δ.       | qq                     | Qy              | qq           | Qy                   | qq                 | Oy         | QQ   | Qy.          | qq                           | Qγ          | qq   | δy                              | QQ                     | Οy                        | qq      | QY              | qq   | Οy            | QQ                               | Óγ                      | qq   | δy  | qq      | Qy                            | Q                  | Οy           | qq                | Qγ             | qq               | Qy          | Q          | Οy        | qq                                    | Qy             |

| qa           | 4540 CATCTGCAACTCCCCAAGCAGCATCCCCGTCACACCGCCAGGCAGGA 4493               | į    |                       |
|--------------|---|------|-----------------------|
| ò            | 629 pHisHisValValValGlnLenGlnLenLvsSerLvsGluThrGlvMetThrPheAlaSerTh 649 | λ    | :::                   |
| <b>3</b> 8   | [   | qa - | 3535 GGCGGGC          |
| Qy           | 649 rSerPheValPheTyrAsnCysSerValHisAsnSerCysLe 663                      | λο d | 986 IValmer           |
| qa           | 11::  | a è  |                       |
| ογ           | 663 uSerCysValGluSerProTyrArgCysHisTrpCysLysTyrArgHisValCysThrHi 683    | G AC |                       |
| qa           | 4372 CICCIGCGIGAGCAACCGCIGGACCIGCCAGIGGGACCIGCCCTACCACGAGIGCCGGGA 4313  | δλ   |                       |
| Oy           |   | qq   | 3385 CCAGATG          |
| qa           | GGCTTCGCCCAACCCTGAGGACGGCATCGTCCGTGCCCACATGGAGGACAG                     | Qy   | 1034 eGlnTyr          |
| Qy           |   | qa   | 3325 CACCIAC          |
| qq           | CTGTCCCCAGTTCCTGGGACCCCAGCCCCTGGTGATCCCCATGAACCACGAGACAGATGT            | Qy   | 1054 yAsnThr          |
| Qy           | nProGlnSerGlyGlnArgGlyTyrGluCysIl                                       | qq   | 3265 TGGCCGC          |
| qq           |   | Qy   | 1074 gAlaLys          |
| Oy           | eLeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArgPheAsnSerSe                  | Db   | 3207                  |
| qq           | ACCGTGAAGGGTTCCTCCCTGCACGTGGCAGTGACTTGCTCAAGTTCATGGAGCC                 | QY   | 1094 tThrCys          |
| Ολ           |   | QO   | 3172 GCCGCGG          |
| qa           | CACGATGC  | Qy   | 1108                  |
| Qγ           | As  | Db   | 3112 CAATGAG          |
| qq           | 4060 CAACGAGACGCTGCCCTGCACCTTTACGTCATACGCGCAAGAATATCGAC 4006            | Qy   | 1119 yPheile          |
| Qy           | 793 nProAlaGlnAsnLysValHisLeuTyrLysCysGlyAlaMetArgGluSerCy 811          | qq   | 3052 CCTCAC           |
| qq           | 4005AGCAAGCICCATGTGACCCICTACGACIGCTCCITTGGCCGCACGACIG 3956              | ΛO   | 1135 nPheTh           |
| . Oy         | 811 sGlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGlnGlyProGlyG1 831    | G QQ |                       |
| <b>q</b> a , |   | Qy   | 1155 uLysPro          |
| Oy           | roAlaGlnGluSerGlnTrpLeuGluLeuSerGlyAl                                   | qa   | 2955                  |
| οp           | 3895 GIGCGIGIAIGAGGCCCIGIGCAACAC 3869                                   | οy   | 1175 yAsnVa           |
| ογ           | 851 aLysSerLysCysThrAsnProArglleThrGluIleIleProValThrGlyProArgGl 871    | ΩĐ   | 11 ::<br>2905 CAATCT  |
| QQ           | 3868 CACCICCGAGIGCCCGCCGCCGTCAICACCAGGAICCAGCCTGAGACGGGCCCCCTGGG 3809   | \    | 1190 sThrVa           |
| Qy           | 871 uGlyGlyThrLysValThrIleArgGlyGluAsnLeuGlyLeuGluPheArgAspIleAl 891    | g qo |                       |
| qa           | 3808 TGGGGGCATCCGCATCACCATCTGGGGTCCAATTTGGGCGTCCAAGCAGGGACATC 3751      | ΛO   | 1209 qHisLy           |
| Qy           | 891 aSerHisValLysValAlaGlyValGluCysSerProLeuValAspGlyTyrIleProAl 911    | g qa |                       |
| qa           | 3750 -CAGAGGATCTCTGTGGCCGGCCGGAACTGCTTTCAGCCGGAACGTTACTCCGTGTC 3692     | ΔÔ   |                       |
| ΟŊ           | 911 aGluGlnIleValCysGluMetGlyGluAlaLysProSerGlnHisAlaGlyPheValG1 931    | g qa | 11Î<br>2725 CGGCTC    |
| q            | 3691 CACCCGGATCGTGTGTGTGTCGAGGCTGCGGAGACGCCTTTCACGGGGGGTGTCGA 3635      | δλ   | 1233 oLeuSe           |
| Qy           |   | qq   | 111111<br>2665 GCTCAG |
| qa           |   | QY   | 1246 yGlyLe           |
| Oy           | -GlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSerArgGlyProMe            | qq   | 2607                  |
| qa           | 3592 CCAGTTCACCTTCCAACAGCCCCAAGCCTCTCAGTGTGGAGCCGCAGCAGGGACCGCA 3536    | •    |                       |

| ٨        | 96   | SerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAlaGlySerAsnValVa 986   |  |
|----------|------|---|--|
| ۵        | 3535 | GGGGCACCACACTGACCATCCACGGCACCCACCTGGACACGGGCTCCCAGGAGGA 347       |  |
| <b>⊼</b> | 98   | ValMetPheGlyLysGlnProCysLeuPheHisArgArgSerProSerTyrIleValCy 100   |  |
| Ω        | 3475 |   |  |
| × 4      | Ō 5  | SASDTHRTHISERSERASPGIUVALLEUGlUMELLYSVALSERVALGINVALASPARGAI 1026 |  |
| Ω :      | 3443 | AAAGTGACGAAGTTTGGGGGGGGGGGGGGGGGGGGGGGG                           |  |
| , д      | 00   | TGGAGGTCTCCTACGGGGGGTCCCCGGTGCCCAACCCCGGCATCTTT 332               |  |
| γ        | 1034 | 31nTyrValGluAspProThrIl   |  |
| q        | 3325 |   |  |
| γ        | 1054 | leAr 10   |  |
| q        | 3265 | GGCCGCAGCATCAACGTCACGGGTTCAGCCTGATCCAGAGGTTTGCCATG 320            |  |
| γ        | 1074 | laLysHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMe 109.   |  |
| Q        | 3207 | GIGGICATCGCGGAGCCCCTGCAGTCCTGGCAGCC 317                           |  |
| Ž.       | 1094 | proalaLeuAlaLeuGlyProAspHis 110                                   |  |
| Q        | 3172 | 099   |  |
| λ        | 1108 | GlnSerAspLeuThrGluArgProGluGluPheGl 1119                          |  |
| ð        | 3112 | GTCGTCTTCCTGTCCCCGGCTGTGCCTGAGGAGCCTACAA 305                      |  |
| λi       | 1119 | sThrAs 113  |  |
| q        | 3052 | CCTCACGGTGCTGATCGAGATGGACGGCACCGTGCCTGCTCAGAACAGAGGCCCGGGGC 2993  |  |
| λ        | 1135 | STHTTYTTYTPTOASNPTOVAIPHEGIUALAPHEGIYPTOSETGIYILCLEUGlULE 115     |  |
| q        | 2992 | racetecteacccacetteagaactic                                       |  |
| λλ       | 1155 | sProGlyThrProllelleLeuLysGlyLy                                    |  |
| q        | 2955 | 3TGGCGTCAAGAAGCTCAGGTCATCCGCGCCCGGGG                              |  |
| λλ       | 1175 | yAsnValLysLeuAsnTyrThrValLeuValGlyGluLysProCy 1190                |  |
| ą        | 2905 | SCAGGAGGCCGAGGCTTCGTGGGTGCCGAGCGCT                                |  |
| λλ       | 1190 | 20  |  |
| q        | 2845 | ACCATGAAGACGCTGACGGAGCCGACCTGTACTGTGAGCCCCCGGAGGTGCAGCCCCC        |  |
| λy       | 1209 | gHisLysvalMetAlaArgVa 1216  |  |
| q        | 2785 | GGCGGCAGAAACGAGACACCACACACAACTGCC                                 |  |
| λy       | 1216 | Ä   |  |
| qc       | 2725 | cectetececadicectecececececideagraceaeaeaegeseaecedececece 266    |  |
| λy       | 1233 | OLEUSETLEU  |  |
| q        | 2665 | dereageerearcrisceserserearesreseerserseresresreareseeres 260     |  |
| 27       | 24   | yGlyLeuLeuIleIlePheIleValAlaValLeuIleAlaTyrLySArgLySSerArgGl 1266 |  |
| მ        | 2607 |   |  |

qq

Qy Db

| 1540   | y 1642 hrProAspLeuGluSerGlyValLySMetTrpHisLeuValLySAsnHisGluHIsGlyA 1662<br>  | 1662 spGlnLysGluGlyAspArgGlySerLysMetValSerG 1675 | 1675<br>1399 | y 1695 euPheGluThrIlePheSerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysT 1715 | y 1715 yrMetPheAspPheLeuAspGluGlnAlaAspLysHisGlyIleHisAspProHisValA 1735 | y 1735 rgHisThrTpLysSerAsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnP 1755 | y 1755 roginphevalpheAspileHisLysAsnSerileThrAspAlaCysLeuSerValValA 1775   1   1   1   1   1   1   1   1   1 | y 1775 laGlnThrPheMetAspSerCysSerThrSerGluHisArgLeuGlyLysAspSerProS 1795 | y 1795 erasnlysleuleuTyralaLysaspileProserTyrLysasnTrpValGluargTyrT 1815<br> | y 1815 yrSerAspIleGlyLysMetProAlaIleSerAspGlnAspWetAsnAlaTyrLeuAlaG 1835 | y 1835 luGlnSerArgMetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePhes 1855<br> | y 1855 erTyrValGlyLySTyrSerGluGluIleLeuGlyProLeuAspHisAspAspGlnCySG 1875 | y 1875 LyLysGlnLysLeuAlaTyrLysLeuGluGlnVal 1886<br>  11 :::      :::::    :::    :::    ::: | 30L<br>198   | AAH98400;<br>12-OCT-2001 (first entry)                                |  | diagnos<br>biodive | S Homo sapiens.<br>X<br>N W0200154477-A2. |
|--|---|---|--------------|--|--|---|--|--|--|--|--|--|---|--|---|--|--------------------|---|
| ΩD   | Qy  | Qy  | Qy           | QY   | da   | Qy<br>Db  | Qy   | QY<br>Db   | QQ<br>Dp   | QY   | Qy<br>Db   | , Oy<br>Db   | QY<br>Db  | RE<br>AAI<br>ID<br>XX  | X D X X   | DE<br>KW<br>KW   | XX KW              | OS<br>XX<br>PN                            |
|  | ,   |   |              |  |  |   |  | <u> </u>   |  |  |  |  |   |  |   |  |                    |   |
| 1266 uSerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeuGluSerArgValAl 1286 ::::::: | aLeuGluCysLysGluAlaPheAlaGluLeuGlnThrAspIleHisGluLeuThrSerAs 1306<br>        ::   <br> GGACGCTGCAAGAAGAACTGAACTGAACTGAATGAATGAA |   |              | snLy<br>::   | 138  |   | ASDH<br>III  | IrpP   | LeuP   |  |  |  |   | 1542 ysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGlySerGlyAlaA 1562<br> | rgMetIleLeuGlnAspGluAspIleThrThrLysIleGluAsnAspTrpLysArgLeuA 1582<br> | snThrLeuAlaHisTyrGlnValProAspGlySerValValAlaLeuValSerLysGlnV 1602         1111111   11111   111111::: ::   11         ACACCCTTATGCACTACAATGTCCGGGATGGAGCCACCCTCATCCTG 1581 |                    |   |

Qy Db

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rGlyValAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAspAs 181
                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of nove-
proteins from a variety of organisms, including human, dog, cat, horse,
cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
urchin and tomato. These were derived from expressed sequence tags (EST)
from the organism of interest. They can be used in diagnostics,
forensics, gene mapping, identification of mutations, to assess
biodiversity and for nutritional purposes. The present sequence is a cD
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TGCCATGAG---GCTGAGATGACTGACAATGTCAACCAGCTGCTGCTGGTCGACCCTCCC
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                                                                                                                                                                                                                                          uPheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAs
                                                                                                                                                                                                                                                                                                                                                                          ------GTGGCGGCCTTCGAGGACGCCCCTACGTCTTCTTTGTCTTCAACCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uAspLeuAlaTrpLeuLysValLys------AspIleProCysSerSerAlaLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5251 GGAGGCCCGTGACATCTTCTACAAGCCCTTCCACGGCGATATCCAGTGCGGCGCCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uLeuThrIleAspAspAsnPhe---CysGlyLeuAsp---MetAsnAlaProLeuGlyVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCGGGCTCCAGCAAGAGCTTCCCATGTGGCTCGGAGCACCTGCCCTACCCGCTGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415 lSerAspMetValArgGlyIleProValPheThrGluAspArgAspArgMetThrSerVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lileAlaTyrValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLe
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                                                                                                          5761 CCGCGTGCTGTTTGTGGGCAAAGGCAATGGGCCACACGACAACGGCATCATCGTGAGCAC
                                                                                                                                                    rArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGl
                                                                                                                                                                                                                                                                                                                                  plleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnPr
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| created and controlle |    | umecuystincyswartytyculii - Valhistrokhaniieeer - Valskio 1772<br>  AAGCAAGTCCTGCGTGGCCGTCACCAGCCCACCAGAACATGAGCCGGCGGGCCCA 4655 | 2 nTyrAsnValLeuLeuValLeuGluThrTyrAsnValProGluLeuSerAlaG1 590 |      |     |      | eGlnCysTyrSerProAlaAlaLysGluValProArgIleIleThrGluAsnGlyAs | CATCTGCAACTCCCCAAGCAGCATCCCCGTCACACCGCCAGGA | 9. PHISHISVALVAIGINLEGUGINLEGULYSSETLYSGLUTNIGLYMETTNIPREALASETTN 649 | CCACOL SOCICOL SOCICOL COLLOCATION CONTROL CANAGE AND THE COLLOCATION CONTROL COLLOCATION CONTROL COLLOCATION CONTROL COLLOCATION CONTROL COLLOCATION CONTROL COLLOCATION CONTROL CONT | CCAGTACCCTTCTACGACTGCCGCCATGAGCCTGGAGGAGAACCTGCGTGCAT | uSerCysValGluSerProTyrArqCysHisTrpCysLysTyrArqHisValCysThrHi | :     | sAspProLysThrCysSerPheGlnGluGlyArqValLysLeuProGluAs | GGCTTCGCCCAACCCTGAGGACGGCATCGTCCTGCCACATGGAGGACAG |     |      | eThrLeuLysAla | : :: | eL    | ::::::!      <br>ACCGTGAAGGGTTCCTCCTGCACGTGGGCAGTGACT | rS    | GGTGACCATGCAGGAATCTGGGACCTTCGCCTTTCGGACCCCAAAGCTGTCCCACGATGC 4061 |        |      |     | :::    ::: |     |      | 1 nCysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGluLeuSerGlyAl 851 | :   <br>5 GTGCGTGTATGAGGCCCTGTGC |     | 3 CACCTCCGAGTGCCCGCCGCCGTCATCACCAGGATCCAGCTGAGACGGGCCCCCTGGG 3809 |
| 535  |    | 4714   | 572  | 4654 | 590 | 4600 | 610   | 4540  | 629   | 649  | 4432  | 663  | 4372  | 683   | 4312  | 700 | 4261 | 720           | 4201 | 740   | 4176  | 758   | 4120  | 777    | 4060 | 793 | 4005       | 811 | 3955 | 831  | 3895                             | 851 | 3868  |
| oy g   | ì  | S &  | Oy   | Ωp   | οy  | qq   | λο i  | go (  | Š á   | 2 0  | g qo  | VO   | οqα   | QŸ  | ΟÞ  | Qy  | Db   | Qy            | QQ   | Qy    | Dp  | ٥y    | Db  | ō      | Db   | Οy  | QQ         | Oy  | Οp   | Qy   | q                                | Qy  | QQ  |

| λ Ф   | 871<br>3808  | uGlyGlyThrLysValThrIleArgGlyGluAsnLeuGlyLeuGluPheArgAspIleAl 891<br>        ::::::                     |
|-------|--------------|--|
| ъ Q   | 891<br>3750  | aSerHisValLysValAlaGlyValGluCysSerProLeuValAspGlyTyrIleProAl 911 :::                                   |
| >ı· 4 | 5 5          | GluGlnIleValCysGluMetGlyGluAlaLysProSerGlnHisAlaGlyPheValGl 931  |
| a k   | 531          | acccosaticatetratearigaoscrecosasacecratarcososositor<br>11eCysValAlaValCysArgProGluPheMetAlaArgSerSer |
| Д     | 3634         | <br>   |
| γ d   | 547<br>3592  | heMetThrLeuT<br>AACAGCCCAAGC   |
| × 4   |              | erGlyGlyThrGlnValThrIleThrGlyTh<br>::         <br>:::  |
| λ     | 98           | ValMetPheGlyLysGlnProCysLeuPheHisArgArgSerProSerTyrIleValCy 100  |
| ą     | 3475         | 3  |
| γĄ    | 1006         | rSerAspGluValLeuGluMetLysValSerValGlnValAspArgAl 1   |
| >     | 0.2          | LysIleHisGlnAspLeuValPh 103  |
| Q     | 6            | 3ATGCTTCTGGAGGTCTCCTACGGGGGGTCCCCGTGCCCAACCCCGGCATCTTCTT 332   |
| γ q   | 1034<br>3325 | eGlnTyrValGluAspProThrIleValArgIleGluProGluTrpSerIleValSerGl 1054                                      |
| · X   | 054          | rHisLeuAspLeulleGlnAsnProGlnIleAr 107  |
| .a    | 265          | GGGCTTCAGCCTGATCCAGAGGTTTGCCAT   |
| Д     | 1074         | galaLysHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMe 1094 :::             :: ::                |
| Y     | 1094         | oAlaLeuAlaLeuGlyProAspHis 110  |
| Q     | 3172         |  |
| γ     | 108          | nSerAspLeuThrGluArgProGluGluPheGl 111.   |
| q     | 3112         | cccgcrgrgccrgagagccagaggccra   |
| ¥     | 119          | nValGlnSerLeuLeuIleLeuAsnLysThrAs 113  |
| ą     | 3052         | CCTCACGGTGCTGATCGAGATGGACGGGCACCGTGCCTGCTCAGAACAGAGGCCGGGGC 2993                                       |
| ۲ ۸   | 13           | eThrTyrTyrTyrDroAsnProValPheGluAlaPheGlyProSerGlyIleLeuGluLe 115:                                      |
| Ω     | ע<br>ע       | CANDIACGIGCTIGACCCCACCIIIGAGAACIIC   |
| , Y   | 15           | sProGlyThrProIleIleLeuLysGlyLysAsnLeuIleProProValAlaGlyGl 117  |
| Ω     | 95           | ACAGGTGGCGTCAAGAAGCAGGTCAACAAGCTCATCCGGGCCCGGGGCAC 290   |
| Y Q   | 1175         | yASnValLySLeuASnTyTThrValLeuValGlyGluLySProCy 1190   |
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|--|----------|-------------|---|--|--------------|------|--|--------------|--|------|--------------|---|------|--|---|--|--------|---|---|---|--|-------|---|------|---|---|---|--|--|---|-----|------|
| 1209   | 2786     | 1216        | 2726  | 1233   | 1246         | 2608 | 1266   | 23/3<br>1386 | 2519   | 1306 | 2459         | 1326  | 2399 | 34   | 2339  | 1362   | 27     | 1382<br>2219  | 1402  | 2159  | 1422   | 2100  | 1442  | 2042 | 1462  | 1982  | 1482  | 1922   | 20   | 1862  | 52  | CORT |
| alSerAspValGlnLeuLeuCysGluSerProAsnLeuIleGlyAr |          |             | 2785 GCCCAAGCGGCGGCAGAACGAGACACCACACACACCTGCCCGAGTTCATTGTGAAGTT ; | 1216 1GlyGlyMetGluTyrSerProGlyMetValTyrIleAlaProAspSerPr | 3 oLeuSerLeu |      | yGlyLeuLeullellePheileValAlaValLeulleAlaTyrLysArgLysScrArgGl |              | dectabled in bedrysal generalises in the state of the sta |      |              | 1306   PLEUASPGIYALAGIYILEPrOPHELEUASPTYrArgThrTyrThrMetArgValLeuPh |      | eProGlylleGluAspHisProValLeuArgAspLeuGluValProGl | 2398 CCTGCCCTCCAAGGACGGCGACAAGGACGTGATGATCACCGGCAAGCTGGACATCCCCGA | 2 yTyrArgGlnGluArgValGluLysGlyLeuLysLeuPheAlaGlnLeuIleAsnAsnLy |        | 1362 sValPheLeuLeuSerPheIleArgThrLeu-GluSerGlnArgSerPheSerMetArgA | 1382 spArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLeuGluTyrAlaT | 2218 CCAAGGTCTACTTCGCGTCCTGCTGACGGTGGCGCTGCACGGGAACTGGAGTACTACA | 1402 hrAspValLeuLysGlnLeuLeuAlaAspLeuIleAspLysAsnLeuGluSerLysAsnH<br>      ::::: ::: ::: |       | SProLysLeuLeuLeuArgArgThrGluSerValAlaGluLysMetLeuThrAsnTrpP |      | 1442 heThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGluProLeuPheSerLeuP | 2041 TGTCCATCTGCCTGTACCAGTACCTCAAGGACAGTGCCGGGGAGCCCCTGTACAAGCTCT | 1462 heCysalaIleLysGlnGlnMetGluLysGlyProIleAspAlaIleThrGlyGluAlaA | 1981 TCAAGGCCATCAAACATCAGGTGGAAAAGGGCCCGGTGGATGCGGTACAGAAGAAGAGCCA | 1482 rgTyrSerLeuSerGluAspLysLeulleArgGlnGlnIleAspTyrLysThrLeuValL :::!  ::::   ::::    : | 1921 AGTACACTCTCAACGACACGGGGCTGCTGGGGGGATGATGTGGGAGTACGCACCCCTGACGG | 5   |      |
| Оу   |          | Oy          | qq  | QY   |              | pp   |  |              | . QZ   | ٥y   | • <b>q</b> 0 | Qy  | QQ   |  | ф   | Qy   | q<br>q | Qy<br>Dp  | Qy  | qq  | Qy   | qq    | Οy  | qa   | QY  | Dp  | ٥y  | Db   | ΟY   | qa ,  | Qy  | Dp   |

| ۵             | 1804 |  |
|---------------|------|--|
| Ý             | 1542 | SSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGlySerGly                  |
| ą             | 1744 | CTGCTGGCCCAGGCCAGACAGCGTGGTCGTGGTGTGTTTTTTTT                             |
| <u>&gt;</u> 4 | in a | rgMetileLeuGlnAspGluAspIleThrThrLysIleGluAsnAspTrpLysArgLeuA 1582 ::     |
| <u> </u>      | 1582 | ThrieualanisTyrGlnValProAspGlySerValValAlaLeuValSerLysGlnV 160           |
| ą             | 1627 |  |
| λ             | 1602 | rAsnAlaValAsnAsnSerThrValSerArgThrSerAlaSerLysTyrG 162:                  |
| Q             | 1580 | CCAAGGTGGGGGTCTCCCAGCAGCCGGAGGACAGCCAGC 154                              |
| λί            | 1622 | <pre>gTyrThrGlySerProAspSerLeuArgSerArgThrProMetIleT 164:</pre>          |
| ą             | 1540 | COTGCCTGGGGAGCGCCATGCCCTC  |
| Δ. «          | 1642 | hrProAspLeuGluSerGlyValLySMetTrpHisLeuValLySAsnHisGluHisGlyA 1662        |
| <b>2</b>      | 1 1  | 57 C20 C4144M211   |
| ξ, q          | 1459 | AGAAGGAGGGACGAAGCCATCACCG 140  |
| λγ            | 1675 | 11eTyrLeuThrArgLeuLeuAlaThrLysG1yThrLeuG1nLysPheValAspAsp                |
| ą             | 1399 |  |
| λλ            | 1695 | 3luThrIlePheSerThrAlaHisArgGlySe   |
| ą             | 1339 | CTTCCAGAGCGTGCTGGCGCTGGGCACGCGGTGCCACCTGCAAG                             |
| λý            | 1715 | isvala 173   |
| q             | 1288 | CTTCTTCGACTTCCTGGACGAGCAGAGAAGCACACATCCAGGAT                             |
| . Ac          | 1735 | rgHisThrTrpLysSerAsnCysLeuProLeuArgPheTrpValAsnMet11eLysAsnP 1755        |
| ۸             |      | oglophevalpheAsplleHisLvsAspSerIleThrAspAlaCvsLeuSerValValA 1            |
| χ . Q         | 16   | ACTICATUTE ACCITACACA CACAGA CACACACACACACACACACATCATA CATACATA CATACATA |
| λy            | 1775 | laGlnThrPheMetAspSerCysSerThrSerGluHisArgLeuGlyLysAspSerProS 1795        |
| qc            | 1108 | GCAGACCTICATGGATGCCTGCACGCACGGAGCATAAGCTGAGCCGCGGATTCTCCCCA 104          |
| Z,<br>qc      | 1795 | erAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLysAsnTrpValGluArgTyrT 1815<br>    |
| λλ            | 1815 | rSerAspIleGlyLysMetProAlaIleSerAspGlnAspMetAsnAlaTyrLeuAla               |
| q             | 988  | SCAGATGG   |
| λy            | 1835 | isMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheS 18                         |
| qc            | 928  | TTTCCCGGGCGCACACGGACTCCTTGAACACCCTCGTGGCACTCCACCAGCTCTACC 86             |
| λy            | ξĊ.  | TyrValGlyLysTyrSerGluGluIleLeuGlyProLeuAspHisAspAspGlnCySG 18            |
| q             | ق    | AATACACGCAGAAGTACTATGACGAGATCATCAATGCCTTG                                |
| Σy            | 1875 | lyLysGlnLysLeuAlaTyrLysLeuGluGlnVal 1886<br>     :::       :::::    :::  |
|               |      |  |

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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities; including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; chammloomodulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; hemostatic, thrombotic or thrombolytic activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; hemostation or metastasis.

CC thrombolytic activity; activin- or inhibin-related activities; or may be invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions cancers, haematopoietic disorders (e.g., my my load or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease,
                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; growth factor;
haematopoiesis regulation; tissue growth; immunomodulator; activin;
                                                                                                                                                                                                                                                                                                      haematopoleals regulation, itsue growth, immunomodulator; activin, fundation, the metastasis; thrombolysts; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoleate disorder; proliferation; metastasis; cancer; tumour; haematopoleate disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; cell culture; drug screening; ene therapy; antiniflammatory; antiacthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                      Human plexin-B1/SEP receptor homologue-encoding cDNA, SEQ ID NO:729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
AGAAGATGCAGCTGGCCTTCCGCCTGCAGCAGATT 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 663-665; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antifungal; vulnerary; antiulcer; ss
                                                                                           ABA08953 standard; cDNA; 7080 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0560875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-2001; 2001WO-US03800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-2000; 2000US-0496914
                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-457740/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ABB11709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157188-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-2000;
                                                                                                                                                                                         11-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                           ABA08953;
                                           RESULT 10
                                                                    ABA0895
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arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incistons and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the dispnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||:::||||||| ::::::||| :::
TATCAGCTGCGGCGCCGAGGCCGGGCGGCCGTGGCGGCCGTGCCG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspAsnProLysCysTyrProProArgileValGln---ThrCysAsnGluProLeuThr 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACAGCCCGCTGTGTCACGCTCCGCAGCTGCCGCAGGCCTCGTGCGAGCACCCCGCGGCGC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrThrAsnAsnValAsnLysMetLeuLeuIleAspTyrLysGluAsnArgLeuIleAla 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 CTCACGGACAACTACAACAAGATCCTGCAGCTGGACCCCGGCCAGGGCCTGGTAGTCGTG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysGlySerLeuTyrGlnGly1leCysLysLeuLeuArgLeuGluAspLeuPheLysLeu 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyGluProTyrHisLysLysGluHisTyrLeuSérGlyValAsnGluSerGlySerVal 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGTGCGCTTCCCGCCCGCCGCCGCCGCCGAGCCCGTCACGGTGTTCCCCAGCATG 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGAACGTGGCGGCCAACCACCGGAACGCGTCCACCGTGGGGCTAGTTCTGCCTCCCGCC 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AspLysLeuPheIleAlaThrAlaValAspGlyLysProGluTyr 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TrcTTCCCGCGCAACCGCAGCCTGGAGGACCACCGCTTCGAGAACACGCCCGAGATCGCC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 SerArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAsp 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AsnHisteuValValAspGluArgThrGlyHisIleTyrLeuGlyAlaValAsnArgIle 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrLysLeuSer---SerAspLeuLysValLeuValThrHisGluThrGlyProAspGlu 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuLeuMetValGly-------MetGlySerSerThrLeuLeuThrArgGlnProAla 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 ProLeuSerGlnLysGlnArgSerPheValThrPheArgGlyGluProAlaGluGlyPhe 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCGGGTCCATCTACCAGGGCTTCTGCCAGCTGCGGGGGCGCGGGGTAACATCTCGGCCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGGCGCGCGCGCCAGCCGCCTGCTCGTGGGCGCCACGTACACCGGTTACGGCAGCTCC
                                                                                                                                                                                                                                                                                                                    Sequence 7080 BP; 1352 A; 2350 C; 2143 G; 1235 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                              7080
652
332
747
304
60
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheGlyValIleValSerTyrSerAsnLeuAsp----
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-964-956-13 (1-1896) x ABA08953 (1-7080)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
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2471.00
48.43$
32.09$
24.73$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
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| AArgC<br>:  <br>:  <br>:  <br>: | ysGluArgSerLysGluProArgArgPheAlaSerGluMetLys 556   |
|---------------------------------|--|
| :::: <br>CGCT<br>LeuI           | :::          ::  |
| ATG/<br>Phe                     | 'GCAGATCTCGGGCAGCCTGCCCAGCCTCAGTGGCATGGAGATGGCCTGTGAC 2099 'GCAGATCTCGGGCAGCCTGCAGCCTCAGTGATGGTGATGGCCTGTGAC 2099 'GCAGATCTCGGGCAGCCTGTGATGATGATGATGGTGATGATGATGATGATGATGATG               |
| AT<br>ln                        | 33GAACAACATCCGCACTGTGGCTCGGGGTCCCAGGCCCTGCCTTTGGTCACAAT<br>CysTyrSerProAlaAlaLysGluValPrOArgIleIleThrGluAsnGlyAspHi<br>::::::  |
| His                             | 650  |
| =                               | a S  |
| CY                              | sValGluSerProTyrargCysHisTrpCysLysTyrargHisValCysThrHisAsp 684   |
| Pr                              | 0 0  |
| G = E                           | uArgvalAspLysIleLeuvalProvalGluva<br>      <br>GCTCTCACCCTGGCACCGTGCCTACGGGTGG   |
| ĽÝ                              | SASnLeuProGlnProGlnSerGlyGlnArgGlyTyrGluCysIleLeuAsnIleGln 744   |
| 61y8<br> <br>                   | SerGluGlnArgValProAlaLeuArg<br>   :::<br> TGGAGGAGATCTTCGAGGCTGTGTGG   |
| AS                              |  |
| ≥ ≤                             | aG<br>GC   |
| . O − E                         | CysGlyAlaMetArgGluSerCysGlyLeuCysLeuLysAlaAspProAspPheAla 822   CysGlyAlaMetArgGluSerCysGlyLeuCysLeuLysAlaAspProAspPheAla 822   CysGlyAlaMetArgGluSerCoAspPocyGGGCGGGAAAACTGGGTCACCTG 2784 |
| Ω-H                             | <b>3</b> .   |
| Š :                             | GlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnPr<br>   |
| 11<br>A1                        | elleProValThrdiyProArgGluGlyGlyThrLysValThrlleArgGlyGluAsn 882   |
| :                               |  |

LeuGluValProGlyTyrArgGlnGluArgValGluLys 1350 ::::::|||| :::
rGGAAGATTCCTGAGAGCTGCCGGCCCAACATGGAAGAG 4425 LeulleAsnAsnLysValPheLeuLeuSerPhelleArg 1370 PheSerMetArgAspArgGlyAsnValAlaSerLeuIle 1390
|||::::::||||||||||
rTTGCGGTGCGCACGAGCTGGCTGGTGCTG 4545 LeuGluTyrAlaThrAspValLeuLysGlnLeuLeuAla 1410 ||||||||||| ||| ::::::||||:::|||||| CTGGAGTACTACACCAGCATCATGAAGGAGCTGCTGGTG 4605 JeuThrAsnTrpPheThrPheLeuLeuTyrLysPheLeu 1450 STCATCTGCAGCGTCCTGCTGCTGCTCCCGTGGTGGCC 4068 ...--Gly1leGlu 1330 GlySerGlyAlaArgMetIleLeuGlnAspGluAspIle 1570 AlaValAlaGlyGlyLeuLeuIleIlePheIleValAla 1255 JysSerArgGluSerAspLeuThrLeuLysArgLeuGln 1275 SerArgValAlaLeuGluCysLysGluAlaPheAlaGlu 1295 4etArgValLeuPhePro----- 1327 ACCCGCACCTTCTTCCCCAAGTGTTCCTCCTTTATGAA 4305 PAGACCCTCAACTCCCAGGGCAGCTCCCAGGCACAGGAA 4365 PhrGlyGluAlaArgTyrSerLeuSerGluAspLysLeu 1490 ysThrLeuValLeuSerCysValSerProAspAsnAla 1510 ysileLeuAsnCysAspThrileThrGlnValLysGlu 1530 GGGCCCATGGACACCGACACGCTGACACAGGTCAAGGAG 4956 ysAsnValProCysSerHisArgProLysAlaAlaAsp 1550 LeuThrSerAspLeuAsp---GlyAlaGlyIleProPhe 1314 AAGAGCCGACGTGCTGACTGGCAGAAGACGCTG

Human cDNA encoding Plexin-D1.

(first entry)

09-MAY-2001

AAS00022;

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neurodegenerative disease; autoimmune disease; lupus; multiple sclerosis; inflammatory bowel disease; diabetes type I; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence encodes Human Plexin-Dl. Plexins are large transmembrane proteins whose extracellular domain shares homology with Scatter factor receptors and contain an approximately 500 amino acid Semaphorin Gomain. The plexin polynucleotides and polypeptides, and plexin-specific binding agents are useful in diagnosis, therapy and in the biopharmaceutical industry. In particular, the plexin polynucleotides and polypeptides are useful for generating compounds (e.g. plexin-specific binding agents or antibodies) for treating or diagnosing a disease or disorder involving aberrant cell growth (e.g. hyperplasia, neoplasia, cancer or neurodegenerative disease), or diseases or disorders involving aberrant bowel disease or biabetes Type I), or immunosuppressive diseases such as lupus, inflammatory bowel disease or biabetes Type I), or immunosuppressive diseases such as multiple sclerosis or rheumatoid arthritis.
                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New plexin polynucleotides and polypeptides, useful in diagnosis, therapy and in producing compounds for treating diseases involving aberrant cell growth (e.g. cancer) or immune regulation (e.g.
                                                                                                       Human; Plexin-D1; semaphorin domain; hyperplasia; neoplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Artigiani S, Comoglio PM, Goodman CS, Tesier-Lavigne M;
Tamagnone L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5892 BP; 1121 A; 1976 C; 1767 G; 1028 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5892
649
334
750
293
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                        /*tag= c
/label= "Mature Plexin-D1"
                                                                                                                                                                                                                                          /*tag= a
/product= "Plexin-D1"
13..138
                                                                                                                                                                                                          Location/Qualifiers
13..5790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 62-64; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.74e-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0150576.
                                                                                                                                                                                                                                                                                                                                                                                                                            25-AUG-2000; 2000WO-US23365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2463.50
48.598
32.088
24.668
                                                                                                                                                                                                                                                                                     /*tag= b
139.5787
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYTO-) UNIV TORINO.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                    immunogen; antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-226610/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAU00017
                                                                                                                                                                                                                                                                                                                                                                 WO200114420-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001.
                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
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US-09-964-956-13 (1-1896) x AAS00022 (1-5892)

RESULT 11 AASO0022 ID AASO0022 standard; CDNA; 5892 BP.

| 651 PheValPheTyrA  | ογ             |  |           |
|--------------------|----------------|--|-----------|
| 2047GTGACTG        | qa             | PILLE SOCIOLARY TO THE STATE OF | 7 음       |
| 631 HisValvalGlnLe | Qy             | The Clark Cortinuated to the test of influence of the test of the  | è         |
| 1987 GCCTACTGCAACC | qa             | zoo Lyseluaspiniala  | r z<br>GD |
| 611 GlnCysTyrSerP  | Qy             | TICATION TO THE TOTAL TO THE TOTAL T | l 8       |
|                    | qa             | 272  | Qy<br>Dp  |
| 595 Phe            | λŎ             | ر  | άn        |
| 1857 ATGATCCTGCAGA | qu             | LI III IIII IIII IIII IIII IIII III III  | 3 2       |
| 576 LeuLeuValLeuG  | QY             | [englnprog]uMetValSerbroproglvser@hrmhr  | ٥         |
| 1807 CGCTGTCCTGCCA | QQ             |  | . qa      |
| 557 GlnCysValArgLe | Qy             | AsplleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThr   | ٥y        |
| 1747 CAGGACTGCACCA | g<br>G         | 787GCCTCCGACGACAAC 801   | qa        |
|                    | Οy             | 221 GluPheValAlaSerWetIleLysIleProSerAspThrPheThrIleIleProAspPhe 240   | Qy        |
|                    | gr é           | 730 ATCGCTCCCTGGACACGCGCGCGCGAGCTCTTCACCTTCGACCTCAAC 786   | qa        |
| 520 LeuGlySerGlyA  | oy<br>1        | 201 SerArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAsp 220   | Qy        |
|                    | QQ ·           |  | qq        |
| 500 ArgGinLeuThra  | δŌ             | 196 PheProThrIleSer 200  | QY        |
|                    | an (           | 610 GCGGGCGCGGGGGCAGCCCTCGTGGCCGCCACGTACACCGGTTACGGCAGCTCC 669   | qa        |
|                    | Š Š            | 181AspLysLeuPhelleAlaThrAlaValAspGlyLysProGluTyr 195   | Qy        |
|                    | an a           | 550 CTGAACGTGGCGGCCAACCACCGAACGCGTCCACCGTGGGGGCTAGTTCTGCCTCCCGCC 609   | qa        |
| 9 GinT             | δδ             | 170 PheGlyvalIlevalSerTyrSerAsnLeuAsp  | Qy        |
|                    | an i           | 490 GCCGTGCGCTTCCCGCCCCCCCCCCCCCGAGCCCGTCACGGTGTTCCCCAGCATG 549 .  | qa        |
| 449 GlyThrLysSerG  | δο             | 150 GlyGluProTyrHisLysLysCluHisTyrLeuSerGlyValAsnGluSerGlySerVal 169   | Qy        |
|                    | g<br>T         | 430 TGCGGGTCCATCTACCAGGGCTTCTGCCAGCTGCGGGGGTAACATCTCGGCCGTG 489  | qa        |
|                    | δo i           | 130 CysGlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAspLeuPheLysLeu 149   | Qy        |
|                    | gr é           | 370 CTCACGGACAACTACAACAAGATCCTGCAGCTGGACCCCGGCCAGGGCCTGGTAGTCGTG 429   | qa        |
|                    | Oy<br>10       | 110 ThrThrAsnAsnValAsnLysMetLeuLeuIleAspTyrLysGluAsnArgLeuIleAla 129   | Qy        |
|                    | QQ ·           | 310 GACAGCCCCTGTGTCACGCTCCGCAGCCTCGTGCGAGCACCCCGGGGCGC 369   | qa        |
|                    | δō i           | 91 AspAsnProLysCysTyrProProArglleValGlnThrCysAsnGluProLeuThr 109   | Qy        |
|                    | q <sub>O</sub> | 111:::       :::::    ::: 250 TATCAGCTGCGGGCCCAACCTGGAGGCCGAGGCGGCCGTGGGCCCGGTGGCCC 309  | qa        |
|                    | δy             | 72 TyrLysLeuSerSerAspLeuLysValLeuValThrHisGluThrGlyProAspGlu 90  | Qy        |
| m i                | qα             | 190 AACAACTTCGCCCTGGACGGCGGGGGGACGTGTACCTGGCGGCGGCGGCGTCAACGGCCTC 249  | QO        |
|                    | δλ             |  | Οy        |
|                    | qq             | 178 CCCACGCCACC 189  | qα        |
|                    | δŏ i           | 32 ProLeuSerGlnLysGlnArgSerPheValThrPheArgGlyGluProAlaGluGlyPhe 51   | Qy        |
|                    | <u>a</u>       | 118 CTGCTGCTGGGGGGGGGGGGGGGGGGGCGGGGATCCAGCGTCCGGTTCCCCTCG 177   | qa        |
|                    | δo d           | Ä-   | Qy        |
|                    | č              |  |           |

| Ωy             | 318         | AlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThr 337     :::      :::      CGCGGCGACCTCTACAGCCGCGGACCGCTCTTGCT 1122 |
|----------------|-------------|---|
| Qy<br>Db       | 338<br>1123 | tLysSerLeuAspGluSerAlaLeuCysIle 3 :::          GGCCGGGCTGCTCCGGCCGCACTCTGCGC 1  |
| Q <sub>V</sub> | 58          | nlleAsnAspArglleLysGluArgLeuGlnSerCysTyrArgGly 37<br>:::  |
| ٥y             | 378         | uAspLeuAlaTrpLeuLysValLysAspIlePro 3  |
| Db             | 1242        | G-ACGTGGTGCCGTGCTC  |
| Oy do          | 393         | CysSerSerAlaLeuLeuThrIleAspAspAsnPheCysGlyLeuAsp 408  |
| Oy             | 40          | JeuGlyvalSerAspMetValArgGlyIleProValPheThrGluAsp 428  |
| 9 2            | 1360        | . 14  |
| QD             |             |   |
| Qy             | 449         | 1 468   |
| QQ             | 1474        | GGCACGGTCAACGGGAGGCTTCTCAAGATCAACCTGAAC   |
| Oy<br>da       | 469         | GlnTyrGluThrValGlnValNalAsp   |
| 2              | 1 .         | מעמימנים מכנים מיום מעמיק שמפים ממנים מערים מיום מיום מיום מערים ביום מיום מיום מיום מיום מיום מיום מיום מ                      |
| Qy<br>Db       | 481         | ValLeuArgAspMetalaPheSerLysaspHisGluGlnLeuTyrIleMetSerGlu 499<br>   |
| Qy             | 500         | ArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCys 519  |
| qq             | 1627        | 16  |
| Οy             | 7           |   |
| QQ             | 1687        | GCAG 17   |
| Qy<br>Db       | 540         | GluArgCysGluArgSerLysGluProArgArgPheAlaSerGluMetLys 556 :::   |
| ٥y             | 55          | 1 575   |
| Dp             |             | 18  |
| QY             | 576         | LeuLeuValLeuGluThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThr 594   |
| QQ             | 1857        | 19  |
| Οy             | 5.9         | 10  |
| qq             | 1927        | ATGGGAACAACATCCGCACTGTGGCTCGGGTCCCAGGCCCTGCCTTTGGTCACCAGATT·19  |
| δy .           | 6.1         | <pre>LnCysTyrSerProAlaAlaLysGluValProArgIleIleThrGluAsnGlyAspHis 630 :::::</pre>  |
| QQ             | 1987        | CTACTGCAACCTCCTGCCGAGGGACCAGTTTCCGCCCTTCCCCCCCAACCAGGACCAC 20   |
| Qy             | 631         | isValValGlnLeuGlnLeuLys   |
| QQ             | 2047        | GTTGAGATGTCTGTGAGGGTCAATGGCGGAACATCGTCAAGGCC  |
| Qy             | 651         | PheValPheTyrAsnCysSer   |

| 9 6 9 6 9 6  | 6 6 6 6 6 6  | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6  | 4   | . 40 00 00 00 00 00 00 00 00 00 00 00 00                             |
|--|--|--|---|--|
| 101 TTCACCATCTACGACTGCACAGGTGTACCCCCACAGGCTGTACCAGC 2160 565 CysValGluSerProTyrargCysHisTrpCysLysTyrargHisValCysThrHisAsp 684 11: :: :: :: | 725 LysAsnLeuProGlnProGlnSerGlyGlnArgGlyTyrGluCysIleLeuAsnIleGln 744 | 2497 AAGGGGCGGCCGGATTCCTGGACCCTTGGGCCCATGACATCATGTCTATAAC 2556 804 CysClyAlaMetArgCluSerCysGlyLeuCysLeuLysAlaAspProAspPheAla 822 | 863 IleIleProValThrGlyProArgGluGlyGlyThrLysValThrIleArgGlyGluAsn 882  111 | 943 AlaArgSerSerGlnLeuTyTTyrPheWetThrLeuThrLeuSerAspLeuLysProSer 962 |
| 6 6 6 6 6  | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                | 90 A Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q   | 64 69 69 69 69 69 69 69 69 69 69 69 69 69                                 | 60 60 60 60 60 60 60 60 60 60 60 60 60 6                             |

| qc   | 3100 A | CCACCATCGCCTGCACCATGCCTGAGGGGGCCCCTGCCGGCTCCGGTGCCTGTG 3153                     |
|------|--------|---|
| λλ   | 1022 G | 03  |
| . qc | 3154 T | CATGCAG 321   |
| λy   | 1039 A | Proile 105  |
| qc   | 3214 A | SCGGTCATCACGGCCATCAGTCCCCGCCGCAGCCCTGTCAGTGGCGGCAGGAC                           |
| 2y   | 059    | AlavalTrpGlythrHisLeuAspLeulleGlnAsnProGlnIleArgAlaLysHisGly 1078               |
| gg   | 4/7    |   |
| λά   | 79     | GlyLysGluHisTleAsnIleCysGluVaLLeuAsnAlaThrGluMeTinCySGlnAta 1090<br>   -        |
| 3 6  | # 000  | GlyproAspHisGlnSerAspLeuThrGluArgProGluGluPhe 111                               |
| 2 g  | 30     |   |
| οy   | 1119 G | GlyPhelleLeuAspAsnValGlnSerLeuLeuIleLeuAsn 1132                                 |
| qq   | 3451 G | CAGACGAGGTGGCTGTGGCTGAGGAGCTACTGGACCCCGAGGAGGCACAGCGGGGCAGC 3510                |
|      | 1133 L | LysThrAsnPheThrTyrTyrProAsnProValPheGluAlaPheGlyProSerGlyIle 1152               |
| Db   | 3511 A | GETTCCGCCTGGACTACCTCCCCAACCCACTTCTACGGCCAAGAGGGAGAAGTGG 3570                    |
| Qy   | 1153 [ | 16  |
| qq   | 3571 P | ATCCACAGGAGCAGGACAGCCT  |
| QY   | 1170 F | oProValAlaGl  |
| Db   | 3631   |   |
| Qy   | 1190   | cValSerAspValGlnLeuLeuCysGluSerProAsn 120                                       |
| Db   | 3676   | GGGACATCCAGATTGTCTCTGACAGAATCATCCACTGCTCGGTCAACGAGTCCCTGGGC 37                  |
| QY   | 1206   | 2   |
| qq   | 3736 ( | ccc 379   |
| Qy   | 225    | roLeuSerLeuProAlaileValSerileAlaVal 124   |
| Db . | 3796 1 | GAGACGGCCATCATCGTGTCCATCGTCATC 384  |
| QY   | 1245 / | LeulleAlaTyrLysArgLysSer 126.   |
| Db   | 3847   | rscascsrcriscriscrererecersissescrsrrcsrteraccaasasc 3903                       |
| Qy   | 265    | 0 0   |
| Db   | 3904 ( | ATCTCAG 396   |
| QY   | 1285   | alAlaLeuGluCysLysGluAlaPheAlaGluLeuGlnThrAspIleHisGluLeuThr 130.<br>      ::::: |
| Db   | 3964   | cgagaggaaarccccaaaggcrifcgcrgagcragacagacagagagagagagagagagagaga                |
|      | 1305   | JeuaspGlyalaGlyIleProPheLeuaspTyrArgThrTyrThrMetArg 132:                        |
| Db   | 4024   | GCAGCCAGGCATCCCCTTCCTGGAGTATAAGCACTTCGTGACCCGC 408                              |
| ΟŶ   | 1324   | 1Leuphepro 132  |
| Db   | 4084   | 414   |
| Qy   | 1328   | Gly1leGluAspHisProValLeuArgAspLeuGlu 133<br>            :::                     |
| Db   | 4144   | CTCAACTCCCAGGGCAGCTCCCAGGCACAGGAAACCCACTGCTGGGAGAGTGGAAG 4203                   |

```
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations creaponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human cream of the produce data for this parent directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                      Claim 1; SEQ ID No 21008; 103pp; English
P-PSDB; ABG21017
                                                                                                                                      biodiversity
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Sequence 6561 BP; 1329 A; 2077 C; 2004 G; 1130 T; 21 other;

|  |                                      | 43   | 178   | 63   | 232  | 83   | 292   | 103  | 352  | 123   | 409   | 143  | 469   | 161  | 529  | 181  |
|--|--------------------------------------|--|---|--|--|--|-------|--|--|---|-------|--|---|--|--|--|
|  |                                      | rPhe   | CTIC  | sile   | GGTG   | lThr   | GCAG  | n-Th   | CCCA   | yrūy  | CTCC  | ArgL   | ၁၁၁၅  | Teus.  | GTGG   | AspA<br>   |
|  |                                      | ValTh  | GACTI   | GlyHi  | GGCGT  | LeuVa  | GAGCA | ValGl  | GCCAG  | eAspī   | CGACC | euLeu  | TGCGC   | isTyr  | CTTTC  | snLeu  |
|  |                                      | erPhe  | AGCTG   | rgThr  | CCTCA  | ysval  | AGCTG | rgile  | TCGAG  | Leuil   | CTGGT | sLysi  | CGCTC   | sGluE  | GAAGI  | rSerA  |
| 6561<br>644<br>345<br>725<br>271   |                                      | ThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPheValThrPhe | ACCCTGCTGGCCTGCTGGGCGCGCAGGTGCCAGCCTGAGGCCCCGCAAGCTGGACTTCTTC | ArgGlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThrGlyHisIle | CGCAGCGAGAAAGAGCTGAACCACCTGGCTGTGGATGAGGCCTCAGGCGTGGGT | TyrLeuGlyAlaValAsnArglleTyrLysLeuSerSerAspLeuLysValLeuValThr | GCTGC | HisGluThrGlyProAspGluAspAsnProLysCysTyrProProArglleValGln-Th | GTGGCCACGGGCCCTGGACAACAAGAGTGCACGCCGCCCATCGAGGCCAGCCCA | rCysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuleAspTyrLy 123 | TGCTG | sGluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIle-CysLysLeuLeuArgL | 410 CAGGAAACGCCTGGTGGAGTGCGGGCAGCTTCTTAAGGGCATCCTGCGCTCTGCGCGCCCC | LeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeuS | 470 TGAGCAACATCTCCCTCCGCCTGTTCTACGAGGACGGCAGCGGGGAGAAGTCTTTCGTGG | 161 erGlyValAsnGluSerGlySerValPheGlyVallleValSerTyrSerAsnLeuAspA ::: |
|  |                                      | Lysg]  | AGGCC   | ValAs  | GTGGA  | SerAs  | GCGAA | TYTPI  | ACGCC  | nLysk   | CCCAC | nGlyl  | GGGC?   | yrHis  | GCAGC  | leval  |
| :<br>s:<br>vativ<br>ches:  |                                      | erGln  | GCCTG   | euVal  | TGGCI  | euSer  | TGGAT | yscys  | AGTGC  | ValAs   | GTCAP | Tyrg]  | CTTA  | uProT  | GGACG  | yVal1  |
| Length: Matches: Conservative Mismatches: Indels: Gaps:                    | (1-6561)                             | oLeus  | TGCCA   | nHisL  | CCACC  | rLysL  | CCAGC | nProL  | CAAGA  | snAsn   | ACAAT | erLeu  | AGCTT   | GlyGl  | TACGA  | PheG1  |
| JECEHO   |                                      | AlaPr  | GCAGG   | Pheas  | CTGAA  | IleTy  | CTCTA | AspAs  | GACAA  | rThrA   | GACTG | sGlyS  | 29992   | ysLeu  | TGTTC  | erval  |
| 184<br>0   | \$8520                               | lnPro  | TGGGC   | luGly  | AAGAG  | snArg  | ATGCC | spGlu  | CCCTG  | ThrTh   | GAGAT | Alacy  | GAGTG   | uPheL  | ၁၁၅၁၁  | rGlys  |
| 3.97e-184<br>2357.50<br>49.858<br>32.468<br>23.608                         | x AA                                 | rArgG  | CCTGC   | oAlaG  | . W  | aValA  | GGTGA | YProA  | 99222  | roLeu   | GCT   | eulle  | TGGTG   | Le   | TCCCI  | Gluse  |
|  | 1896)                                | LeuTh  | CTGGG   | GluPr  | GAG  | GlyAl  | 29999 | Threl  | ACGGG  | nGluP   | TGAG- | nArgL  | ACGCC   | ds   | ACATO  | alAsn<br>:::   |
| s:<br>ity:<br>larit  | 3 (1-                                | hrLeu  | CCCTG   | rgGly  | GCAGC  | yrLeu  | ACCTG | isGlu  | TGGCC  | CysAs   | TGCCA | GluAs  | AGGAA   | euGluAsp                                       | GAGCA  | rGlyV  |
| Scores<br>milari<br>Simil<br>h:  | 956-1                                | 24 T   | 119 A   | 44 A   | 179 ¢  | 64 T   | 233 T | 84 н   | 293 G  | 103 r   | 353 G | 123 s  | 410 C   | 143 e  | 470 T  | 161 e<br>:   |
|  | US-09-964-956-13 (1-1896) x AAS85204 |  |   |  |  |  |       |  |  |   |       |  |   |  | •  |  |
| Alignment<br>Pred. No.<br>Score:<br>Percent Si<br>Best Local<br>Query Matc | 18-09                                | QY   | οgo   | οy   | QQ   | ٥ý   | q     | Qy   | Db   | ٥y  | QQ    | οy   | qq  | Οy   | QQ   | οy   |
| 7-5.2401   | _                                    | ~  |   | _  | _  | •  | _     | •  | _  | •   | _     | _  | _   | -  | _  | -  |

| . qa           | ñ           | NGCAATGATGAGGGCGTGGCCACAGTGGGGCTGGTGAGCTCCACGGGTCCTGGTGGTG 58   |
|----------------|-------------|---|
| Qy<br>Db       | 181<br>590  | <pre>spLysLeuPhelleAlaThrAlaValAsp61yLysProGluTyrPheProThrIleSerS 201   ::::::   :::::  </pre>  |
| Qy             | 201         | nrLysAsnSerGluAlaAspGlyMetP   |
| Db             | 650         | TCGCTGTTGGACCGGACTGACAGCAGGGCCTTTGAAGCCTACACGGACCACGCCA 70  |
| Qy<br>Db       | 221         | LuPheValAlaSerMetileLysileProSerAspThrPheThrIleIleProAspPheA 241  |
| oy (           | 4           | =TyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnP 26   |
| qq             |             |   |
| Qy             | 261         | oGluMetValSerProProGlySerThrThrLysGluGlnValTyrThrSer  |
| . qq           | 800         |   |
| Qy             | 281         |   |
| Dp             | 836         | GCATGTGCAGAAGACCCCAACTACTCCTACCTGGAGATGGACCTGCAGTGCC 8  |
| Qy             | 301         | TyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAl<br>      :::  |
| QQ             | 968         | 3CACGCCGCTGCCTTTGGCACCT 93  |
| Qy             | 321         | GlyValHisPro<br>GCTGCGCCTGGO  |
| : ;            |             | 26 100 10 10 10 10 10 10 10 10 10 10 10 10  |
| oy<br>oy       | 34 L<br>992 | Lyshig LysmerLysserreunsboluserhalaeurysiternelieleur 3<br>:::  |
| Qy             | 361         | 3lnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGl   |
| qq             | 4           | CCTGTTACACAGGCACCC 1  |
| Qy             | 381         | spLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaL 39  |
| qq             | 0           | GACATCTTCTACAAGCCCTTCCACGGCGATATCCAGTGCGGCGGCCACG 11  |
| Qy             | 397         | In the constant of the control of |
| Db             | 1160        | TICCCAIGIGGTCGGAGCACCTGCCCTACCGGCTGGGCA 12  |
| Qy             |             | <pre>spMetValargGly1leProValPheThrGluAspArgAspArgMetThrSerV 43     </pre>   |
| Db             | 1220        | CGCGACGGCTCAGAGGCACAGCCGTGCTGCAGGCGTGAGGCCTGAACCTCACGGCCG 1   |
| Qy             | 435         | erLeuAlaPheValGlyThrLysSerGlyLysL 45  |
| q <sub>Q</sub> | 1280        | GACGGTCGCCGCGAGAACAACCACTGTTGCTTTTCTGGGCACCTCTGATGGCCGGA 13   |
| Qy             | 455         | rgGlyAsnAlaLeuGlnTyrGl  |
| Db             | 1340        | ccrcaaggrgraccrcaccccagarggcaccrccagagracgacrcrarg 13   |
| Qy             | 475         | euT 49  |
| Dp             | 1397        | GGAGATAAACAAGAGGGCACCTGGTACTGTCTGGAGACCTGGGCAGCCTGT 14  |
| Qy             | 495         | yrileMetSerGluArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnS 515  |
| Dβ             |             | GCCATGACCCAGGACAAGGTGTTCCGGCTGCGGGTGCAGGAGTGCCTGAGCTACCCGA 151  |
| Oy<br>S        |             | ω r   |
| QQ             |             | CTGCACCCAGTGCCGCGACTCCCAGGACCCCTACTGCGGCTGGTGCGTCGTCGAGGGAC 15/   |

| 871 luGlyGlyThrLysValThrIleargG<br>        :::::        <br>2543 GTGGGGCATCCGCATCACCATCGTGG | 891 laSerHisValLysValAlaGlyValG:::               | 911 laGluGlnTleValCysGluMetGlyG<br>:: ::         <br>2660 CCACCGGATCGTGTGTGTGATCG | -  | 947GlnLeuTyrTyrPheMetThrLeuT<br>   <br>2759 TCCAGTTCACCTTCCAACAGCCCAAGC |   | 986 alValMetPheGlyLysGlnProCysL<br>   <br>2876 ACGTG  | 1006 ysAsnThrThrSerSerAspGluValL<br>  | 1026 laLysile   |  | 1054 lyAsnThrProIleAlaValTrpGlyT<br>                                       | 1074 rgAlaLysHisGlyGlyLysGluHisI<br>3145   | 1094 etThrCysGlnAlaP 3179 cGCCGCGGGGGCTGATCCCTGCAGC   | 1108G   | 1119 lyPheIleLeuAspA<br>:::   <br>3299 ACCTCACGGTGCTGATCGAGATGGACG | 1135 snPheThrTyrTyrProAsnProValP<br>                    3359 CCTTCGAGTACGTGCCTGACCCACCT                | . 1155 euLysProGlyThrProlleIleLeuL<br>      ::  <br>  3397ACAGGTGGCGTCAAGA | 1175 lyAsnValLysLeuAsnTyrThrVal-<br>   :::<br>3446 CCAATCTGAACAAGGCGATGACGCTGC | 1190 ysThrValThrValSerAspValG |
|---|--|---|--|---|---|---|---|---|--|--|--|---|---|--|--|--|--|-------------------------------|
| Qy  | Qy<br>Db   | Q Q   | Qy   | Qy  | Oy<br>OD  | Qy  | Qy  | Qy  | Oy   | Qy   | Qy<br>Dp   | Qy<br>Db  | Qy  | Qy   | Qy   | qa   | qa .   | Οy                            |
| 535 hrCysThrArgLysGluArgCysGluArgSerLysGluProArgArgPheAlaSerG 554                           | Db 1577 GATGCACCGGGAAGGCCGAGGGCCGAGGGCCAGCCAGCCA | 572 InTyrAsnValLeuLeuValLeuGluThrTyrAsnValProGluLeuSerAlaG                        | Oy 590 lyvalAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnI 610 :::              :: Db 1751 AGTTGCTGTGCCTTTTGGGGAGTCGCCGCCACACCCCGCCGTGGAGGCGAGGCCG 1810 | Oy 610 leGlnCysTyrSerProAlaAlaLysCluValProArgileIleThrCluAsnGlyA 629 :: | InLeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerT ::: | . Qy 649 hrSerPheValPheTyrAsnCySerValHisAsnSerCysL 663 :::      :::    Db 1919 ACCAGTACCCCTTCTACGACGCCAGGCCATGACCTGGAGGAGAACCTGCCGTGCA 1978 | Qy 663 euSerCysValGluSerProTyrArgCysHisTrpCysLysTyrArgHisValCysThrH 683 ::             ::: :: | 683 isAspProLysThrCysSerPheGlnGluGlyArgValLysLeuProGluA | 700 spcysprodinceuleuArgValAspLyslleLeuValFroValGluValIleLysProd | Oy 720 leThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyGlnArgGlyTyrGluCysI 740 :: | Oy 740 leLeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArgPheAsnSerS 758 ::::::       ::: | 758 erSerValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGlulleAsnAsn 2231 CGGTGACCATGCAGGAATCTGGGACCTTCGCCTTTCGCACCCAAAGGTGTCCCACGATG | Qy 777LeuprovalGluLeuThrValValTrpAsnGlyHisPheAsnIleAspa 793 |  | 811 ysGlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGlnGlyProGlyG 1   1   1   1   1   1   1   1   1   1 |  | 851 laLysSerLysCysThrAsnProArgileThrGluileileProValThrGlyProArgG               |                               |

| λ           | 871  | eArgAspileA 89  |
|-------------|------|---|
| Ф           | 2543 | SGGGCATCCGCATCACCATCTGGGGTCCAATTTGGGCGTCCAAGCAGGGGACAT  |
| γ           | 891  | laSerHisValLysValAlaGlyValGluCysSerProLeuValAspGlyTyrIleProA 911                                  |
| Q           | 2602 | -CAGAGGATCTCTGTGGCCGGCCGGAACTGCTCTTTCAGCCGGAACGTTACTCCGT  |
| ¥           | Ç.1  | uGlnileValCysGluMetGlyGluAlaLysProSerGlnHisAlaGlyPheValG       931         :::                ::: |
| Ω           | 09   | CGTGTGTGTGTGTCGAGGCTGCGGAGACGCCTTTCACGGGGGGTGTCG 27   |
| <b>&gt;</b> | 931  | oGluPhe 946<br>     :::   |
| Д           | 17   | :TTCGGGAAACTGGGCCGTTCGCCTCCCAATG 27   |
| X           | 4    | -GlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSerArgGlyProM 966                                   |
| q           | 2759 | CAGTTCACCTTCCAACAGCCCAAGCCTCTCAGTGTGGAGCCGCAGCAGGACC  |
| X.          | 95   | erGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAlaGlySerAsnValV 986<br>::           :::                 |
| q           | 2816 | ວອອອວອ  |
| λ           | 85   | ValMetPheGlyLysGlnProCysLeuPheHisArgArgSerProSerTyrIleValC 100<br>    ::: :::                     |
| Q           | 2876 | 3CGGGTGACCCTCAACGCCGTCC   |
| γ           | 1006 | AsnThrThrSerSerAspGluValLeuGluMe  |
| Q           | 2906 | rccastrateactescececasses   |
| γ           | 1026 | LysIleHisGlnAspLeuVal   |
| Q           | 2966 |   |
| Ā           | 034  | ValSerG 105   |
| Q           | 3026 | <pre>2TACCGCGAAAACCCCGTACTGCGAGCCTTCGAGCCGCTACGAGGTTTGCCAGT</pre>                                 |
| λ           | 1054 | AsnThr  |
| Д           | 3086 | <br>TGGCCGCAGCATCAACGTCACGGGTCAGGGCTTCAGCCTGATCCAGAGGTTTGCCAT                                     |
|             | 1074 | gAlaLysHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluM 10<br>:::            :: ::            |
| Q           | 3145 | GTGGTCATCGCGGAGCCCCTGCAGTC  |
|             | 1094 | 31nAla  |
| Q           | 3179 | GCCGCGGGAGCTGAATCCCTGCAGCCCATGACGGTGGTGGG   |
| γ           | 1108 | GlnSerAspLeuThrGluArgProGluGluPheG 1119   |
| Q           | 3239 | ACAATGACACCAAGGTCGTCTTCCTGTCCCCGGCTGTGCCTGAGGAGCCAGAGGCCTACA 3298                                 |
| γ           | 1119 | lyPheIle  |
| ą           | 3299 | ACCTCACGGTGCTGATCGAGATGGACGGCACCGTGCCCTGCTCAGAACAGAGGCCGGGG 3358                                  |
| Ϋ́          | 1135 | snPheThrTyrTyrProAsnProValPheGluAlaPheGlyProSerGlyIleLeuGluL 1155                                 |
| Ω           | 3359 | CCTTCGAGTACGTGCCTGACCCCCACCTTTGAGAACTTC3396   |
| γ           | 1155 | uLysProGlyThrProlleIleLeul  |
| Q           | 3397 | gcaggtcaacarctcaccggggg 3   |
| γ           | 1175 | AsnVal  |
| Q           | 3446 | AATCTGAACAAGGCGATGACGCTGCAGGAGGCCGAGGCCTTCGTGGGTGCCGAGCGCT 35                                     |
| Y           | 1190 | ysThrValThrValSerAspValGlnLeuLeuCysGluSerProAsnLeuIleGly- 1208                                    |

| 4559 CCATCT<br>1544 isArgP<br>4619 GCTGGC<br>1564 leLeu6<br>11111<br>4676 TCCTGT<br>1584 euAlaH<br>1736 TTATGC | 1604 laTyrA<br>4777<br>1624 etileA<br>4798<br>1642 hrProA<br>162 spG1n1<br>1662 spG1n1<br>1662 spG1n1<br>1662 spG1n1<br>1663 spG1n1<br>1664 pgG1<br>1665 liliii | 4960 AGATCH 1695 Leuphe 5020 TTCTTC 1715 TYPMET 5071 TACTTC 1735 ATGH15 5131 ATCCACA 1755 ProG11 5191 CCCCACA |   |
|--|---|---|---|
| 9  | 64 65 65 65 65 65 65 65 65 65 65 65 65 65   | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0   |   |
| GCACCATGAAGACGCTGACGGAACGACCTGTGAGCCCCCGGAAGTTGCAGCCC  | 3686 TGCGGCTCAGCTCCTCTTGCCGCTGGTCATC  | TCCAAGGACGCGACAGGACGTGATCACCGGCAAGCTGGACATCCCTGAGCCGCGGGGGGGG   | 4205 CATGCACACGTCTTCCTGGAGCACTAGGTGGTGGTGTGTTTTTTTT |
| 8 6 8 8 6  |   |   |   |

| 45   | 59 CCAICIC                           | CCAGGTCAAGGAGAAGATCATTGACCAGGTGTACCGTGGGCAGCCCTGCTCCT 461:  |
|------|--------------------------------------|---|
| 2    | 4 isAr                               | DLysalaalaaspMetAspLeuGluTrpArgGlnGlySerGlyAlaArgMetI 156          :::                                |
| ف    | 9 6016600                            | CAGGCCAGACAGCGTGCTGGAGTGGCGTCCGGGCTCCACAGCGCAGA 467   |
| 15.  | 64 leLeuGl<br>      <br>76 TCCTGTC   | nAspGluAspIleThrThrLysIleGluAsnAspTr<br>  |
| 151  | 84 euAlaHi:<br>     <br>36 TTATGCA   | sTyrGlnValProAspGlySerV<br>                :::<br>CTACAATGTCCGGGATGGAGCCA                             |
|      | 1. A                                 | nalaValAsnAsnSerThrValSerArgThrSerAlaSerLysTyrGluAsnM 1.  |
|      | 4 etileA<br>8                        | JTyrThrGlySerProAspSerLeuArgSerArgThrProMet11eT   |
|      | ProAs<br>    <br> CCCTC              | July SerGlyValLysMetTrpHisLeuValLysAsnHisGluHisGlyA       16  |
| 16   | 62 spglnLy<br>  :::<br>00 ACGAGGG    | LysMetValserG<br>    ::::: <br> AAGGCCATCACCG   |
| 16   | 75 lulleTy<br>         <br>  AGATCTA | rLeuThrArgLeuLeuAlaThr-LysGlyThrLeuGlnLysPheValAspAsp 169<br>                   :::::                 |
| 16   | 95 LeuPhed<br>   :<br>20 TTCTTCC     | SluthrilePheSerthralaHisArgGlySerAlaLeuProLeuAlaileLys 1  |
| 17   | r Ke                                 | PheAspPheLeuAspG]<br>   |
| 17   | 35 ArgHisT<br>   <br>31 ATCCACA      | thrTrpLysSerAsnCysLeuProLeuArgPheTrpVe<br>        ::   <br>  httgGaAGAGGAACAGCTTACCGCTCCGGTTCTGGG     |
| 17   | 55 ProglnF<br>     <br>91 CCCCACT    | nPheValPheAspileHis-LysAsnSerIleThrAspAlaCysLeuSerValVa 1774<br>   :::       :::    :::               |
| 17   | ag – 20                              | rcysSerThrSerGluHisArgLeuGlyLysAspSerPr 179.<br>    :::::   |
| . 53 | 94 oSerAsr<br>        <br>11 CAGCAAC | SerTyrLys<br>:::       <br>ACCTACAAG  |
| 18   | 14 yr-Tyr<br>         7<br>71 ACTTAC | etProAlaIleSerAspGln-Asp-MetAsnAlaTyr 18<br>  |
| 18   | 33 LeuAla<br>    <br>31 CTTGGC       | GlnSerArgMetHisMetAsn(<br>   <br>GATTTCCCGGGCGGCACACGGACT   |
| 18   | 52 GluilePl<br>::::::<br>91 CAGCTCTA | neSerTyrValGlyLysTyrSerGluGluIleLeuGlyProLeuAspHisAsp 1   |
| 18   | 72 AspGln<br>51 CCTGCC               | sGlyLysGlnLys-LeuAlaTyrLysLeuGluGlnVa<br>    :::      ::::   :::<br>:CAGAAGATGCAGCTTGGCCTTCCGCCTGCAGT |

64

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180 AspAspLysLeuPheIleAlaThrAlaValAspGlyLys---ProGluTyrPheProThr 198
                                                                                                                                                                                                                                                              TCCGCACCTAATACCACTCTCAACCACTTGGCACTGGCACCTGGCCGAGGCACACTTT11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 AsnGluProLeuThrThrAsnAsnValAsnLysMetLeuLeuIleAspTyrLysGlu 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --LeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeu 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 SerGlyValAsnGluSerGly---SerValPheGlyValIleValSerTyrSerAsnLeu 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               436 GTGGCTGCCAATACCCCGGGAGTGGCAACGGTGGGGCTGGTGGTGCCCTTGCCCGGC--- 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493 CGGGACCTCCTGCTFGTGGCCAGAGGCCTGGCGGGCAAGCTGTCGGCAGGGGTGCCACCC 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysAlaClyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPhe 336
                                                                                                                            LeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPheValThrPheArg 44
                                                                                                                                                                                                                                                                                                                                                          CAGGAGCTGGTGGCCTGCGGGCAGGTGCGGCGTGTGTGAGACACGGCGCCTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 GTCACTGGCCCTGTAATCGACAGCCCTGACTGCGTGCCCTTCCGTGACCGAGCCGAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 CCACAG---GCCCAGCTCACTGACAATGCCAACCAGCTGCTGCTGGTGAGCAGCCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 IleSerSerArgLysLeuThrLysAsnSer-----GluAlaAspGlyMetPheAlaTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 CTGGCCATCCGCCAGCTGGCCGGGTCTCAGCCCTTCTCCCAGCGAGGGCCTGGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTCCGACTACAACAGCTACGTCGGGGCCTTTGCCGACGCCCGCTCCGCCTACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuThrLeuGlnProGluMetValSerProProGlySerThrLysGluGlnValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 ThrSerLysLeuValArgLeuCysLysGluAspThrAlaPheAsnSerTyrValGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProlleGlyCysGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSer
                                                                                                                                                                                                                           GlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThrGlyHisIleTyr
                                                                                                                                                                                                                                                                                                                                LeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysValLeuValThrHis
                                                                                                                                                                                                                                                                                                                                                                                                                                  85 GluThrGlyProAspGluAspAsnProLysCysTyrProProArgIleValGlnThrCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValPheHisAspGluPheValAlaSerMetIleLysIleProSerAspThrPheThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 IleProAspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          613 GTGGTGGCGAC------
                                                                                                                                                                         43 CTGCTGTCCCCACCGCCACTGCCCTTGACAGGGGCCCATCGCTTC-
597
  Indels:
                                                                          US-09-964-956-13 (1-1896) x AAS00021
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                                                                                                                                                                                                                                                                      Human; Plexin-B3; semaphorin domain; hyperplasia; neoplasia; cancer;
neurodegenerative disease; autoimmune disease; lupus; multiple sclerosis;
inflammatory bowel disease; diabetes type I; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins whose extracellular domain shares homology with Scatter factor receptors and contain an approximately 500 amino acid Semaphorin domain. The plexin polynucleotides and polypeptides, and plexin-specific binding agents are useful in diagnosis, therapy and in the biopharmaceutical fludustry. In particular, the plexin polynucleotides and polypeptides are useful for generating compounds (e.g. plexin-specific binding agents on antibodies) for treating or diagnosing a disease or disorder involving neurodegenerative disease), or diseases or disorders involving aberrant fumune regulation (e.g. hyperplasia, neoplasia, neoplasia, inflammatory bowel disease or biabetes Type I), or immunosuppressive diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence encodes Human Plexin-B3. Plexins are large transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New plexin polynucleotides and polypeptides, useful in diagnosis, therapy and in producing compounds for treating diseases involving aberrant cell growth (e.g. cancer) or immune regulation (e.g. autoimmune diseases)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tesier-Lavigne M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 919 A; 1834 C; 1708 G; 906 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bowel disease or Diabètes Type I), or immur
multiple sclerosis or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
/label= "Mature Plexin-B3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "Plexin-B3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 56-58; 79pp; English.
                                                                       AAS00021 standard; cDNA; 5367 BP
                                                                                                                                                                                                                         Human cDNA encoding Plexin-B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.46e-142
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CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                        immunogen; antibody; ss.
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Tamagnone L;
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Pred. No.:
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                     RESULT 13
AASO0021
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684

296

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Length: Matches: Conservative: Mismatches:

Percent Similarity: Best Local Similarity:

ThrValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCys

| Οy         | IlePheIleLeuLysGln1leAsnAspArgIleLysGluArgLeuGlnSerCysTyr 3  | qa     | 1815                       |
|------------|--|--------|----------------------------|
| qq         | GCCTTCCCCATGGTGGAGCTGGGTGCCAGCATGGAGCCCCGGAGGCTCTGCTACACG  | Qy     | 710 IleLeuValPro           |
| Οy         |  | qa     | :::<br>1816GTCCAGGCC       |
| අධ         | GCGGGCGGCCGCCCCAGCGGCGCAGAAGCCACCGTGGAGTACGGCGTCACGTCG   | QY     | 730 ProglnSerGly           |
| δλ.        | ValLysAspIleProCysSerSerAlaLeuLeuThrIleAspAspAspAsnPheCysGLY   | qa     | 1849 CCCCAGGCCTG           |
| q<br>Q     |  | QY     | 750 ValProAla              |
| οy         |  | Db     | 1909 CIGCCGGCCACC          |
| ପୁ         | GACGAGCACACCCCCAGCCCCCATTGCTGGCCGCCAGCCCCTGGAGGTCCAGCCTCTGCTG  | δλ     | 766 SerTyrSerTyr           |
| δλ         | ArgGlylleProvalPheThrGluAspArgAspArgMetThrSerValIleAlaTyr 438  | qa     | 1963                       |
| qa         | AAGCTCGGGCAGCCGGTCAGCGCCGTGGCAGCTCTC   | QY     | 786 AsnGlyHisPhe           |
| ολ         | ValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLye  | Dp     | 2005 GGTGAAGCCCAC          |
| අධ .       |  | QY     | 795                        |
| δ t        | 459 ArgyalAspelyProArgelyAsnAraLedentHiyreLuinrvaleinvalvalAspelo 470  | qq     | 2065 GCAGGCGGGC            |
| a d        | TITUICCACGCICCCAGGCCCAGGGIIIACCACICCCAGGCAAGGGGCCCCCCAAGGGGGCCCCCCAAGGGGGG   | QY     | 799 -ValHisLeuTy           |
| λ <i>Έ</i> | 4/9 GIYELOVALLEUNAIG***ASDWELALGENESELDYSASPALGENINGULY-LIEWEC 49/<br>   | Db     | 2125 AGTGATCCTGT           |
| 3 8        | 1001 01 00 00 00 00 00 00 00 00 00 00 00   | Qy     | 818 pProAspPheA]<br>:      |
| ć d        | 490 SELGIULIGONILIEGIIII ALGAMININA MARTINA MA | qa     | 2185 CAGGAGCCTGG           |
| ò          |  | δδ     | 824                        |
| 3 dd       | AGGGCCTCCAGGCCCAGGACCCGCTGTGTGCTGCTGTGTCCTCCAGGGCAGGTGTACC   | . qa   |                            |
| ž ô        | ArgLysGluArgCysGluArgSerLysGluProArgArgPheAlaSerGlu  | Qy     | sProAl<br>                 |
| qq         | :::         ::: :::  | QD ::0 |                            |
| Οy         | 555 MetLysGlnCysValArgLeuThrValHisProAsnAsnIleSer 569  | Š d    | Salo OALGILLES             |
| qq         | 1510 GACAGCCACGTGCCACATCCAGAGCCTGCTGCCGGCCACCACCCCGCCAG 1563   | 2 6    | 4                          |
| θŷ         | 570 ValSerGlnTyrAsnValLeuLeuValLeuGluThrTyrAsnValProGluLeuSerAla 589   | Z d    |                            |
| qq         | 1564GAGCAGGCCAGGTCACTTTGTCTGTCCCCGGCTGCCCATCCTGGATGCAGATGAA 1620   | ΔO     |                            |
| Οy         | 590 GlyValAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGln 609   | 7x dd  |                            |
| QQ         | 1621 TACTICCATIGLEGGITCGGGGACTATGACAGCTIGGCTCATGTGGAAGGCCCCAC 1677   | λŎ     | 918 tGlyGluAlaL            |
| Qy         | 610 IleGlnCysTyrSerProAlaalaLysGluValProArgIleIleThrGluAsnGlyAsp 629   | 7 dd   | 1 1                        |
| qα         | 1678 GTGGCCTGTGTCACCCCTCCCCAAGACCAGGTGCCACTTAACCCTCCAGGCACAGAC 1734  | }      | 938 aProGluPheM            |
| Qy         | 630 HisHisValValGlnLeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThr 649   | G dd   |                            |
| qa         | 1735 CACGICACTGICCCCTGGCCCTGATGITCGAGGACGIGACTGGCTGCCACC 1788  | 2 2    | 958 of a spread of spreads |
| οy         | 650 SerPheValPheTyrAsnCysSerValHisAsnSerCysLeuSerCysValGluSerPro 669   | ୍ଷ ପ୍ର |                            |
| qq         | 1789 AACTICICCTITIAIGACIGCAGIGCC   | ^O     | 978 nLeuAsnAlaG            |
| Qy         | 670 TyrargCysHisTrpCysLysTyrArgHisValCysThrHisAspProLysThrCysSer 689   | qq     |                            |
| qa         | 1815 1815  | Qy     | 995LeupheH                 |
| Qy         | 690 PheGinGluGlyArgValLysLeuProGluAspCysProGlnLeuLeuArgValAspLys 709   | _      | =                          |

|     | 1815        | 181  | 815       |
|-----|-------------|--|-----------|
|     | 710         | rovalgluvallleLysProlleThrLeuLysAlaLysAsnLeuProGln 72                                  | 58        |
|     | 1816        | :::<br>GTCCAGGCCTTGGAGGCGGCTGCCCCGTCCTT  | 848       |
|     | 730         | ProgliserglyglnargglyTyrgluCysileLeuAsnileglnGlySerGluGlnArg 749<br>         :::       | 49        |
|     | 200         | alProAlaLeuArgPheAsnSerSerValGlnCysGlnAsnThr 76 :::          ######################### | 65<br>962 |
|     | 992         | rTyrSerTyrGluGlyMetGluIleAsnAsnLeuProValGluLeuThrValValTrp 78                          | S         |
|     | 1963        | <br> CCCAGTGCCCATCTACGTCACCCAG 20  | 004       |
|     | 786         | Interpretation   | 4         |
|     | 50          | 9666466646 20  | *<br>00 6 |
|     |             | GGTGGGTGGCAGACAGGAGGCCTCAGCACACACTGACCCTCCCT   | ١ -       |
|     | 199         | euLysAlaAs 81  | 18        |
|     | 2125        | SATCCTGTACGACTGCGCCATGGGCCACCCGGACTGCAGCCACTGCCAAGCGGCCAA 21                           | _         |
|     | 81          | DASpPheAlaCys82  | 23        |
|     | 2185        | AGAGCCTGGGCTGCCTGTGACCAGCCCTGCCCCAGGCCCCCAAACCCCAGGCTGCGG ZZ                           | N         |
|     |             | GlyTrpCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCy 83  |           |
|     | 7 4         | Prvalacing in Cinternal of troited in Leuser (1 vA la Lus Ser Lus Cost hir Asn Pr 85   | 58        |
|     | 00          | AGAGT-GGAGGGGGGGCACCCATCTGCCATCATTGC 23  | 3         |
|     | 858         | OARGILETHRGLUIJEILEProValThrGlyProArgGluGlyGlyThrLysValThrIl 878 ::::::::::            | 178       |
|     | 1 (         | 0.0 [] = [   | 0         |
|     | 878<br>2385 | 24   | y 4.      |
|     | 898         | 1GluCysSerProLeuValAspGlyTyrIleProAlaGluGlnIleValCysGluMe 91                           | 118       |
| _   | 2421        | 24   | 421       |
|     | 91          | GlyGluAlaLysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysAr 93                         | 38        |
| _   | 2422        | CAGTACGCCGACCTGTC  | 7         |
|     | 93          | ProGluPheMetAlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAs 95                         | 58        |
| 0   | 2440        | CTGCTGAG 24  | ₹.        |
| S 0 | 958         | PLEULYSPROSERAGGLYPROMETSERGLYGLYTHIGLINVALTHRILETHIGLYTHIAS 97.                       |           |
| _   | 978         | ASNAlaGlySerAsnValValValMetPheGlyLysGlnProC  |           |
| . 0 | 0           |  |           |
| _   | 366         | LeuPheHisArgArgSerProSerTyrlleValCysAsnThrThrSerSerAspGl 10                            | 1013      |
|     |             |  |           |

| QY 1342 yTyrArgGlnGluArgValGluLy Db 3606 GGAGGACGCCACTGTGCCACTGTGCGCCC QY 1360 nAsnLysValPheLeuLeuSerPheIleAr Db 3666 CAGCAACCTCTTCCTCCTCACGGTGAC QY 1380 tArgAspArgGlyAsnValAlaScrLeuI Db 3714 QY 1400 rAlaThrAspValLeuLysGlnLeuLeuAl Db 3715 | Qy         1420 sAsnHisProLysLeuLeuLeuh           Db         3738 GAACTACTGGCCTGAGACAAAGGTGGGGG           Qy         1438 uThrAsnTrpPheThrPheLeuLeuTyrL           Db         3798 CACCAACTGGCTGTCCATCTGCTGTAGG           Qy         1458 uPheSerLeuPheCysAlaIleLysGlnG           Inii         IIII           Db         3358 GTACTGCTTCTGCGCCATCTGTAGG           Qy         1478 rGlyGluAlaArgTyrSerLeuSerGluA           Qy         1478 rGlyGluAlaArgTyrSerLeuSerGluA           II         IIII           IIII         IIII           IIII         IIII           II         AGGCAAGGCCAAACGGACCTGAATGATAC           Qy         1498 sThrLeuValleuSerCysVal           II         III           II         II           II         II           II         II           II         II           II         II           II         II           II         II           II         II           II         II           II         II           II         II           II         II           II         II           II         II | 4038<br>1531<br>4098<br>1551<br>4158<br>1571<br>1571<br>1591 | 4222<br>1631<br>4233<br>1650<br>4293<br>1663  |
|--|---|--|---|
| 2568 GCGACTGATCCGTGTCAGGGCCACGGCCTAGACGTGGTGCAGCGGCCCCTACTGTCTGT   | yGlyLysGluHislleAsnIleCysGluValLeuAsnAlaThrGluMetThrCysGlnAl  | aGlyGlyAsnValLysLeuAsnTyrThrValLeuValGlyGluLysProCysThrVal-  | 1262 glysserkrgGluserAspleuThrLeuuysArgLeuGluMetGlnMetGspAsnleuGl 1282 1366 CAAGAGCAGCCCTGCGGGACTACCGGAGGTGCTAGTGCAGCTGGAGGGCTGGGAGGAGCCTGATGACGGAGGATGACCGAGGGGAGCCGCGAGGGGAGGAGGAGCCTGAGGAGGAGCCGCAAGGGGTTGCCAAGGACTCATGACGCAGCACCTACCGGAGGGCAGCGGAGGGAG |
|  |   |  |   |

| j                 |              | ,   |
|-------------------|--------------|---|
| ξ, q              | 3606         | YTYFArgganGineluargValciuLySciyLeuLysLeuPheAlaGinLeulicAs 1360<br>  |
| λ                 | 1360         | 138   |
| q                 | 3666         |   |
| λλ                | 1380         | rgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLeuGluT   |
| q                 | 3714         | 3714  |
| ·λζ               | 1400         | aThrAspValLeuLy   |
| q                 | 3715         |   |
| · Κα              | 420          | 43  |
| q                 | 738          | 379   |
| <i>≿</i> ;        | 438          | 45  |
| g.                | 86/          | 385   |
| ≿ 4               | 1458<br>3358 | UPheserLeuPheCysAlalleLysGlnGlnMetGluLysGlyProlleAspAlalleTh 1478<br>   |
| } ;               | 2 6          | 1 0   |
| <sup>2</sup> − 20 |              |   |
| λ                 | 198          | 151   |
| q                 | 78           | 03  |
| ٨                 | 1511         | nSerProGluValProValLysIleLeuAsnCysAspThrIleThrGlnValLysGluLy 1531   |
| q                 | 4038         | 0   |
| λλ                | 1531         | rHisArgPr   |
| q                 | 4098         |   |
| λy                | 1551         | MetileLeuGlnAs  |
| q                 | 41.58        | ပ္  |
| λy                | 1571         | LeuAsnThrLeuAlaHisTyrGlr  |
| q                 | 41.83        |   |
| . YS              | 1591         | lThrAlaTyrAsnAlaValA  |
| q                 | 4197         |   |
| λλ                | 1611         | JASnMetIleA   |
| qc                | 4222         | CTGGAGCCCC 4232   |
| λλ                | 1631         | oAspSerLeuArgSerArgThrProMetIleThrProAspLeuGluSerGlyValLy 1650  |
| qç                | 4233         |   |
| λλ                | 1650         | SMetTrpHisLeuValLysAsnHisGluHisGlyAsp1662   |
| q                 | 4293         | CCTCTGGCACCTGGTGAAAGCCACCGAGGAGCCAAGGGGCCAAGGTGCGGTGCAGGAGGAGGAGGGCCAAGGTGCAGGAGGAGGAGGGGCCAAGGTGCAGGAGGAGGGGCCAAGGTGCGGTGCAGGAGGAGGGGCCAAGGTGCGGTGCAGGAGGAGGGGCCAAGGTGCGGTGCAGGAGGAGGGGCCAAGGTGCAGGAGGAGGGGCCAAGGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG |
| λy                | 1663         | GlnLysGluGlyAspArgGlySerLysMetValSerGluIleTyrLeuThrAr 1680  |
| q                 | 4353         | CCTGCGGGAGCGCGAGCAGCAAGGCGCCAAGGCCATTCCGGAAATCTACCTCACCG 4409   |

cell proliferation; cell differentiation; growth factor; squlation; tissue growth; immunomodulator; activin;

cytokine;

haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;

myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial isohaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiniflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antiflungal; vulnerary; antiulcer; ss.

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                   nLysLeuLeuTyrAlaLysAspIleProSerTyrLysAsnTrpValGluArgTyrTyrSe
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                                                                                                                                                                     TGTGGACGACGTTCCAGGCCATTCTCAGGGTG------AACCGGCCCATCCCCAT
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                                                                                                -----AlaThrLysGlyThrLeuGlnLysPh
                                                                                                                       4530 CCACACCCTGCCCTCCACACACCCTTATCCCCTGCCTCGCAGGCACGCTGCTGCAGAAGTT
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Tang YT, Liu C, Drmanac RT;

(HYSE-) HYSEQ INC

2000US-0496914. 2000US-0560875.

03-FEB-2000; 27-APR-2000;

05-FEB-2001; 2001WO-US03800.

WO200157188-A2

09-AUG-2001

Homo sapiens.

P-PSDB; ABB11753.

P-PSDB; ABB11753.

Treating or ameliorating a medical condition in a mammalian subject treating or ameliorating a medical condition in a mammalian subject treating or ameliorating a medical condition in a mammalian subject are grant and cancer — the sequences ABB10991-ABB1230 represent 1350 novel human polypeptides, and sequences ABB10991-ABB1230 represent 1350 novel human polypeptides, and sequences ABB10991-ABB1230 represent 1350 novel human polypeptides, and recorded a invention also relates to vectors and recombinant bost cells comprising a invention also relates to vectors and recombinant bost cells comprising a invention also relates to be purposed to the invention. Although novel, many of the nucleotides of the invention have homology to known proteins, thereby gyving an insight into their probable biological activities, and hence to polypeptides of the invention have homology to known proteins, thereby gyving an insight into their probable biological activities, and hence to polypeptides of the invention may have arious activities; including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; daranatopolates of cultivity; activity; tissue growth activity; daranatopolatic or themanianetic activities; has memorably activity; tissue growth activity; cemorated activities; neglected or thromboly or thromboly or thromboly or thromboly or thromboly or thromboly or thromboly or thromboly or thromboly or thromboly or the invention are useful for preventing, treating or maniparial or properties or gene therapy. Such conditions includes or pepending on their biological activities; promple or language or submatography, abore to growth, bolypeptides and nucleotides or pepending on their biological activities; promple or submatography, abore to growth, bolypeptides and nucleotides involved with tissue regeneration or metal growth. Polypeptides with growth factor activity may be used to promote vell growth. For example, such polypeptides with growth fac

Human NOV/plexin-A1 homologue-encoding cDNA, SEQ ID NO:773.

(first entry)

11-JAN-2002

ABA08997

DXXXXXX

ABA08997 standard; cDNA; 1088

us-09-964-956-13.p2n.rng

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a human cDNA easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
   SerAsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnProGlnPheValPhe
                                       LeuAspGluGlnAlaAspLysHisGlyIleHisAspProHisValArgHisThrTrpLys
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T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length cDNA clones and
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                                                                                                                                    ASPILOHISLYSASNSETILOTHRASPATACYSLOUSERVALVAL 1774
                                                                                                                                                                                                                                                                                                           Human; full length cDNA; cDNA synthesis; oligo-capping;
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  and in drug
                                                                                                                                                                                             may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                            1460 SerLeuPheCysAlaIleLysGlnGlnMetGluLysGlyProIleAspAlaIleThrGly
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1573.50
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| 1140 ProAsnProValPheGluAlaPhe | heGluAlaPheGlyProSerG  | ProAsnProValPheGluAlaPheGlyProSerGlyIleLeuGluLeuLysProGlyThr 1 | 1159  | qq              |                  |
|                               | ysglyLysAsnLeuIleProP  |  | 1179  | δy              |                  |
| 33 GGTGGCGTCAAGA              |  |  | 92    | qa .:           |                  |
| 1180 AsnTyrThrVal-            |  |  | 1193  | λη<br>Op        | 137 CAG          |
| 93 GCGATGACGCTGC              | CAGGAGGCCGAGGCCTTCGTGG   | GCGATGACGCTGCAGGAGGCCGAGGCCTTCGTGGGTGCCGAGCGCTGCACCATGAAGACG   | 152   | ß è             |                  |
|                               | 31nLeuLeuCysGluSerProA   | ValSerAspValGlnLeuLeuCysGluSerProAsnLeuIleGlyArgHisLys 1       | 1211  | a a             |                  |
|                               | BACCTGTACTGTGAGCCCCCGG   |  | 212   | Qy              | 1547 Lys         |
| 1212                          |  |  | 1220  | qa              | 1254 AGG         |
|                               | Apt Val Tyrt I pA  |  | 1236  | QY              | 1567 Asp         |
|                               | <br>       <br>  | TGGGTGCTGGGCCGCGTGGGGTGACGGCTGACGGCTGACGTCACCTCACCTCCATC       | 332   | QQ              |                  |
|                               | ProAlaIleValSerI   |  | 1250  | δλ              |                  |
| 333 TIGCCGCIGGTCA             | :::        ATCGTGCCATGGTGGTCGTCA                               | :::   TIGCCGCIGGICATCGTGTCGTGTCTCTCTT                          | 377   | ag .            |                  |
| 1251 IlePheIleVal             | AlaValLeuIleAlaTyrLysA   | IlePhelleValAlaValLeulleAlaTyrLysArgLysSerArgGluSerAspLeuThr   | 1270  | λο<br>Q         | 160/ Ala<br>1404 |
| 378                           | GTCTACTGCTACTGGA   |  | 419   | ΔO              | 1627 TVE         |
|                               | 31nMetGlnMetAspAsnLeuG   | LeuLysArgLeuGlnMetGlnMetAspAsnLeuGluSerArgValAlaLeuGluCysLys   | 1290  | qa              |                  |
| 420 TAIGAGAAGAICE             | addiccederiesassectiss   |  | 1310  | δλ              | 1647 Ser         |
|                               | 3ACCTGATGATCGAGATGGAGG   |  | 539.  | ΟP              |                  |
|                               | LeuAspTyrArgThrTyrThrM   |  | 1326  | δλ.             |                  |
|                               | TITITITITE STATE STATES CTACACCG                               |  | 299   | qq              |                  |
|                               | AspHisProValLeuArqAspL   |  | 1346  | ΟŊ              | 1680 Arg         |
|                               | 3ACGTGATGATCACCGGCAAGC   | GACGGGGACAAGGACGGATGATGATCACCGGCAAGCTGGACATCCCCGAGCCGGGGGGCG   | 629   | qq              |                  |
|                               | 31.yLeuLysLeuPheAlaGlnL  |  | 1366  | ΟŊ              |                  |
| 660 GTGGTGGAGCAGG             | <br>   |  | 719   | QQ ű            |                  |
| 1367 SerPhelleArg             | ThrLeuGluSerGlnArgSerP   |  | 1386  | δ               |                  |
| 720 AATTTCATCCAC              |  | :::  | 977   | ag <sub>(</sub> |                  |
| 1387 AlaSerLeuIleM            | $\mathtt{MetThrValLeuGInSerLysL}$                              |  | 1406  | ζ               |                  |
| 11111111::: 780 GCGTCCCTGTG   | <br>acgtggcgctgcacgggaaac                                      |  | 839   | ପୁପ             | 1770 ACG         |
| 1407 GlnLeuLeuAla             | AspLeulleAspLysAsnLeuG   |  | 1426  | λο<br>·         | 1/60 ASF         |
| 840 ACGCTCTTCCTGC             | GAGCTCCTGGAGCAGTACGTGG   | :::   :::::::::::::::::::::::::::                              | . 968 | <u>a</u> :      | 1830 GAC         |
| 1427 LeuArgArgThro            | GluSerValAlaGluLysMetL   | LeuArgArgThrGluSerValAlaGluLysMetLeuThrAsnTrpPheThrPheLeuLeu   | 1446  | 5 6             | 1890 ASE         |
| 897 CTGCGCAGGTCTC             | GAGACTGTGGAGAGGATGC  |  | 956   | 2 6             |                  |
| 1447 TyrLysPheLeul            | TvrI.vsPhelenI.vsG]uCvsAlaGlvGluProLeuPheSerLeuPheCvsAlaIleLvs |  | 7766  | 7               |                  |

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APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Melanie K. Spriggs, Michard S. Johnson
APPLICANT: Robert F. DuBose, Richard S. Johnson
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/958,598 (converted to APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,706
FILING DATE: October 28, 1998
                                                                                                   US-08-121-7131-53
US-08-835-268-53
US-09-606-610-53
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US-08-133-391-59
US-08-835-268-59
US-08-833-391-59
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US-08-308-872B-5
US-09-026-001A-5
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STREET: 51 University St.
CITY: Seattle
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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|  | 3 6 6 6 6 6<br>  | 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1   | 8 8 8 8 8   | 0 1 0 1 0 1   |
| ATTORNEY/AGENT INFORMATION:  NAME: Henry, Janis C REGISTRATION NUMBER: 34,347 REFERENCE/DOCKET NUMBER: 2631-A TELECOMMUNICATION INFORMATION: TELEPHONE: (206)470-4189 TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 4707 base pairs TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-SENSE: NO REATURE: SENSE: NO REATURE: 1.4707 09-181-706-1  | 1.9e-134   Length: 4707     1349.00   Matches: 291     13-78   Mismatches: 291     13.50%   Gaps: 74     13.50%   Gaps: 74     14.77%   Mismatches: 591     15.60%   Mismatches: 591     16.61%   Mismatches: 591     17.60%   Mismatches: 591     18. | AsnProLysCysTyrProProArgileValGinThrCysAsnGiuProLeuThrThrill  | 400 TGCGAGGTGCGCCCCTGGGCAACCTG  | ValaspGlyLysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSer 20 ::: ATGGGGCTCAAGGAGGGGCGAGGCTGGCAGGAGTGGGGGCTCAAG 20 GluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheValAlaSerMetIle 22 ::: |
| ATTORNEY/A  NAME: H  REGISTRENC  REFERENC  TELECOMUNI  TELEPHONI  TELEPHONI  TELEPHONI  TYPE: N  TYPE: | Alignment Scores: Pred. No.: Score: Score: Percent Similarity Best Local Similar Query Match: DB: US-09-964-956-13 ( QY 72 TyrL  | 67 69 69 69 69 69 69 69 69 69 69 69 69 69   |   |   |

| 942 MetalaargSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysPro 961 :::::: | 962 SerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAla 981<br> | 982 GlyserAsnValValValMetPheGlyLysGlnProCys 994              | 995 LeupheHisArgArgSerProSerTyrIleValCysAsnThrThrSerSerAspGluVal 1014 :::             ::  | 1015 LeuGluMetLysValSerValGlnValAspArgAlaLysIleHisGlnAspLeuVal 1033 | 1034 PheGlnTyrValGluAspProThrIleValArgIleGluProGluTrpSerIleValSer 1053 | GLYASnThrProlleAlaValTrpGlyThrHisLeuAspLeulleGlnAsnProGlnIle                     | 1074 ArgAlaLysHisGlyGlyLysGluHisTleAsnIleCysGluValLeuAsnAlaThrGlu 1093 11 | 1094 MetThrCysGlnAlaProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGlu 1113<br>       :::   <br>2416 TGCGGGTTTTTAGCCCCCAGTTTA2439 | 1.14 ArgProGluGluPheGlyPheIleLeuAspAsnValGlnSerLeuLeulleLeuAsnLys 1133 ::: | 1i34 ThrasnPheThrTyrTyrProAsnProValPheGluAlaPheGly 1148      | 1149 ProserGlyIleLeuGluLeuLysProGlyThrProIleIleLeuLysGlyLysAsnLeu 1168 :::   :::    :::   ::: | 1169 IleProProValAlaGlyGlyAsnValLySLeuAsnTyrThrValLeuValGlyGluLys 1188 | 1189 ProcysThrValThrValSerAspValGlnLeuLeuCysGluSerProAsn 1205 :::   : | 1206 Leulle 1207<br>   | GlyArgHisLysValMetAlaArgValGlyGlyMetGluTyrSer 122 | 1223 ProGlyMetValTyrileAlaProAspSerProLeuSerLeuProAlaIleValSer 1241 :::!  ::: 2800CTCTACGTCGAGGAGTCATTCCACAAGGTATTTTCTGATTGTG 2850 |   | ArgLysSerArgGluSerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeu |
|---|--|--|---|---|--|--|---|--|--|--|--|--|---|--|---|--|---|--|
| Oy<br>Db  | dQ<br>Db   | do Oy  | QY  | Qy  | VQQ .  |  | QV  | Qy   | da<br>Db   | . Oy   | QY   | QY   | da .  | QY   | ζ.<br>δο<br>αο                                    | Qy   | δλ  | - Oy   |
| 591 ValAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIle 610        | GlnCysTyrSerProAlaAlaLysGluValProArgIlelleThrGluAsnGlyAspHis             | HisValValGlnLeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThrSer | 1579 TTCTCTCCAAGACAAGACAAAGACAAAGACTGACTATGGTGGGAAGC 15/8 651 PhevalPheTyrAsnCysSerValHisAsnSerCysLeuSerCysValGluSerPro 669 111 | TyrArgCysHisTrpCysLysTyrArgHisValCysThrHisAspProLysThrCysSer        | PheGlnGluGlyArgValLysLeuProGluAspCysProGlnLeuLeuArgValAs               | 1638 1638  710 IleLeuValProValGluValIleLysProIleThrLeuLysAslaLysAsnLeuProGln 729 | ProGlnSerGlyGlnArgGlyTyrGluCyslleLeuAsnIleGlnGlySerGluGlnArg              | ValProAlaLeuArgPheAsnSerSerSerValClnCysGlnAsnThrSerTyrSerTyr   | GluGlyMetGluIleAsnAsnLeuProValGluLeuThrValValTrpAsn                        | HisPheAsnIleAspAsnProAlaGlnAsnLysValHisLeuTyrLysCysGlyAlaMet | ArgGluSerCysGlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGln :::   | GlyProGlyGlnCysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGlu           |   | GlyProArgGluGlyGlyThrLysValThrlleArgGlyGluAsnLeuGlyLeuGluPhe | GCT   |  | AGTGTCCAGTGGCTGTCGAGAAGACATCAGGAGGAGGAG<br>heValGluIleCysValAlaValCysArgProGluPhe | 1936 AGACCCAAGGAACAAGGGG                                     |
| Qy  | 8 % E  | Q V  | oy da   | ,<br>,  | δ <sup>λ</sup>   | oy<br>Oy   | G V   | a ko   | oy o   | Qy de  | oy G   | 6 V  | 0y ob   | QY   | Db<br>Qy  | g &  | da vo   | qq   |

| 3907<br>1631<br>3937<br>1651<br>3988<br>1671  |  | Db . 4258 GTAAACATCCTGAAGAACCCTCAGTT  Qy          | Db 4498 ATGGAAGAATTTTAACTCAGGAATC  Qy 1849 AlaLeuSerGluIlePheSerTyrVa  | US-09-458-791-1 Sequence 1, Application US/09458791 Sequence 1, Application US/09458791 Sequence 1, Application US/09458791 Sequence 1, Application US/09458791 Sequence 1, Spriggs, Melanie TITLE OF INVENTION: VIRAL ENCODENTION: VIRAL ENCODENTION: VIRAL ENCODENTION: VIRAL ENCODENTION: VIRAL ENCODENTIAL SECEPTOR DN UNMERE OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Janis C. Henry STREET: 51 University St. CITY: Seattle STATE: WA COUNTRY: US COUNTRY: US COUNTRY: US CONPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPATIBLE IBM PC |
|---|--|---|--|--|
| 2902 CACAAATCGAAGGAGCTGAGTCGAAACGAGTCAACAACTAGAATTGCTG 2952  1282 GluserArgValalaLeuGluCysLysGlualaPheAlaGluLeuGlnThrAspIleHis 1301 | GluValProGlyTyrArgGlnGluArgValGluLysGlyLeuLysLeuPheAla | AGCTGGTCTACCTGACCACATCTTGAGGTGTTGTAGGGACCTGTGTGTG | 14/7 ILETRIGINGIALIZARGENERGENERGIANSPLYSLEAULEATGGINIEASP 1496 11/11/11   1/11/11/11/11/11/11/11/11/11/11/11/11/1 | 1531 LysIleLeuAspAlailePheLysAsnValProCysSerHisArgProLysAlaAlaAsp 1550 11111 13706 AAGATTTCCAAGCATTCTTAAGCAAAATGGCTCTCTTATGGACTTCAGCTTAATGAA 3765 1551 MetAspLeuGluTrpArgGlnGlySerGlyAlaArgMetIleLeuGlnAspGluAspIle 1570 1551 MetAspLeuGluTrpArgGlnGlySerGlyAlaArgMetIleLeuGlnAspGluAspIle 1570 1571 ThTTLYSILGGCTCAAATGGCACACGACAGAAAATTCTGGCATTCGAGTTCC 3825 1571 ThTTLYSILGGUASNASPTPLYSATGLEUASNThTLeuAlaHisTyTGlnValPro 1590 1571 ThTTLYSILGIUASNASPTTPLYSATGLEUASNThTLeuAlaHisTyTGlnValPro 1590 1591 ASpGlySerValValAlaLeuValSerLySGlnValThTAATTATGAGATATCA 3885 1591 ASpGlySerValValAlaLeuValSerLySGlnValThTAATTATAATAANAN 1610 11611 SerThrValSerArgThTSErAlaSerLySTyTGluAsnMetIleArgTyTThTGlySer 1630 1611 SerThrValSerArgThTSErAlaSerLySTyTGluAsnMetIleArgTyTThTGlySer 1630  |
| 90 Oy Oy Oy Oy Oy   | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                  | 40 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0            |  | 6  |

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||TCTAAGAAACATGAAATTTAATGAAGAGTG 4557
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|ATCTGACAAGCTGCTGTCGACCAAGGTGGCAATT 4083
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\GAAGCATTTGGAGTTTACCCAAC-----AGCAGA 4137
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1306 AATATCTACATTTATCTAACAGCTGGAAAGAGGTGAGGAGAATTCGTGTTGCAAACTGC 1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1102 TCATCTACCTTGATCCATTCCGACCTGACATCCGTTTATGGCACCGTGGTAATGAACAGG 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GGTGAGAATTTGACTTCAAATTGTCCAGAGGTTATCTATGAAATTAAAGAAGAGACA 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1072 -----GAAAGAGTCCAACCT-----GAAAGAGTCCAACCAATCGCA 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 ValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrValTyrLysAsnHis 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysIleArgValAspGlyPro 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------AspProGlyProValLeuArgAspMetAlaPheSerLysAsp 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValLeuHisAsnThrCysThrArgLysGluArgCysGluArgSerLysGluProArgArg 550
   189 ValAspGlyLysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSer 208
                                                                                                     CTGTGGGAGGGGGGGGGCGGCTTGGTGGACGCCTTTCTCTGGAACGGCAGCATC 732
                                                                                                                                                    LyslleProSerAspThrPheThrIleIleProAspPheAspIleTyrTyrValTyrGly 247
                                                                                                                                                                                         -----TACTACCCCTACAAC 756
                                                                                                                                                                                                                          PheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProPro 267
                                                                                                                                                                                                                                             288 ThrAlaPheAsnSerTyrValGluValProIleGlyCysGluArgSerGlyValGlu--- 306
                                                                                                                                                                                                                                                                                                                                                                                                                 GTGCTGTTCCAGGGC-----CAGGCATCCCTCGACTGCGGCCACGGCCACCCCGACGGC 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyValHisProAspAspAspLeuLeuPheThrValPheSer-----LysGlyGlnLys 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 ArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLysGlnIleAsn 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 AspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThrLeuAspLeuAla 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trp---LeuLysValLysAspIleProCysSerSerAlaLeuLeuThrIleAspAspAsn 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404 PheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValArgGlyIlePro 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyGlnTyrGlnSerCysGlyGluCysLeuGlySerGlyAspProH3eCysGlyTrpCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HisGluGlnLeuTyrIleMetSerGluArgGlnLeuThrArgValProValGluSerCys
                                                                             GlualaAspGlyMetPheAlaTyrValPheHisAspGluPheVal---AlaSerMetIle
                                                                                                                                                                                                                                                                                                    GlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------CTGGACGTCTGGGCGGGAGTGTTCAGCGCGGCCGCTGGAGAGGGC
                                        ATCGCGCTCAAGGACACGGAGGGGCGCAGCCTGGCCACGCAGGAGCTGGGGGCGCCTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           871 CGCCGCCTGCTCCTCCTCCTCCAGCGAGGCC-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           464 ArgGlyAsnAlaLeuGlnTyrGluThrValGlnValVal----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1270 CCTGTTTTCTACAAACTCGTTCCTGATCCTGTG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1012 GCGCGCCCAAGAGG------
                                                                                                                                                                                                                                                                                                                                         805 CAGAGCACC-----
                                                                                                                                                                                         733 TACTTCCCC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||||||
553 CTGCCTGAGCCGGAGCCGCTGCAACCCCGCGGCATCCGACCACGACACGGCC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnProLysCysTyrProProArgIleValGlnThrCysAsnGluProLeuThrThr 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----AsnAsnValAsnLysMetLeuLeuIleAspTyrLys 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HisTyrLeuSerGlyVal------AsnGluSerGlySerValPheGlyVal 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ThrAla 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHisLysLysGlu 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 CCCCCGCGGGCCCCGGGGAGCTTCAGCAAG---CTGCTGCTGCTCTACCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 IleValSerTyrSerAsnLeuAspAspLysLeuPheIleAla-----
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480
291
591
576
74
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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OPERATING SYSTEM: MS-DOS/Windows SOFTWARE: Word for Windows 95, 7. CURRENT APPLICATION DATA:
                                                      APPLICATION NUMBER: US/09/458,791
                                                                                                           PRIOR APPLICATION DATA:

**RAPLICATION NUMBER: 08/958,598

**FILING 'DATE: 28-007-1997

**ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..4707
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                     NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEFRAX: (206)233-0644
                                                                          FILING DATE: 10-Dec-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH 4707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.9e-134
1349.00
39.78%
24.77%
13.50%
                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
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Best Local Similarity:
Query Match:
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| Qy 1571 ThrThrLyslleGluAsnAspTrpLysArgLeuAsnThrLeuAlaHisTyrGlnValPro 1590 ::: ::    :::             :::: Db 3826 TCGTGATTCTTGAAGATGCAATCACCAAGCTAAACACCATTGGCCACTATGAGATATCA 3885  Qy 1591 AspGlySerValValAlaLeuValSerLysGlnValThrAlaTyrAsnAlaValAsnAsn 1610 :::       ::: ::: | Db 3886 AATGGATCCACTATAAAAGTC 3906 Qy 1611 SerThrValSerArgThrSerAlaSerLysTyrGluAsnMetIleArgTyrThrGlySer 1630 | 3907TTTAAGAAGATAGCAAATTTACTTCAGAT. 3  | Qy 1631 ProAspSerLeuargSerArgThrFroMet11eThrProAspLeuGluSerGlyValLys 1650 :::                   | Qy 1651 MetTrpHisLeuValLysAsnHisGluHisGlyAspGlnGlyAspArgGlySer 1670 111   1   1   1   1   1   1   1   1 |  | 1689  | Oy :709 LeuProLeuAlaIleLysfyrMetPheAspPheLeuAspGluGInAlaAspLysHisGly 1728   11 | Qy 1.729 IleHisaspProHisValargHisThrTrpLysSerAsnCysLeuProLeuArgPheTrp 1748 | Oy 1749 ValasnMetIleLysasnProGlnPheValPheAspIleHisLysasnSerIleThrasp 1768 |          | Oy 1789 LeuGlyLysAspSerProSerAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLys 1808  | Qy 1809 AsnTrpValGluArgTyTTyrSerAspIleGlyLysMetProAlaIleSerAspGlnAsp 1828                 | Oy 1829 MetAsnalaTyrLeualaGluGlnSerargMetHisMetAsnGluPheAsnThrMetSer 1848 | Oy 1849 AlaLeuSerGluIlePheSerTyrValGlyLysTyrSerGluGluIleLeuGlyProLeu 1868       | Oy 1869 AspHisAspAspGlnCysGlyLysGlnLysLeuAlaTyrLysLeu 1883 ::: ::::: | RESULT 3<br>US-09-459-066-1<br>; Sequence 1, Application US/09459066<br>; Patent No. 6187909 | GENERAL INFORMATION:  APPLICANT: Sprigss, Melanie  TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  NUMBER OF SEQUENCES: 10 |
|--|--|---|---|---|--|---|--|--|---|----------|--|---|---|---|--|--|---|
| 1223 ProGlyMetValTyrIleAlaProAspSerProLeuSerLeuProAlaIleValSer 1241 :::   ::: 2800CTCTACGTCGAGGAGTCAGTTCCTTCCACATGGTATTTCTGATTGTG 2850 1242 IleAlaValAlaGlyGlyLeuLeuIleIlePheIleValAlaValLeuIleAlaTyrLvs 1261  | CICCCIGICTIGCIAGIGALIGICALITITGCGGCCGIGGGGGGGCACAGG  | 1262 ArgLysSerArgGluSerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeu 1281<br>      :::   <br>2902 CACAAATCGAAGGAGCTGAGTCGCAAACAGAGTCAACAACTAGAATTGCTG 2952 | 1282 GluserArgValAlaLeuGluCysLysGluAlaPheAlaGluLeuGlnThrAspIleHis 1301<br>        :::      :::: | 1302 GluLeuThrSerAspLeuAspGlyAlaGly-7-IleProPheLeuAspTyrArgThrTyr 1320<br>                              | 1321 ThrMetArgValLeuPheProGlyIleGluAspHisProValLeuArgAspLeu 1338 | 1339 GluValProGlyTyrArgGlnGluArgValGluLysGlyLeuLysLeuPheAla 1356 :::::::::::::::::::::::::::::::::::: | 1357 GInLeuileAsnAsnLysValPheLeuLeuSerPheileArgThrLeuGluSerGinArg 1376<br>     |  | sAsn<br>:<br>GTGT   | 14<br>34 | 1437 MetLeuThrasnTrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGlu 1456<br> | 1457 ProLeuPheSerLeuPheCysAlaIleLysGlnGlnMetGluLysGlyProIleAspAla 1476     :::        ::: | eAsp 14<br>:::<br>GGAA 35   | 1497 TyrLysThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerPro 1513 :::    :::    ::: | 1514GluValProValLysIleLeuAsnCysAspThrIleThrGlnValLysGlu 1530<br>     | 1531 LysileLeuaspalailePheLysasnValProCysSerHisArgProLysalaalaasp 1550<br>                   | 1551 MetaspLeugluTrpargGlnGlySerGlyAlaargMetIleLeuglnAspGluaspIle 1570<br>:::        :::        3766 ATTGGTCTTGAAATGGGCACACGACAGAAAGAACTTCTGGACATCGACAGTTCC 3825                    |

| CORRESPONDENCE ADDRESS: ADDRESSEE: Janis C. Henry   | Oy 173 IleValSerTyrSerAsnLeuAspAspLysLeuPhelleAla186   |
|---|--|
| STREET: 51 University St. CITY: Seattle   | Db 496 GIGTACCGCGGGGCCGGAACCGCTGGTACCTGGGGGGGCCGCCACCTACGTG 552  |
| 2   | Qy 187ThrAla 188   |
| ZIP: 98101<br>COMPUTER READABLE FORM:   | Db 553 CTGCCTGAGCCGGAGACGGCGAGCCGCTGCAACCCCGGGGCATCCGACCACGACACGGCC 612  |
| MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible  |  |
| OPERATING SYSTEM: MS-DOS/Windows 95 SOFTWARE: Word for Windows 95, 7.0a   | Db 613 ATCGCGCTCAAGGACACGGAGGGGCGCAGCCTGGCCACGCAGCTGGGCGCCCTCAAG 672   |
| CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/09/459,066  FILING DATE:  | Qy 209 GlualaaspGlyMetPhealaTyrValPheHisaspGluPheValAlaSerMetIle 227 :::   |
| PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/958,598 FILING DATE:   | Qy 228 LysileProSerAspThrPhcThrIleIleProAspPheAspIleTyrTyrValTyrGly 247  |
| ATTORNEY AGENT INFORMATION: NAME: Henry Janis C RESISTRATION NUMBER: 34,347  REFERENCE/DOCKET NUMBER: 2631                    | 248  |
| ; TELECOMMUNICATION INFORMATION:<br>; TELEPHONE: (206)470-4189<br>; TELEFAX: (206)233-0644<br>; INFORMATION FOR SEQ ID NO: 1: | 268 GlySerThrThrLysGluGlnVa  |
| ; SEQUENCE CHARACTERISTICS:<br>; LENGTH: 4707 base pairs<br>; TYPE: nucleic acid<br>crabandenness: double                     | 288 ThrAlaPheAsnSerTyrValGluValProIleGlyCysGluArgSerGlyValGlu:::::::::::::::::::::::::::::::::   |
| TOPOLOGY: linear MOLECULE TYPE: cDNA HYDOPHETICAL: NO   | Tecescratesc |
| ž   | 871  |
| ; NAME/KEY: CDS<br>; LOCATION: 14707<br>US-09-459-066-1   | Oy 327 GlyValHisProAspAspLeuLeuPheThrValPheSerLysGlyGlnLys 344   |
| 1.9e-134 Length:<br>1349.00 Matches:  | Oy 345 ArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLysGlnIleAsn 364 ::::   |
|   | 365  |
| US-09-964-956-13 (1-1896) x US-09-459-066-1 (1-4707) Oy 72 TyrLysLeuSerSerAspLeuLysValLeuValThrHisGluThrGlyProAspGluAsp       |  |
| 208   | AspMetValArgGlyIlePro  |
| Qy 92 ASnProLysCysTyrProProArgileValGinThrCysAsnGluProLeuThrThrThr  | 1 Db 1072  |
| Db 256ACTGCAGAGCCGGTCTGGCGGCCGGCGGCGGCGGCGGGCG  | 282<br>123 OY  |
| 283 CCCCCGCGGGCCCGGGCCGGGAGCTTCAGCAAGCTGCTGCTGCCGT  | 339 Db IIO2 TCATCTACCTTGATCCGACCIGACATCCGACTTGACATCTGACATCTGACCTTGATGATGATGATGATGATGATGATGATGATGATGATGA  |
| Qy 124 GluasnArg  | 1162 ACTGTTTATTCTTGGGGACTGGAGATGGCCAGTTACTTAAGGTTATCTT   |
|   | Oy 464 ArgGlyAsnAlaLeuGlnTyrGluThrValGlnTyrGlvTh (11::- 157 Db 1213GGTGAGAATTTGACTTCCAGAGGTTATCTATGAATTAAAGAAGAGACA 1269   |
| Db • 400 receasedcececeresecancersAsceceance  | 435 Oy 477   |
| Qy 158 HisTyrLeuSerGlyValAsnGluSerGlySerValPheGlyVal ::   | 172 Db 1   |

| Dp       | 2626 GACATTGAAATTACTCTTCCATGGGGAAAATGGGCAATTAAAATTGCAGTTTTGAAAAT 2685                         | ΛΟ             | 1531 LvsI         |
|----------|---|----------------|-------------------|
| Qy       | 1206 LeuIle 1207  | 7 E            |                   |
| qa       | 2686 ATTACTAGAAATCAAGATCTTACCACCATCCTTTGCAAAATTAAAGGCATCAAGACTGCA 2745                        | 3 3            | 264076            |
| QY       | 1208GlyArgHisLysValMetAlaArgValGlyGlyMetGluTyrSer 1222  | Š E            |                   |
| qa       | 2746 AGCACCATTGCCAACTCTTCTAAGAAGTTCGGGTCAAGCTGGGAAACCTGGGAG 2799                              | 2 2            |                   |
| QY       |   | qa<br>Z        |                   |
| Ob       | 2800  | ,<br>Oy        | 1591 AspG         |
| . Оу     | 1242 IleAlaValAlaGlyGlyLeuLeuIleIlePheIleValAlaValLeuIleAlaTyrLys 1261                        | · 6            |                   |
| QQ       | 2851 CICCCIGICIIGCIAGIGATIGICATITITICCGGCCGIGGGGGIGACCAGG 2901                                | Oy             | 1611 SerT         |
| Οy       | erAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeu  | qa             | 3907              |
| qq       | 2902 CACAAATCGAAGGAGCTGAGTCGCAAACAGAGTCAACAACTAGAATTGCTG 2952                                 | ογ             | 1631 ProAs        |
| ΟY       | GluSerArgValAlaLeuGluCysLysGluAlaPheAlaGluLeuGlnThrAspIleHis                                  | QQ             | :<br>3937 GTGG    |
| qq       | GAAAGCGAGCTCCGGAAAGAGATACGTGACGGCTTTGCTGAGCTGCAGATGGATAAATTG                                  | ÓΣ             | 1651 MetT         |
| oy<br>;  | GluLeuThrSerAspLeuAspGlyAlaGlyIleProPheLeuAspTyrArgThrTyr                                     | qq             | 3988 T            |
| g<br>G   | GATGTGGTTGATAGTTTTGGAACTGTTCCCTTCCTTGACTACAAACTTTT  | Qy             | 1671 Lys-         |
| Vo       | ThrMetArgValLeuPheProG1ylleGluAspHisProValLeuArgAspLeU<br>:::                                 | q <sub>0</sub> | 4024 CACA         |
| <b>Q</b> | GCTCTGAGAACTTTCTTCCCTGAGTCAGGTGGCTTCACCCACATCTTCACTGAAGATATG                                  | Qy             | 1689 GlnL         |
| ΟŊ       | GluValProGlyTyrArgGlnGluArgValGluLySGlyLeuLySLeuPheAla<br>::::::::::::::::::::::::::::::::    | qa             | 4084 CATT         |
| qa .     | 3124CATAACAGAGACGCCAACGACAAGAATGAAAGTCTCACAGCTTTGGAT 3171                                     | δò             | 1709 LeuP         |
| δÿ       | GlnLeulleAsnAsnLysValPheLeuLeuSerPhelleArgThrLeuGluSerGlnArg                                  | 1 <b>Q</b>     |                   |
| QQ       | 3172 GCCCTAATCTGTAATAAAAGCTTTCTTGTTACTGTCATCCACACCCTTGAAAAGCAGAAG 3231                        | ٥٥             | 1729 Ilен         |
| ٥y       | SerPheSerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSer :::       :::                    | 7 A            |                   |
| qa       | AACTTTTCTGTGAAGGACAGGTGTCTGTTTGCCTCCTTCCT   | Qy             | 1749 ValA         |
| ΟŊ       | 1397 LysLeuGluTyrAlaThrAspValLeuLysGlnLeuLeuAlaAspLeuIleAspLysAsn 1416<br>                    | Db             | <br>4258 GTAA     |
| qa       | 3292 AAGCTGGTCTACCTGACCAGCATCCTAGAGGTGCTGACCAGGGACTTGATGGAACAGTGT 3351                        | 0              | 1769 AlaC         |
| Qy       | 1417 LeuGluSerLysAsnHisProLysLeuLeuLeuArgArgThrGluSerValAlaGluLys 1436                        | 4d             |                   |
| qa       | 3352AGTAACATGCAGCCGAAACTCATGCTGAGACGCACGGAGTCCGTCGAAAAA 3405                                  | ì ô            |                   |
| Qy       | 1437 MetLeuThrAsnTrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGlu 1456                        | QQ<br>QQ       |                   |
| qq       | 3406 CICCICACAAACIGGAIGICCGICIGCCTIICIGGAITICICCGGGAGACIGICGGAGAG 3465                        | <b>^</b>       | 1809 AsnT         |
| Οy       | 1457 ProLeuPheSerLeuPheCysAlaIleLysGlnGlnMetGluLysGlyProIleAspAla 1476                        | og<br>O        |                   |
| qa       | 3466 CCCTTCTATTTGCTGGTGACGACTCTGAACCAGAAATTAACAAGGGTCCCGTGGATGTA 3525                         | δ              | 1829 MetA         |
| ΟŊ       | IleThrGlyGluAlaArgTyrSerLeuSerGluAspLysLeuIleArgClnGlnIleAsp<br>        :::       :::     ::: | qq             |                   |
| qa       |   | QY             | 1849 AlaL         |
| Ολ       | TyrLysThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerPro 151                                       | Dp             | 1111<br>4558 GCCT |
| ΩΩ       | TTCAGTACTGTGGCATTAAACGTCGTCTTTGAAAAATCCCGGGAAAACGAGAGTGCAGAT                                  | Qy             | 1869 AspH         |
| Oy<br>2  | GluValProValLysIleLeuAsnCysAspThrIleThrGlnValLysGlu   | qu             | 4618 GAAA         |
| QQ       | 3646 GTCTGTCGGAATATTTCAGTCAATGTTCTCGACTGTGACCATTGGCCAAGCCAAAGAA 3/U5                          |                |                   |

| <u> </u>   | 1531         | IvstletenasnalallephetwsasnvalproCvsSerHisArgProLvsAlaAlaAsp 1550                                    |
|------------|--------------|--|
| , g        |              | 97   |
| λy         | Ľ            | MetAspLeuGluTrpArgGlnGlySerGlyAlaArgMetIleLeuGlnAspGluAspIle 1570                                    |
| qc         |              | <br> TGAGCTTCAAATGGGCACACGACAGAAAGAACTTCTGGACA1  |
| λλ         | 57.          | <pre>cThrLyslleGluAsnAspTrpLysArgLeuAsnThrLeuAlaHisTyrGlnValPro 159 :::   :::                 </pre> |
| qc         | 3826         | CGTGATTCTTGAAGATGGAATCACCAAGCTAAACACCATTGGCCACTATGAGATATCA 388                                       |
| λy         | 1591         | rAlaTyrAsnAlaValAsnAsn 161   |
| qc         | 3886         | IGGATCCACTATAAAAGTC 390  |
| λy         | 1611         | erThrValSerArgThrSerAlaSerLysTyrGluAsnMetIleArgTyrThrGlySer 163                                      |
| qc         | 3907         | TTTAAGAAGATAGCAAATTTT  |
| λy         | 1631         | <pre>spSerLeuArgSerArgThrProMetIleThrProAspLeuGluSerGlyValLys 165 ::</pre>                           |
| qc         | 3937         | TGGAGTACTCGGATGACCACTGCCATTTGATTTTACCAGATTCGGAAGCA 398   |
| λy         | 1651         | tTrpHisLeuValLysAsnHisGluHisGlyA   |
| qc         | 3988         | rccaagatgtgcaaggaaagagattcGa   |
| ٥y         | 1671         | alSerGlulleTyrLeuThrArgLeuLeuAlaThrLy  |
| qc         | 4024         | :::IIIII<br>rcgaccaaggrggc   |
| λχ         | 1689         | lnLysPheValAspAspLeuPheGluThrIlePheSerThrAlaHisArgGl   |
| qq         | 4084         | TTCTGTGCTTGAAAAACTTTTAGAAGCATTTGGAGTTTACCCAACAG  |
| Σy         | 1709         | euProLeuAlaIleLysTyrMetPheAspPheLeuAspGluGlnAlaAs  |
| qq         | $\leftarrow$ |  |
| ργ         | 1729         | HisThrTrpLysSerAsnCysLeuProLeuArgPheTrp 174  |
| qq         |              | CACAGATCCTGACGTCGTACATATTTGGAAAACAAACAACCTTCCTT  |
| Οy         | 1749         | alAsnMetIleLysAsnProGlnPheValPheAspIleHisLysAsnSerIleThrAsp 176                                      |
| qq         | 4258         | AAACATCCTGAAGAACCCTCAGTTTGTCTTTGACATTAAGAAGACACCACATAT   |
| ٥y         | 1769         |  |
| qq         | 4318         | CTGTTTGTCAGTGATTGCCCAGGCATTCATGGATGCATTTTC   |
| ΟY         | 1789         | LeuGlyLysAspSerProSerAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLys 1808                                    |
| qq         | 4378         | TAGGGAAGGAAGCACCAACTAATAAGCTTCTTTTTTTTTT   |
| Qy         | 1809         | AsnTrpValGluArgTyrTyrSerAspIleGlyLysMetProAlaIleSerAspGlnAsp 1828                                    |
| qq         | 4438         | AGTAAAATCTTATTACAAAGCAATCAGGGATTTGCCTCCATTGTCATCCTCAGA   |
| Qy         | 1829         | MetAsnalaTyrLeualaGluGlnSerArgMetHisMetAsnGluPheAsnThrMetSer 1848                                    |
| ДD         | 4498         | TGGAAGAATTTTTAACTCAGGAATCTAAGAAACATG   |
| ٥y         | 1849         | AlaLeuSerGluilePheSerTyrValGlyLysTyrSerGluGluileLeuGlyProLeu 18                                      |
| Db         | 4558         | CITGACAGAATITACAAAIACATCGIAAAAIATITGATGAGATTCTAAAIAA   |
| Qy         | 9 8          | AspHisAspAspGlnCysGlyLysGlnLysLeuAlaTyrLysLeu 188:   |
| <b>q</b> 0 | 4618         | Ö  |

| Db 606 AGAGGACCTGCCAGCGACATGTCTTTCCCCAAAT | Qy 155 LysLysGluHisTyrLeuSerGlyValAsnGluSer |  | Qy 167 GlySerValPheGlyValIleValSerTyrSerAsnLeuAsp                           | Db 702 AGCCAGTGTCCTGACTGTGGGGGGCCCCTGGGGAGCCAAAGTCCTTTGATCTGTAAAG | Qy 181 AspLysLeuPhellealaThralaValAspGlyLysProGluTyrPhePro |                      | OY 198ThilleSerSerArgLysLouThilysAsnSerGluAlaAspGly 111111 Db 816 GATCATCGATTCGATATCACTGAGAAGCTAAAGGAAACGAAAGATGGT | Oy 213 MetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAsp | 870 | Qy 233 ThrPheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPhe         | Db 900GATGTTTACCTGAGTTCAGAGATTCTTACCCCATTAAGTATGTCCATGCCTTT | Qy 249 SerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProPtroGly  Dh GAA CRARGERARTHTHISTER | # 00°   | 66   | Qy 289 AlaPheAsnSerTyrValGluValProlleGlyCysGlu  | Db 1053 GGATTGCATTCCTACATGGAAATGCCTCTGGAGTGTATTCTCACAGAAAAGAGAAAAAA | Oy :02 ArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGly                              | Qy 320 AlaValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPhe | 340     | 123                                     | Qy 360 LeuLysGlnIleAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGly                            | 1293       | Qy 380 ThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaLeuLeuThr | Db 1322 | Qy 400 IleAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetVal | Db 1322   | 420 ArgGlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAla |  | Oy 440 TyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysTleArg 1329 AACAAAAACHATGTG | Ov 460 ValAspGlvProArgGlvAsnAlaLenGlnTvrGlnThrValGlnValValAspProGlv     |
|---|---|--|---|---|--|----------------------|--|---|-----|---|---|---|---|--|---|---|--|---|---------|---|---|------------|---|---------|---|---|--|--|--|---|
| RESULT 4                                  | מ   | GENERAL INFORMATION  STATEMENT CALIFORMATION | APPLICANT: Calabretta, Bruno APPLICANT: Skorski, Tomasz APPLICANT: ANTENNES |   | SS<br>Ce   | ; CITY: Philadelphia | SOUNTRY: U.S.A. ZIP: 19102   | E B   | ٠,  | SOLTWARENT APPLICATION DATA: APPLICATION NUMBER: US/08/306,691B | 겉   | BE  | ATTORNEY/AGENT INFORMATION: NAME: Monaco, Daniel A. | ; REGISTRATION NUMBER: 30,480<br>; REFERENCE/DOCKET NUMBER: 8321-8 | ; TELECOMMUNICATION INFORMATION:<br>; TELEPHONE: (215) 568-8383<br>: TELEFEAX: (215) 568-5549 | TELEX: NO. 5734039e   | SEQUENCE CHARACTERISTICS:  LENGTH: 4626 base pairs  TYPE: nucleic acid  croaningness: Acid | ine   | Length: | 629.50 Matches:<br>35.47% Conservative: | DEST LOCAL SIMILATICY: 20.38* MISMATCHES: 409 Query Match: 6.30% Indels: 475 DB: 1 Gaps: 59 | 22 (1-4626 | rrLys   |         | Ile   | 435 GTTGCTGAGTACAAGACTGGGCCTGTGCTGGAACACCCAGATTGTTTCCCA | AsnValAsn  |  | 116 LysMetLeuLeulleAspTyrLysGluAsnArgLeulleAlaCysGlySerLeu<br>   :::::           :::     | Db 546 ATGGCTCTAGTTGTCGAÇACCTACTATGATGATCAACTCATTAGCTGTGGCAGCGTCAAC 605 |

|      |        |  | _   |
|------|--------|--|-----|
| Qy   | 480 E  | ProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrIleMetSerGlu 499 | •   |
| qq   | 1359   | TTTTACGGACCCAATCATGAG  |     |
| ΟY   | 200    | ArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCys 519 |     |
| Db   | 1379   | 1379   |     |
| Qy   | 520 1  | LeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsnThrCysThrArgLys 539 |     |
| Db   | 1380   | TITAATAGGACACTICTGGAAAT 1409                                     | •   |
| Qy   | 540 (  | GluargCysGluargSerLysGluProArgArgPheAlaSerGluMetLys 556          |     |
| · qa | 1410   | ICAICAGGCIGIGAAGCGCGCCGGGAGAAAAAACAGAGTTTACCACAGCTTTGCAG 1469    |     |
| QY   | 557 (  |  | _   |
| qq   | 1470 ( | CGTT   |     |
| ٥y   | 577    | LeuvalLeuGluThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThr 594       |     |
| qq   | 1506 ( | CTCTTAACATCTATATCCACCTTCATTAAAGGAGACCTCACC 1547                  |     |
| Qy   | 595    | PheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSer 614 |     |
| qa   | 1548   | ATAGCTAATCTTGGGACATCAGAGGTCGCTTCATGCAGGTTGTGGTTTCTCGATCAGGA 1607 |     |
| ٥y   |        | rGluAsnGlyAspHisHisValValGln                                     | -   |
| qq   | 1608   | CCATCAACCCCTCATGTGAATTTTCTCCTGGACTCCCATCCAGTG 1652               | *** |
| Qy   | 635    | LeuglnLeuLysSerLysgluThrGlyMetThrPheAlaSerThrSerPheValPheTyr 654 |     |
| qq   | 1652   | 1652   |     |
| ΟY   | 655    | AsnCysSerValHisAsnSerCysLeuSerCysValGluSerProTyrArgCysHisTrp 674 |     |
| Db   | 1653   | 1658   |     |
| Qy   | 675    | CysLysTyrArgHisValCysThrHisAspProLysThrCysSerPheGlnGluGlyArg 694 |     |
| qq   | 1658   | 1658   |     |
| Qy   | 695    | ValLysLeuProGluAspCysProGlnLeuLeuArgValAspLysIleLeuValProVal 714 |     |
| Dþ   | 1658   | 1658   |     |
| Οy   | 715    | LysAlaLysAsnLeuProGlnProGlnSe                                    |     |
| qa   | 1659   |  |     |
| Qy   | 735    | ArgGlyTyrGluCys1leLeuAsn1leGlnGlySerGluGlnArgValProAlaLeuArg 754 |     |
| qq   | 1689   | CTACACACTG   |     |
| Qy   | 755    | PheAsnSerSerValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIle 774    |     |
| qa   | 1713   | GGGAAGATC 1724   |     |
| Qy   | 775    | luLeuThrValVal   |     |
| qa   | 1725   | ACGAAGATCCCAFTG 1763   |     |
| Οy   | 791    | IleAspAsnProAlaGlnAsnLysValHisLeuTyrLysCysGlyAlaMetArgGluSer 810 |     |
| qa   | 1764   |  | _   |
| ٥y   |        |  |     |
| qq   | 1770   | TGCAGTCAATGCCTCTCTGCCCCACCCTTTGTTCAGTGTGGCTGGTGCCCACGAC 1823     |     |

| δy   | 83   | SThrLeuArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGluLeuSerGly 850       |
|------|------|---|
| QΩ . | C) I | TGTGTGCGATCGGAGGAATGC   |
| Qy   | 851  | LysSerLysCysThrAsnProArglieThrGlullellePFOVAlInfGly 808<br>:::::: |
| Db   | 1857 | CAACAGATCTGTCTGCCTGCAATCTACAAGGTTTTCCCAAATA                       |
| Qy   | 869  | AsnLeuGlyLeuGluPheArg 888   |
| qq   | 1914 | CCCTTGAAGGAGGGACAAGGCTGACCATATGTGGCTGGGACTTTGGATTTCG              |
| Qy   | 889  |   |
| QQ   | 1968 | rtctccttggaaatg   |
| Οy   | 904  | uAl   |
| . da | 2028 | ACTTTAAGTGAGAGCACGATGAATACATTGAAATGCACAGTTGGT                     |
| Οy   | 924  | AlaGlyPheV  |
| Db   | 2079 | ATGAAT  |
| QY   | 944  | ArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSerArg 963  |
| qq   | 2136 | CAGTACATTCTCCTATGTGGATCCTGTAATAACAAGTATTTCGC                      |
| δÿ   | 964  | 83  |
| qq   | 2193 | CCTATG  |
| Qy   | 984  | AsnValValValMetPheGlyLysGlnProCysLeuPheHisArgArgSerProSerTyr 1003 |
| QO   | 2253 | TCTAGACACATTTCAATTGGTGGAAAAACATGTACTTTAAAAAGTGTGTGT               |
| Qγ   | 1004 | leValCysAsnThrThrSerSerAspGluValLeuGluMetLysValSerValGlnVal 102   |
| Dp   | 2313 | AIGTTATACCCCAGCCCAAACCATTCAACTGAGTTTGCTGTTAAATTGAAAATT 2377       |
| Qy   | 1024 | gAlaLysIleHisGlnAspLeuValPheGlnTyrValGluAspProThr                 |
| . qa | 2373 | CGAGAGACAAGCATCTTCAGTTACCGTGAAGATCCCATTGT                         |
| Qy   | 1044 | Ψ-  |
| qq   | 2430 | CATCCAACCAAAT   |
| QY   | 1053 | SerGlyAsnThrProlleAlaValTrpGlyThrHisLeu 1065                      |
| Db   | 2490 | CTATTTTGCTTTGCCAGTGGTGGGGGCACAATAACAGGTGTTGGGAAAAACCTG            |
| Qy   | 1066 | eulleGlnAsnProGln   |
| qq   | 2550 | AATTCAGTTAGTGTCCCGAGAATGGTCATAAATGTGCATG                          |
| Qy   | 1084 | snAlaThrGluMetThrCysGlnAlaProAlaLeuAl.                            |
| . qa | 2610 | GIGGCATGTCAACATCGCTCTAATTCAGAGATAATCTGTTGTACCACTCCTTCC            |
| QY   | 1103 | ren(  |
| . da | 2667 | CAACAGCTGAATCTGCAACTCCCCTGAAAACCAAAGCCTTTTTCATGTTA 2717           |
| Qy   | 1123 | AspasnValGlnSerLeuLeuIleLeuAsnLysThrAsnPheThrTyrTyrProAsnPro 114  |
| Dβ   | 2718 | GAIGGGAICCITICCAAAIACIIIGAICTCAITIAIGIACAIAAICCI 276              |
| Qy   | 1143 | ValPheGluAlaPheGlyProSerGlyIleLeuGluLeuLysProGlyThrProIleIle 116  |
| Db   | 2766 | GIGITTAAGCCTTTTGAAAAGCCAGTGATGATCTCAATGGCAATGAAAATGTACTGGAA 282   |
| Qγ   | 1163 | LeuLysGlyLysAsnLeuIleProProValAlaGlyGlyAsnValLysLeuAsnTyrThr 1182 |

us-09-964-956-13.p2n.rni

| ; LENGTH: 4626 base pairs<br>; TYPE: nucleic acid<br>; STRANDEDNESS: double<br>; TOPCLOGY: linear<br>; MOLECULE TYPE: DNA (genomic)<br>PCT-US93-06251-27 | Alignment Scores: 1.22e-56 Length: 4626  Pred. No.: 629.50 Matches: 282  Percent Similarity: 35.47% Conservative: 204  Best Local Similarity: 20.58% Mismatches: 475  DB: 5 Gaps: 59 | US-09-964-956-13 (1-1896) x PCT-US93-06251-27 (1-4626)  Oy 62 HislleTyrLeuGlyAlaValAsnArglleTyrLysLeuSerSerAspLeuLysVal 80  11     :::   | 81 LeuvalThrisGluThrGlyProAspGluAspAsnProLySCySTyrProProArgile 10 81 sinnill   | Oy 116 LysMetLeuLeuIleAspTyrLysGluAsnArgLeuIleAlaCysGlySerLeuTyr 134 | AGGGACCTGCCAGCGACATGTCTTT  | Oy 167 GlySerValPheGlyValIleValSerTyrSerAsnLeuAsp 180 ::::       Db   702 AGCCAGTGTCCTGAGCGCCCTGGGAGCCAAAGTCCTTCATCTGTAAAG 761  Qy             | 198ThrileSerSerArgLysLeuThrLysAsnSerGlualaAspGly 21 :: | Oy 233 ThrPheThrIleIleProAspPhe  | 269 SerThrThrLysGluGlnValTyrThrSerLysLeuValargLeuCysLysGluAspThr 28: |
|--|--|--|--|--|--|--|--|--|--|
| 1   1   1   1   1   1   1   1   1   1  | Oy 1202 GluserproAsnLeuileGlyArgHisLysValMetalaArgValGlyGlyMetGlu 1220  12931 ACGGTCCCCAATGACTGCTGAAATTGAACAGCGAGCTAAATATAGAG 2978  Oy 1221 TyrSerPro                                | Oy 1234 LeuserLeuProAlaIIeValSerIleAlaValAlaGlyGlyLeuLeuIleIle 1251  3039 TTCACAGGATTGATTGTTGTCTCAATATCAACAGCACTGTTATTACTACTTGGG 3098  Oy 1252 PheIleValAlaValLeuIleAlaTytLysArqLysSerArqGluSerAspLeuThrLeu 1271 | 3099 TTTTCCTGTGGGTGAAAAAGAGAAATTAAAGATCTGGGCAGTGAATTAGTTCGC 315 1272 LysArgLeuGlnMetAspAsnLeuGluSerArgYalAlaLeuGluCysLysGlu 129 3159 TACGATGCAAGAGTACACTCCTCATTTGGATAGGTCTCTGAAGTGTAAGGC 321 1292 AlaPheAlaGluLeuGlnThrAspIleHisGluLeuThrSerAspLeuAspGlyAlaGly 131 | Db 3219 CCAACTACAGAAATGGTTTCAAAT                                     | Oy 1332 HisProValLeuArgAspLeuGluValPro 1341  Db 3300 AACGGTTCATGCCGACAAGTGCAGTATCT 3329  RESULT 5  PCT 1133 - A6751 - 27 | plication PC/TUS9306251 Mickstrom, Eric and Rife, Jason ENTION: Trivalent Synthesis of ENTION: Stereospecific Alkylpho QUENCES: 93 CE ADDRESS: | SEE: SC<br>400 G<br>Garden<br>NY<br>Y: USA<br>11530    | MELLOW TIFE: FIDEPY dish  COMPUTER: IN PC COMPATIBLE  COMPUTER: PATENTIN RELEASE #1.0, Version #1.25  SOSTWARE: PATENTIN RELEASE #1.0, Version #1.25  CURRENT APPLICATION DATA:  FILING DATE: 19930630  CLASSIFICATION:  ATTORNEY AGENT INFORMATION: | NAME: DiGiglio, Frank S.   |

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181 CATATGAACGAAGATCGAGATACG-----CTCTATGTGGGAGCCATGGATCGCGTATTC 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 ProLysCysTyrProProArgIleValGlnThrCysAsnGluProLeuThrThrAsn 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TTGGAGCCAACACGGGATGATGTGGTTAGCTGCGTC 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 AsnValAsnLysMetLeuLeuIleAspTyrLysGluAsnArgLeuIleAlaCysGlySer 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535 CGTGTG-----AACCTGCAGAATATCTCCTCATCCAATTGTAATCGGGATGCGATCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-964-956-13 (1-1896) x US-08-121-713D-61 (1-2670)
                                                                                                          APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: Timothy applicant: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                               ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/121,713D
FILING DATE: 13-SEP-1993
CLASSIFICATION: 514
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                                                           Sequence 61, Application US/08121713D Patent No. 5639856
                                                                                                                                                                                                                                                                                                                                                                                                                      : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNIEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (4.15)343-4341
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227.00
37.22%
20.42%
2.27%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2670 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
268..2439
                                                                                                                                                                                                                                                                                                                      San Francisco
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                                                                                                  GENERAL INFORMATION:
APPLICANT: GOODMAI
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                      RESULT 6
US-08-121-713D-61
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2313 CTTGAATGTTATACCCCAGCCCAAACCATTTCAACTGAGTTTGCTGTTAAATTGAAAATT 2372
                                                             AspLeuIleGlnAsnProGln-----IleArgAlaLySHisGlyGlyLySGluHisIle 1083
                                                                                                                                                                                                                                                                                                                                                        1084 AsnileCysGluValLeuAsnAlaThrGlu----MetThrCysGlnAlaProAlaLeuAla 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CAACAGCTGAATCTGCAACTCCCCTGAAAACCAAAGCCTTT---TTCATGTTA 2717
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                                       AspArgAlaLysIleHisGlnAspLeuValPheGlnTyrValGluAspProThrIleVal
                                                                                                                                                       2430 GAAATTCATCCAACCAAATCTTTATTAGTACTTGGTGGAAAGAACCTCTCAACATTGTC
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| ΩP    | 625 TCCAAAGGCAAAAGTCAGATCTTCGACTGCAAGAACCATGTGCGTGTCATCCAGTCA 681                         |   |
|-------|---|---|
| àC    | 133 LenTvrGlnGlvIleCvsLvsLeuLeuArqLeuGluAspLeuPheLysLeuGlyGluPro 152                      | 455 1561 481  |
| QO QO | ATGACCAGGG  | -   |
| QY    | 153 TyrHisLysLysGluHisTyr   | Qy 433 Yuxshenryshyshterigvarnsportyrons<br>  :::::                             |
| qq    | 111 :::   | 472   |
| Qy    | 168 ServalPheGlyvalIleValSerTyrSerAsnLeuAspAspLys 182                                     | 1728  |
| qa    | 83  | Qy 492 uGlnLeuTyrIleMetSerGluArgGlnLeuThn                                       |
| 6y    | LeuPh   | Db 1788 GAGCCTCTACATTGGCACCGATCATCACATCAA                                       |
| අු සි | 21  | Qy 512 -GlnTyrGlnSerCysGlyGluCysLeuGlySer                                       |
| ර් රි | 200 SEISELAIGLÝSLEGITILLISARISSELGIANIARSPOLJANCH MAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 1848  |
| Qy    | 220 AspGluPheValAlaSerMetlleLyslleProSerAspThrPheThrIlelleProAsp 239                      | OY 531 ILEUHISABITHICVSTHIATULYSCHUATU<br>                                      |
| qa    | 940 actgatchtaataattcggctaaacgtttggaatataaattcaagaggactctgaaa 999                         | 542   |
| Qy    | 240 Pheaspile   | Db 1962 GAGTGACATTTGCGATTCGAGTGTGCTGAAAAA                                       |
| οp    | 1000 TACGACTCCAAGTGGTTGGACAAACCAAACTTTGTCGGCTCCTTTGATATTGGGGAGTAC 1059                    | Qy 558 sValArgLeuThrValHisProAsnAsnIleSe  |
| Qy    | <pre>nProGluMetValSerProProGlySerThrTysGl<br/>:   </pre>                                  | Db 2022 TGTACATCTGGGCTGTTTC   |
| qa    | ACCGCCGTGGAATACATCAACTGCGCC   | Qy 578 lLeuGluThrTyrAsnValProGluLeuSerAl  |
| QY    | uValArgLeuCysLysGluAspThrAla  | Db 2041GTCAAAATACCGAAGTGCTGAA   |
| qa    | 1108 AAGGCTGTC-TATTCGCGCATCGCACGGGTGTGCAAGAAGGATGTGGGTGG                                  | Qy 598 uSerGluMetAspGlyLeuValValGlyAsnGl  |
| Qy    | 290   | :::<br>  Db   |
| QΩ    |   | Qy 618 sGluValProArgIleIleThrGluAsnGlyAs  |
| Qy    | LeuSerLysAlaGlyAlaValLe   | Db 2137TACATTGAGACCACGA   |
| qa    | 1227 ATTTCCGTTCTATTTCAACGAGATCCAATCGGTCTAC  | Qy 638 sSerLysGluThrGlyMetThrPheAlaSerTh  |
| Qy    | LysGl   | :::    <br>Db 2181 CGAAGCCGATGGTGGTCGG  |
| qa    |   | Cys   |
| Οỳ    | yGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLysGl                              | :   |
| qa    | ACGAGCACTAATGGCCTGATTGGATCTGCCGTATGCAGTTTCCACATTAACGA                                     | Qy 678 gHisvalCysThrHisAs   |
| Ολ    | nileAsnaspargileLysGluArgLeuGLnSerCysTyrArgGLYGL  | Db 2241 CATTACAGTGGATGCCCACAGATGCACTCCGCC                                       |
| qa    | GATTCAGGCTGCCTTCAATGGCAAATTCAAGGAGCAATCTTCATCG  | RESULT 7  |
| δλ    | 378 uGlyThrLeuAspLeuAlaTrpLeuLysValLysAsp1lePrOCysSerSerAl 390                            | . Sequence 61, Application US/08835268<br>. Datont No 5807826                   |
| qq    |   | ; GECEL INFORMATION: ; GENERAL INFORMATION:                                     |
| δλ    | aLeuLeuThrIleAspAspAsnPheCysGlyLcuAspMetAsnAlaProLeuGlyVaLSe                              | APPLICANT: GOODHEN, COLEY 3. , APPLICANT: Matthew David                         |
| qa    | A   | Bentley,  |
| δλ    | 416 IAspMetValArgGlyIlePro:   | TITLE OF INVENTION: The Semaphorin Gene   |
| qa    | GAATTTCATCAGATCCCATCCCATCCCATCCACAAAGCCGTAAATCACGAGCACACAACAACAACAACAACAACAACAACAACAA     | CORRESPOND DESCRIPTION CORRESPONDED TO A ADDRESSED SCIENCE & TECHNOLOGY LAW GRO |
| oy.   | 424   | 268 Bush Street, Suite 3200<br>n Francisco                                      |
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AspHisHisValValGlnLeuGlnLeuLy 638
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---------TGCAGCTACAA 2240
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\AGGGAGAGTGGTGTCCAAGCTTCTGGA 1727
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:AGTGATGGAAATCAGCCAGACGTAA 1787
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ATTTACTGCAGGATGTGGCCAATGAAAC 1961
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                                                                                                                                                                                                                                                                                                          rgArgPheAlaSerGluMetLysGlnCy 558
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                                                                                                    rgAspMetAlaPheSerLysAspHisGl 492
                                                                                                                                                      hrArgvalProvalGluSerCysGly-- 511
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1000 TACGACTCCAAGTGGTTGGACAAACCAAACTTTGTCGGCTCCTTTGATATTGGGGAGTAC 1059
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183 LeuPhelleAlaThrAlaVal.-----AspGlyLysProGluTyrPheProThrIle 199
                                                                         SerSerArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHis 219
                                                                                                                                                220 AspGluPheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAsp 239
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                                                                                               TACTCCGCCACCAATGCGGAGTTCACCAAGGCGGGTT----ACGGTTATTTCCGC
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                        B94-002-1
                                                                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,268
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: B9
TELECOMMUNICATION INFORMATION:
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227.00
37.22%
20.42%
2.27%
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TELEFAX: (415) 343-4342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
                                                                                                                                                                                      FILING DATE:
                               94104
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US-08-835-268-61
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sValArgieuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeuLeuVa 578
                                                                                                                                                                                                                                                                                                                          -----CysGluArgSerLysGluProArgArgPheAlaSerGluMetLysGlnCy 558
                                                                                    -GlnTyrGlnSerCysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCysVa 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
                                                                                                                                                                                                               lLeuHisAsnThrCysThrArgLysGluArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCIENCE & TECHNOLOGY LAW GROUP 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/060,692 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 61, Application US/09060692
Patent No. 5935865
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTACATCTGGGCTGTTTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       datent No. JOHN GENERAL INFORMATION:
APPLICANT: GOOdman, Corey S.
APPLICANT: Kolodkin, Alex L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2214 GGGCGCTCGCTTTTG---
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CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 LeuphelleAlaThrAlaVal------AspGlyLysProGluTyrPheProThr1le 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 AsnValAsnLysMetLeuLeuIleAspTyrLysGluAsnArgLeuIleAlaCysGlySer 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyGluPro 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 HisLeuValValAspGluArgThrGlyHisIleTyrLeuGlyAlaValAsnArgIleTyr 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         940 ACTGATCTGTATAATACTTCGGCTAAACGTTTGGAATATAAATTCAAGAGGACTCTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 ProLysCysTyrProProArglleValGlnThrCysAsnGluProLeuThrThrAsn
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Conservative:
Mismatches:
Indels:
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                                          NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFRENCE/DOCKET NUMBER: B94-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 PheAspIle------
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227.00
37.22$
20.42$
2.27$
FILING DATE: 13-SEP-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 2670 base pairs
                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                          268..2439
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Best Local Similarity:
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us-09-964-956-13.p2n.rni

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                                                                                                                                                                                                                                                                           LysLeuSerSerAspLeuLysValLeuValThrHisGluThrGlyProAspGluAspAsn 92
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Matches:
Conservative:
Mismatches:
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                                            CDS
268..2439
TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                         , NAME/KEY:
, LOCATION:
US-08-833-391-61
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| Qy   | 305 -    | uSerLysAlaGlyAlaVal  | 7      |
|------|----------|--|--------|
| qq   | 1227 ₽   | TCAACGAGATCCAATCGGTCTAC  | 1263   |
| Qy   | 322 u    | lyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPheSerLys                     | 342    |
| qq   | 1264 -   | sccotccdataagagtcgattcttcgccacattcacg  | 1305   |
| Qy   | 342      | GlnLysArgLysMetLysS  | 62     |
| Dρ   | 1306     | ACGAGCACTAATGGCCTGATTGGATCTGCCGTATGCAGTTTCCACATTAAUG                         |        |
| QY   | 362 1    | <pre>snAspArglleLysGluArgLeuGlnSerCysTyrArgGly(</pre>                        |        |
| qa   | 1359 (   | CAGGCTGCCTTCAATGGCAAATTCAAGGAGCAATCTTC                                       | 1404   |
| Qγ   | 378      | 31yThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCysSe                              | 396    |
| Db   | 1405     | - AATTCCGCATGCTGCCGTGCTTAACTCCCG   | 1454   |
| QY   | 9        |  | 416    |
| qq   | 55       | GTACATGTGTCAACGATACATCAAACCTGCCGATACCGTA                                     | 14     |
| Qy   | 16       |  | 423    |
| qq   | 00       | :::   <br> TCATCAGATCCCATCCACTTATGGACAAA                                     | 1559   |
| Qy   | 424      | SpArgMetT  | 4      |
| Dp   | 0        | CTTCACCAAGCTCGTCGTTGACAAATTCGC   | 1614   |
| QY   | 33       | rVal   | 453    |
| QQ   |          | TGACATCCTCAACCAGGAATACATTGTGTACTATGTGGGCACCAATCTGG                           | 16     |
| ОУ . | 453      | LysLeuLysLysIleArgValAspGlyProArgGlyAsnAlaLeuGlnTyrGluT<br>::::::        ::: | 472    |
| qq   | 89       | NITTACAAAATCGTGCAGTACTACCGTAACGGAGAGTCGCTGTCCAAGCTTCTG                       | 17     |
| Qy   | 472      | rvalGlnvalValAspProGlyProValLeuArgAspMetAlaPheSerLysAspHisGl                 | 492    |
| Db   | 1728     | :<br>:TTCGAGGTGGCTCCAAACGAGGCCATCCAAGTGATGGAAATCAGCAGACACGT                  |        |
| Qy   | 492      | uGlnLeuTyrIleMetSerGluArgGlnLeuThrArgValProValGluSerCysGly                   | 511    |
| QQ   | 88       | SCICIACATIGGCACCGATCATCAAGCAAATCGACCTGGCCATGT                                | 1847   |
| Qγ   | $\vdash$ | GlnTyrGlnSerCysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCys                    | 53     |
| QQ   | 1848     | GTTACGACAACTGCTTCCGCTGCGTCCGTGATCCCTACTGCGGCTGGGATA                          | 19     |
| Qy   | 531      | 31uArg   | 541    |
| qa   | 1902     | 3AGGCCAATACGTGCCGACCGTACGAGCTGGATTTACTGCAGGATGTGGCCAA                        | 19     |
| Qy   | 542      | GluM   | 55     |
| QQ   | 1962     | agtgacatttgcgattcgagtgtgctgaaaagaagattgtggtgacctatggcca                      | , 2021 |
| Qy   | 558      | valargLeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeuLeuV                   | 578    |
| Db   | 2022     |  | 2040   |
| QY   | 578      | LeuGluThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThrPheGluA                      | 598    |
| Db   | 2041     | TCAAAATACCCGAA   | 20     |
| Qy   | 598      | <pre>\spGlyLeuValValGlyAsnGln1leGlnCysTyrSerProAlaAlaL \!! \!\ \!\\</pre>    | 618    |
| QQ   |          | AAGGACAAGGACGCTACGAGATTCGT   | 21     |
| ΟŸ   | 618      | sGluValProArgIleIleThrGluAsnGlyAspHisHisValValGlnLeuGlnLeuLy                 | 638    |

Page 21

us-09-964-956-13.p2n.rni

| . US-09-964-956-13 (1-1896) x US-09-060-610-61 (1-2670)                   | Oy 53 HisLeuValvalAspGluArgThrGlyHisIleTyrLeuGlyAlaValAsnArgIleTyr 72  | Qy 73 LysLeuSerSerAspLeuLysValLeuValThrHisGluThrGlyProAspGluAspAsn 92 ::::: ::: | Qy 93 ProLysCysTyrProProArgIleValGInThrCysAsnGluProLeuThrThrAsn 112   11   11   11   11   11   11   11 | Qy 113 AsnValAsnLysMetLeuLeuIleAspTyrLysGluAsnArgLeuIleAlaCysGlySer 132 | QY 133 LeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyGluPro 152 :::                             | Oy 153 TyrHisLysLysGluHisTyrLeuSerGlyValAsnGluSerGly 167  | Oy 168 SerValPheGlyValIleValSerTyrSerAsnLeuAspAspLys 182   | Oy 183 LeuPhellealaThralaValAspGlyLysProGluTyrPheProThrIle 199 :::   | OY 200 SerSerArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHis 219   | OY 220 ASPGIUPheValalaSerMetIleLysIleProSerAspThrPheThrIleIleProAsp 239 ::: | Oy 240 PheaspileTyrTyrValTyrGlyPheSerSerGlyAsnPhe 253 :::                                     | Qy 254 ValTyrPhe-LeuThrLeuGlnProGluMetValSerProProGlySerThrThrLysGl 273  | Qy 273 uGlnValTyrThrSerLysLeuValArgLeuCysLysGluAspThrAla 289 ::::::      :::   | Oy 290 | Qy 305ValGluTyrArgLeuGeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAlaValLe 322 :: | Qy 322 uGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPheSerLysGl 342 :: 1 | Oy 342 yGlnLysArgLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLysGl 362   11   | Oy 362 nIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGl 378 :: |
|---|--|---|--|---|---|---|--|--|---|---|---|--|--|--------|---|--|--|--|
| ::: ::    ::: ::: Db 2137TACATTGAGACCACCGAACGTGGCTGGTTGTGGTTTCCGTGAA 2180 | Oy 638 sSerLysGluThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerVa 658 ::       ::       ::       ::       :: | Qy 658 lHisAsnSerCysLeuSerCysValGluSerProTyrArgCysHisTrpCysLysTyrAr 678<br>     | Oy 678 gHisValCysThrHisAspProLysThrCysSerPheGlnGlu 692<br>   | RESULT 10<br>US-09-060-610-61<br>; Sequence 61, Application US/09060610 | ; Paten No. 634454 ; GENERAL INFORMATION: ; APPLICANT: Goodman, Corey S. ; APPLICANT: Kolodkin, Alex L. | APPLICANT: MACLUES, DAYIG  APPLICANT: Bentley, David R.  APPLICANT: O'Connor, Timothy  TITLE OF INVENTION: The Semaphorin Gene Family | CORRESPONDENCE ADDRESS:  ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP  STREET: 268 Bush Street, Suite 3200 | STATE: CA COUNTRY: USA COUNTRY: USA COUNTRY: TO COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY C | MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  COPERATING SYSTEM: PC-DOS/MS-DOS  COFFMANDE: DefantT baloace #1 06 | FECULARION DATA: ON NUMBER: US/09/060,610 TE: AFTOM:                        | PRIOR APPLICATION DATA:  APPLICATION NUMBER: 08/835,268  FILING DATE:  APPLOADENT INDOMARTON. | CONDITION OF THE CONTROL OF THE CONT | ; TELEPHONE: (415)343-4341<br>; TELERA: (415)343-4342<br>; THERRY: (715) 343-4342<br>; THERRAMATION FOR SECTION OF 61. | Ľ      | 90 7  |  | Pred No.: 1.47e-13 Length: 2670. Score: 227.00 Matches: 147 Percent Similarity: 37.23 Conservative: 121 Rest Local Similarity: 20.43 Mismatches: 250 | 2.27% Indels:  |

| RESULT 11<br>PCT-US94-<br>; Sequenc<br>; GENERA     | APPL ; TITL ; NUMB ; CORR |       | COMP                                 | SC SCURP |   | ; RELE   | IT :   |  | MOLI<br>FEAN                        | PCT-US94 Alignmen   | Score: Percent Best Loc  |   | da da  | da . | QQ Qp  | QY<br>Dp  | da .     |
|---|---------------------------|-------|--------------------------------------|----------|---|--|--|--|-------------------------------------|---|--|---|--|------|--|---|----------|
| 1359 GATTCAGGCTGCCTTCAATGGCAAATTCAAGGAGCAATCTTCATCG | aLeuLeuTh<br>GGGTACATG    |       | 424ValpheThrGluAspArgAspArgMetTh 433 |          | 453 yLysLeuLysLysIleArgValAspGlyProArgGlyAsnAlaLeuGlnTyrGluTh 472<br> | 472 rValGlnValValAspPrOGlyPrOValLeuArgAspMetAlaPheSerLysAspHisGl 492 ::: | 492 uGlnLeuTyrIleMetSerGluArgGlnLeuThrArgValProValGluSerCysGly 511 | 512 -GLnTyrGlnSerCysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCysVa 531 | 531 lleuHisasnThrCysThrArgLysGluArg | 542CysGluargSerLysGluProArgArgPhealaSerGluMetLysGlnCy 558<br> | 558 svalArgLeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeuLeuVa 578<br> | 578 lLeuGluThrTyrasnValProGluLeuSerAlaGlyValAsnCysThrPheGluAspLe 598 :::        ::: | 598 uSerGluMetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSerProAlaAlaLy 618<br> |      | 638 sSerLysGluThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerVa 658 1::     ::: | 658 lHisashSerCysLeuSerCysValGluSerProTyrArgCysHisTrpCysLysTyrAr 678<br>: |          |
| oy oy   | g & d                     | 8 % a | QY<br>Db                             | QY<br>Dp | Sy da   | QY   | Qy<br>Dp   | Oy<br>Dp   | QY                                  | Qy  | Oy<br>Db   | QY  | QY   | QY   | Qy<br>Db   | Oy do   | Qy<br>Op |

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113 AsnValAsnLysMetLeuLeulleAspTyrLysGluAsnArgLeulleAlaCysGlySer 132
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APPLICANT: The Regents of the University of California APPLICANT: The Regents of the University of California TITLE OF INVENTION:
AUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT STREET: San Francisco Center, Suite 3400
CITY: San Francisco
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ZIP: 94111-4187

CONDUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPA: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10151A
FTLING DATE: 13-SEP-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,627
REGISTRATION NUMBER: 36,627
REGISTRATION NUMBER: 36,627
FEELENCE/DOCKET NUMBER: 8P-58750-PC/RAO
TELEFAX: (415) 398-3249
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Matches:
Conservative:
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LOCATION: 268..2439
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CATTTACAAAATCGTGCAGTACTACCGTAACGGAGAGTCGCTGCTGCTGCTTCTGGA 1727
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TGACATTTGCGATTCGAGTGTGCTGAAAAGAAGATTGTGGTGACCTATGGCCAGAG 2021
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sLeuLysLysIleArgValAspGlyProArgGlyAsnAlaLeu---GlnTyrGluTh 472
                                                                                    IGlnValValAspProGlyProValLeuArgAspMetAlaPheSerLysAspHisGl 492
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                                                                                                                                                                                                                                                                                                                                                    uHisAsnThrCysThrArgLysGluArg--------
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Kolodkin, Alex L.
Matthes, David
Bentley, David R.
O'Connor, Timothy
SEQUENCES: 100
BENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCIENCE & TECHNOLOGY LAW GROUP
68 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCCGATGGTGGTCGG----A
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PE: Floppy disk
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1180 TGTAAACATGACAAGGGGGGCCCTCATCAGGGTGGTGACAGATGGACTTCTTTTGAAA 1239
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                                                                                                                                                                                                                              -------TTCTTCTTCTTCGAGAGACTGCTGTTGAG 1134
165 GluSerGlySerValPheGlyValIleValSer---TyrSerAsnLeuAspAspLysLeu 183
                                                                                                                                                                                                                                                                                                                                                                                            SerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAACAAGTGACATCATTGAAGGAAATTATGGTGGT-----CAAGTGGAGAAACTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1507 CCAAGGCCTGGACAATGTGTGAATGACAGTCGTACACTTCCTGAT------GTG
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                                955 AGTGAGGGACAATTGTACTCAGCAACAGTGGCAGACTTCTCTGGAACTGACCTCTCATA
                                                                                           -------CCTCTAAGAACAGAGATCT
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                                                               184 PhellealaThrAlaValAspGlyLysProGluTyrPheProThrIleSerSerArgLys
                                                                                                                               204 LeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheVal
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121
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234
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                                           PatentIn Release #1.0, Version #1.25
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Mismatches:
Indels:
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Matches:
                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713D
FILING DATE: 13-SEP-1993
CLASSIFICATION: 514
ATORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 85,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECHONE: (415,343-4341
TELEPHONE: (415,343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 57:
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207.00
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19.36%
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LENGTH: 2854 base pairs
TYPE: nucleic acid
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STRANDEDNESS: double
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; LOCATION: 451..2640
US-08-121-713D-57
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MOLECULE TYPE: CDNA
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Best Local Similarity:
Query Match:
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| Percent Similarity: 36.964   Mismatches: 234                                 | Qy         264 ValSerProProGlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeu           Db         1162TCAAGAGTTGCCAGAGTC           Qy         284 CysLysGluAspThrAla |
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|  | · · · · · · · · · · · · · · · · · · ·   |
| 1840 AACCTGTATGGGGGGAATGATGGGGGGATGATGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG | 1.0   |

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NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                       MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible ODERATING SYSTEM: PC-DOS/WG-
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                       36,627
                                                                                                                                                                                                                                                                                                                                                                                   NAME: Osman, Richard A. REGISTRATION NUMBER: 36,6 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2854 base pairs
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36.96%
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STRANDEDNESS: double
                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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451..2640
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                                                                                                                           94104
                                                                                            CA
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                                                                                                            COUNTRY:
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   1240 TCACGICIGAACTGITCCGICCCIGGA---GAITAICCAITTIACTICAAIGAAAIICAG 1296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 GlnLeuThrArgValProValGluSerCysGly-----GlnTyrGlnSerCysGlyGlu
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                                                                           297 TCAACAAGTGACATCATTGAAGGAAATTATGGTGGT----CAAGTGGAGAAACTCATC
                                                                                                                PheThrValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeu
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                                      316 SerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeu
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APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David R.
APPLICANT: Bentley, David R.
APPLICANT: O'Conon', Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      454 LysteuLysLysIle-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57, Application US/09060692 Patent No. 5935865 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 TrpAsnTrpThrCysLeuLeuSerHisLeuLeuMetValGlyMetGlySerSerThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 LeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPheVal---ThrPheArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt GlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThrGlyHisIleTyr}
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Mismatches:
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SOFTWARE: Patentin Release #1.0, Version #1...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,692
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Matches:
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                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
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| 1135 1<br>264 V<br>1162<br>284 C  | 296 1<br>1240 3<br>316 316 1297  | 336   | 1399   | 1447   | 1507                                       | 1555       | 428                             | 441                      | 454   | 1735   | 1789                         | 1840  | 501       | 1900   | 1960   | 539      | 554  |  |
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| pairs<br>ble<br>ble   | 2.44e-11 Length: 2854<br>36.96% Matches: 121<br>36.96% Mismatches: 110<br>19.36% Mismatches: 234<br>2.07% Indels: 161<br>3 Gaps: .30 | 13 (1-1896) x US-08-833-391-57 (1-2854)  TrpAsnTrpThrCysLeuLeuSerHisLeuLeumetValGlyMetGlySerSerThrLeu 25  ::: | LeuThrargGlnProalaProLeuSerGlnLysGlnArgSerPheValThrPheArg 44<br> | GlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThrGlyHisIleTyr 64      ::: | LeuglyalavalasnargileTyrLysLeuSerSerAspLeu |            | ThrasmasmvalasmLysMet           | GGGAAGTCAGAGGACGACTGCCAG | ACGATGACCGCGTACTCATCTGCGGTACGACGCCTATAAGCCA 846 | Ilevyslysleuleuargleucluaspleuriglysleudryslyslusistyristyristyristyristyristyristyristy | GluHisTyrLeuserGlyvalasn 164 | GluserGlyservalPheGlyVallleValSerTyrserAsnLeuAspAspLysLeu 183 |           | PhellealaThralaValAspGlyLysProGluTyrPheProThrIleSerSerArgLys 203<br> | LeuThriysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheVal 223 |          |      | TyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMet 263 |
| 2854 base panucleic acid<br>nucleic acid<br>nucleic acid<br>Y: linear<br>TYPE: CDNA<br>Y: CDS<br>Y: CDS | :<br>ty:<br>arity:   | 13 (1-1896)<br>   | LeuThrArgG<br>   <br> ACGTCAG                                    | SlyGluProA<br>    <br>GGCAATGAAT   | LeuGlyAlaV<br>:::      <br>GTAGGAGČTA      | LysValLeuV | CAGAGGATCG<br>ProArgileV<br>::: | GGGAAGTCAG<br>LeuLeuIleA | GCGAAAATTC                                      | Ilecyslysi<br>:::   :::<br>CTATGTCGG   | Glu;                         | GluSerĠly   | AGTGAGGGA | PhelleAla'<br>:::<br>TACCGCGGC                                       |  |          |      |  |
| LENGTH: 2854 TYPE: nuclei. STRANDEDNESS: TOPOLOGY: li MOLECULE TYPE: FATURE: NAME/KEY: CD LOCATION: 45  | Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match:   | US-09-964-956-13<br>Qy 6 TXI<br>Db 485 TT   | 26 I<br>521 '-   | 45 G<br>577 G  | 65 1                                       |            | 697 (                           | 751 (                    |   | 137  | 157                          |   | 955       | 184  |  | 1045     | 1105 | 244  |
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| qq       | <br>1135 T |   |
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| Qy       | 264 V      | alSerProProGlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeu 283   |
| . qa     | 1162 -     | rcaagagTTGCCAGAGT 11  |
| о до     | 28         | ysLysGluAspThrAlaysLysGluAspThrAla  |
| qa       | 08         | GTAAACATGACAAGGGGGCCCTCATCAGGGTGGTGGACAGGAGGGCTTCTTTTTTTT   |
| Qy<br>H  | 296 V      | alprolleGlyCysGluArgSerGlyValGluYYArgLeULeULeULAAra1Y1LeU or<br>  |
| 20 '     | , ,        | CACCATACA AND AND AND AND AND AND AND AND AND AN  |
| Oy<br>Op | 316 S      | CAAGTGGAGAAACTCATC 13   |
| Qy       | 36         | heThrvalPheSerLysGlyGlnLys  |
| qa       | 1351       | ATTGGTGGCTCTGCTGTT 13   |
| Qy       | 356        | nlleAsnAspArglleLysGluArgLeuGlnSerCysTyr 375  |
| Db       | 66         | GTGCCTTCAGTATGAAGTCAATACTTGAGTCATTTGATGGTCCATTT 14  |
| Qy       |            | lyGluGlyThrLeuAspLeuAlaTrpLeuLysValLysAspIle 391  |
| QQ       | 47         | AAGAGCAGGAAACGATGAACTCAAACTGGTTGGCAGTGCCAAGCCTTAAAGTGCCAGAA L>  |
| QŸ       | 392        | roCysSerSerAlaLeuLeuThrIleAspAspAsnPheCysGlyLeu 407   |
| Db       | 1507       | stgaatgacagtcgtacacttcctgatGtg 15   |
| QY       | 408        | SerAspMetValArgGlyIleProValPheThrGlu 42   |
| qq       | 1555       | SAATTTTGTAAAGTCACATACAGGTGGATGAGGCCGTGCCAGCATTTTTACT 16   |
| QY       | 428        | ThrservalileAlaTyrvalTyr  |
| qq       | 1615       | GCCAATICTCATICGGATCAGCTTACAGTACAGATTTACAAAAATAGCTGTTGATCAA 16   |
| Qy       | 441        | LysAsnHisSerLeuAlaPheValGlyThrLysSerGly 453   |
| qq       | 1675       | AGATGGGAAAGCGTATGATGTCCTGTTTATAGGAACTGATGATGGC 1/   |
| Qy       | 454        | ArgvalAspGlyPro 463   |
| QQ       | 1735       | srgaraaaagcittgaactctgcctcctttgattcatctgatactgtagat 170   |
| QY       | 464        | rgGlyAsnAlaLeuGlnTyrGluThrValGlnValValAspProGlyProValLeuArg 483   |
| qu       | 1789       | AGTGTTGTAATAGAAGAACTGCAAGTGTTGCCACCTGGAGTACCTGTTAAG 18  |
| ΟY       | 484        | 100   100 |
| qq       | 1840       | rgtatgtggtgcgaatggatgggatgatagcaagctggtggttgtgtctgatgat i8  |
| Oy       | 501        | rgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGlu 518  |
| Db.      | 1900       | rgccaattaagcttcatcgttgtggctcagataaaataacaaattgtcgagaa 19  |
| Qy       | 51.9       | lyAspProHisCysGlyTrpCysValLeuHisAsnThrCysThrArg 538   |
| QQ .     | 1960       | STGTCCTTGCAAGATCCTTACTGTGCATGGGACAATGTAGAATTAAAATGTACAGCT 20  |
| οy       | 539        | -Alaser 553   |
| qa       | 2020       | actggagtgctggaaaaagacg  |
| Qy       | 554        | GluMetLysGlnCys 558<br>   |
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APPLICANT: Klimczak, Leszek
APPLICANT: Laeng, Pascal
APPLICANT: Laeng, Pascal
APPLICANT: Palfram Michael
APPLICANT: Rajan, Prithi
TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REFERENCE: 3235/J1795-0433
CURRENT APPLICATION NUMBER: US/10/175,523
CURRENT FILING DATE: 2002-06-18
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PRIOR FILING DATE: 2001-06-18
PRIOR PELLING DATE: 2001-06-18
PRIOR PELLING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-25
PRIOR PAPLICATION NUMBER: US 60/315,150
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-11-14
PRIOR PELLING DATE: 2002-01-18
PRIOR PELLING DATE: 2002-01-18
PRIOR PELLING DATE: 2002-01-18
PRIOR PELLING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 95, Application US/10175523; Publication No. US20030096264A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brockman, Jeffrey
  APPLICANT: Evans, David APPLICANT: Hook, Derek
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Sequence 313, App
Sequence 91, Appl
Sequence 91, Appl
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SOFTWARE: Patentin version
SEQ ID NO 95
LENGTH: 6730
                                                       NAME/KEY: misc_feature LOCATION: (1)..(6730)
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                                                                                  {\tt AspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValVal---AspProGly}
     ValArgLeuCysLysGluAspThrAlaPheAsnSerTyrValGluValProIleGlyCys
                                                  ValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPheSer
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|  | 1059 AlaValTrpGlyThrHisLeuAspLeuIleGlnAsnProGlnIleArgAlaLysHisGly 107 :::  | 10.99   FrootaleudialeudiaphrodsphisGinSerdspleuThrGiudrgprodiugluphe 1118 | Qy         1159 ThrProIleIleLeuLysGlyLysAsnLeuIleProProValAladlyGlyAsnValLys 1178           ::: | Oy 1199 LeuLeuCysGluSerProAsnLeulleGlyArgHisLysValMetAlaArgValGlyGly 1218  | 9 IleValSerIleAlaValAlaGlyGlyLeuLeuIleIlePheIleValAlaValLeuIle 1 | Oy 1279 AspasnLeuGluSerArgValAlaLeuGluCysLysGluAlaPheAlaGluLeuGlnThr 1298 | Db 4504 ACCTATCCCATCAGGGCCTCCCAGGCACCCCCCCCTCTCTGCGGGAACTG 4563  Qy 1339 GluvalProGlyTyrArgGInGluurgValGluLySGJyLeuLySLeuPheAlaGInLeu 1358 |
|--|--|--|---|--|--|---|--|
|  | 2007 CICIGCACACATGACCCCACIACTICCTTCCAGGAAGGCAGGATCAATGTTTC 700 ASpCySProGlnLeuLeuArgValAspLysIleLeuValProValGluValIleLy 11 |  | 2947<br>2947<br>820   | 840 AlaGlnGluSerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnProArg 859 850 AlaGlnGluSerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnProArg 859 8510 AscartranaGcccTdGcTTactagGcTCCAGCCAAGCCCCAA 312 850 IleThrGluLlelleProValThrGlyProArgGluGlyGlyThrLysValThrIleArg 879 85127 ArcAcAAAATTTGAAAATCAAGACCACCTCAAGGAGGGGAGTCGTGTGACCCTA 318 | GlyGluAsnLeuGlyLeuGluPheArgAspIleAlaSerHisValLysValAlaGlyVa      | gPro 9<br>:111<br>GCCA 3<br>GCCA 3<br>pLeu 9<br> 11                       | 3427 AGCCCGATCCGGGACCAGAGTACCATGGTGACCATCACGTGACCATTACTTTTTTTT   |

us-09-964-956-13.p2n.rnpb

| 40 00 00 00 00 00 00 00 00 00 00 00 00 0 | 4624 ATCAACAACAAGTGTTCTTGCTGACCTTCATCGTACACTGGAACTACAGGCGCGCTTC 4683  1379 SerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLeu 1398  1189 HILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII  |  |
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|  | 9 11eLe<br>1::[1]<br>4 GTACT<br>9 ASNVA<br>9 ASNVA<br>1   1   1   1   1   1   1   1   1   1  | 1899 Lentrally Lystell 11   1   1   1   1   1   1   1   1  |
| \( \frac{1}{2} \)                        | 1599 SerLysGinValThrAlaTyrAsnalaValAsnAsnSerThrValSerArgThrSerAla 1618  1514 CCTAAGCAGCTCCTACAACATCCTGCCTGCCAGCATCTCTGGACATCCTT 5403  1619 SerLysTyrGluAsnMetIleArgTyrThrGlySerProAspSerLeuArgSerArgThr 1638  1619 AGCAGATATGATACATCTTCAGGTACAGGGCCCCAGACAGCCTCGGTCCGGGTC  1639 ProMetIleThrProAspLeuGluSerGlyValLysMetTrpHisLeuValLysAsnHis 1658  1639 ProMetIleThrProAspLeuGluSerGlyValLysMetTrpHisLeuValLysAsnHis 1658  1644 CCCATGATCACCCCAGACTTGGAGAGCGGTCTAGGTTTGGCATCTGGTGAAGATCAT 5523 |  |
| Qy<br>Db<br>Qy                           | 1659   GluHisGlyAspGlnLySGluGlyAspArgGlySerLySMetValSerGluIleTyrLeu  | .21e-270 Length:<br>580.00 Matches:<br>0.63% Conserva<br>3.18% Mismatch<br>5.83% Indels:                                       |
| OY<br>OY<br>OY                           | 1699 IlePheSerThralaHisArgGlySeralaLeuProLeuAlaileLySTyIMetPheAsp 1718 :::   | US-09-964-956-13 (1-1896) x US-09-964-824A-313 (1-6252)  Qy 24 ThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPheValThrPhe 43 |

| Oy 10  |                            |     | Qy 11   |    | Qy 11   | _ 32 | Oy 11  | DP 33  | Qy 11                      | Db 33 | Oy 11 | Db 34  | Qy 12 | Db 34 | 0y 12 | Db 35 | 0y 12  | Dp 36   | Oy . 12   | Db 36 | ΣT - ΛΌ .   |     |  |   |          |  |                                | 7. Db 31              |  |  | Qy 1.          | Db 33 | Qy . 1   | Db 4  | Oy 1  |
|--|----------------------------|-----|---|----|---|------|--|--|----------------------------|-------|-------|--|-------|-------|-------|-------|--|---|---|-------|---|-----|--|---|----------|--|--------------------------------|-----------------------|--|--|----------------|-------|--|---|---|
| 759 SerValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIleAsnAsn 776 | CIGGGACCITCGCCTTTCGGACCCCA | 777 | 2207 AACGAGACGCTGCCCTGCACCTCTACGTCAAGTCTTACGGCAAGAATATCGAC 2260 |    | 2261AGCAAGCTCCATGTGACCCTCTACAACTGCTCTTTGGCCGCAGCGACTGC 2311 |      | 2312 AGCCTGTGCGGGCCGCTAACCCCGACTACAGGTGTGCGTGC | 832 CysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGluLeuSerGlyAla 851 | 2372 TGCGTGTATGAGGCCCTGTGC |       |       | 872 GlyGlyThrLysValThrIleArgGlyGluAsnLeuGlyLeuGluPheArgAspIleAla 891 | 1     | 911   |       |       | 2576 ACCCGGATCGTGTGTGTGTCGAGGCTGCGGAGACGCCTTTCACGGGGGGTGTCGAG 2632 | 932 IleCysValAlaValCysArgProGluPheMetAlaArgSerSer 946 | 2633 GIGGACGICTICGGGAAACIGGGCGTICGCCTCCCAAIGIC 2674 |       | 2675 CAGTICACCTICCAACAGCCCCAAGCCTCTCAGTGIGGAGCCGCAGGGACCGCAG 2731 | 296 | 2732 GCGGGCGCACCACACACACATCCACGCCACCTGGACACGGGCTCCCAGGAGGAC 2791 | 987 ValMetPheGlyLysGlnProCysLeuPheHisArgArgSerProSerTyrIleValCys 1006 | 2792 GTG | 1007 ASDThrihrSerSerAspGluValLeuGluMetLysValSerValGlnValAspArgAla 1026 | 2822 AAAGTGACGAAGTTTGGGGCGCAGC | 1027 LysIle 1034 1034 | 2882 CAGAIGCITCIGGAGGICICCIACGGGGGGGTCCCCCGTGCCCCAACCCCGGCATCITCTIC 2941 | 1035 GlnTyrValGluAspProThrIleValArgIleGluProGluTrpSerIleValSerGly 1054 | 2942 ACCTACGGC | 1055  | 3002 GGCCGCAGCATCAACGTCACGGGTCAGGGCTTCAGCCTGATCCAGAGGTTTGCCATG | 1075 AlaLysHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMet :::             ::: | 3059GTGGTCATCGCGAGCCCCTGCAGTCTGGCAGCCG 3094 |
| Qy   | qq                         | Qy  | qa  | QY | QQ  | Qγ   | QQ   | QY   | qa                         | δλ    | qa    | QY   | qa    | Qy    | qa    | Qy    | qa   | Οy  | qa  | Οy    | qq  | Qy  | qa   | οy  | qa       | δŏ   | qa                             | QY                    | qa   | Qy   | qa             | Qy    | qa   | Qy  | qa  |

| Oy<br>Db       |   | ualaLeuGlyProAspHis 1107<br>:::       :::<br>GGTGGTGGGTACGACTACGTGTTCCAC 3154  |          |
|----------------|---|--|----------|
| Qy             | 108   | y 11   |          |
| qq             | 55 AATGACACCAAGGTCGTCTTCCTGTCCCC                  | CAAC 321   |          |
| Οy             | 120 PheIleLeuAspAsnVâ                             | hrAsn 113  |          |
| qa             | 215 CTCACGGTGCTGATCGAGATGGACGGGC                  | GCTCAGAACAGAGCCGGGGCC 327  |          |
| Qy             | 136 PheThrTyrTyrProAsnProValPheGl                 | apheGlyproSerGlyIleLeuGluLeu 1155  |          |
| a .            | Z/S TTCGAGTACGTGCCTGACCCCACCTTTG                  |  |          |
| 0y             | 156 LysProGlyThrProllelleLeuLysGl                 | ulleProProValAlaGlyGly 117 :::   |          |
| g<br>D         | 311ACAGGTGGCGTCAGAAGC                             | SCICALCACOCCOGGGCACC   |          |
| οy             | 176 AsnValLysLeuAsnTyrThrVal                      | LeuValGlyGluLysProCys 119<br>       :::  | <b>-</b> |
| Q<br>O         | 36Z AATCTGAACAAGGCGATG                            | A FOR ADDITIONAL PROPERTY OF THE PROPERTY OF T |          |
| OY<br>Db       | 1191 ThrvalThrvalSerAspvalGinbeubeucyss-<br>  118 | user<br> <br> GCCC   |          |
| O <sub>Y</sub> | 210 HisLys  | ValMetAlaArgVal 121  | .9       |
| QΩ             | <br>82 cccaagegegegaaaa                           | ::: :::<br>recccastrcattstaagttc 35  | -        |
| οy             | yGlyMetGluTyrSerProGlyMet                         | /alTyrIleAlaProAspSerPro 1233  | <u>۾</u> |
| qa             |   | CGGGTGAGCGACGTGCCG 36  | 1        |
| Qy             | 234 LeuserLeu                                     | SerIleAlaValAlaGly 124   |          |
| qq             | AGCCTCATCTTGCCGCTGGTCATCG                         | GTGGTCGTCATCGCGGTGTCT 365  |          |
| Qy             | lyLeuLeuIleIlePheIleValAlaVa                      | AlaTyrLysArgLysSerArgGlu 126   |          |
| QΩ             | 3659  | CAGCAG 368   |          |
| . σу           | 267 SerAspLeuThrLeuLysArgLe                       | etAspAsnLeuGluSerArgValAla 128   | 92       |
| QQ             | CCGAACGAGAGTATGAGAAGAT                            | GGAGGGCCTGGAGGAGCGTGCGG 374  |          |
| QY             | 1287 LeuGluCysLysGluAlaPheAlaGluLeuGlnTh          | rAspIleHisGluLeuThrSerAsp 130  |          |
| QQ             | ACCGCTGCAAG                                       | CAACGAC 380  |          |
| δy             | AspGlyAla   | uPhe 132   |          |
| qq             | ACGAGGCC  | CTTCTTC 386  |          |
| Qy             | 1           | GluValProGly 134   |          |
| qq             | 3869 CTGCCCTCCAAGGACGCGACAAGGACGTGA               | SGACATCCTGAG 392   |          |
| Oy             | 3 Ту  | IlleAsnAsnLys 136  | 52       |
| qO             | 3929 ccecedececeredresacecerer                    | SCIGAACAGCAAG 398  | . 88     |
| QY             | 3 Val   | SerMetArgAsp 138   |          |
| QΩ             | 3989 TCTTTCTCATCAATTTCATCCACACCCTGGAGAACC         | Accessarrerescecesce 404   |          |
| . 40           | GlyAsnValAlaSerI                                  | InSerLysLeuGluTyrAlaThr 140  |          |
| qq             | 49 AAGGTCTACTTCGCGTCCCTGCTGACGGTG                 | screcacegeaaacregaeracace 410  |          |
| Qy             | 1403 AspValLeuLysGlnLeuLeuAlaAspLeuI              | leAspLysAsnLeuGluSerLysAsnHis 1422   | 22       |
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Goddard, Audrey Grimaldi, J. Christopher Gurney, Austin Smith, Victoria

Eaton, Dan Filvaroff, Ellen

Baker, Kevin

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                                         Mismatches:
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Sequence 91, Application US/10245107 Publication No. US20030068779A1

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                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                        FILE REFERENCE: P3630R101 CURRENT ADDITOR: D3630R1071 CURRENT FILING DATE: 2002-09-16 PRIOR ADDITORNET D3630R1
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PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-09-16
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PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-24
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PRIOR APPLICATION NUMBER: 60/0669
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/08901
PRIOR APPLICATION NUMBER: 60/08069
PRIOR PELING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090657
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Stephan, Jean-Phillippe
Watanbe, Colin
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       PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR PELING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR PELING DATE: 1998-06-24
PRIOR PELICATION NUMBER: 60/090689
PRIOR APPLICATION NUMBER: 60/090689
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILLE REPERENCE: P$630RLC90
CURRENT APPLICATION NUMBER: US/10/245,143
CURRENT FILLING DATE: 2002-09-16
PRIOR PILLING DATE: 2002-07-18
PRIOR FILLING DATE: 1997-09-17
PRIOR FILLING DATE: 1997-09-17
PRIOR FILLING DATE: 1997-10-24
PRIOR FILLING DATE: 1997-11-10
PRIOR PLICATION NUMBER: 60/065027
PRIOR PLICATION NUMBER: 60/065027
PRIOR PLILING DATE: 1997-11-10
PRIOR FILLING DATE: 1997-11-10
PRIOR PLILING DATE: 1998-03-27
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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Publication No. US20030068780A1
GENERAL INFORMATION:
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ValTyrPheLeuThrLeuGlnProGluMetValSerProProGlySerThrThrLysGlu
                                                     Phe Thille I Le Pro Asp Phe Asp I Le Tyr Tyr Val Tyr GlyPhe Ser Ser Gly Asn Phe \\
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
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Watanbe, Colin
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Fong, Sherman
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APPLICANT: GAITHGALLAY: CINTESCRIES
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: SCRETCED NUD TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C98
CURRENT APPLICATION NUMBER: U5/19742
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR PELICATION NUMBER: 60/063046
PRIOR PELICATION NUMBER: 60/063046
PRIOR PELICATION NUMBER: 60/063046
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-05-22
PRIOR PELING DATE: 1998-05-22
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PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-24
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PRIOR RAPLICATION NUMBER: 60/090657
PRIOR PELING DATE: 1998-06-24
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Mismatches:
Indels:
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephen, Jean Phillippe
Watanbe, Colin
Wood, William
                                                                                                                                                            ; sequence 91, Application US/10245771; Publication No. US20030068781A1; GENERAL INFORMATION:
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1372.00
100.00$
99.62$
                                                                                LysLeuLysLysIle 458
                                                                                              PRIOR FILING DATE: 1998-06-25
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Best Local Similarity:
Query Match:
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APPLICANT: FONG, STERRED
APPLICANT: APPLICANT:
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R170
CURRENT APPLICATION NUMBER: US/10/245,883
CURRENT FILING DATE: 2002-09-16
PRIOR PAPLICATION NUMBER: US/13/942
PRIOR PAPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-09-17
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
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APPLICANT: Eaton, Dan
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Matches:
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PRIOR FILING DATE: 2002-07-18
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PRIOR FILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/090569
PRIOR APPLICATION NUMBER: 60/090689
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US-10-245-851-91
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Best Local Similarity:
Query Match:
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LENGTH: 2597
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APPLICANT: Fong, Sherman TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACCESS ENCODING THE SAME FILE REFERENCE: P3630R1C3
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/237,535
CURRENT FILING DATE: 2002-09-06
                                                                                                                                                                                                                                CURRENT FILING DATE: 2002-07-09
PRIOR FILING DATE: 2002-07-18
PRIOR PELICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/075027
PRIOR PELING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/086478
PRIOR PILING DATE: 1998-03-27
PRIOR PELING DATE: 1998-05-02
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PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
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FILING DATE: 1999-07-20
APPLICATION NUMBER: 60/144790
                Grimaldi,J. Christopher
Gurney,Austin
Smith,Victoria
                                                                  Stephan, Jean-Phillippe
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Wood, William
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APPLICANT:
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Publication No. US20030073188A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Filen
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C11
CURRENT APPLICATION NUMBER: 0210/2038,183
CURRENT PILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
PRIOR FLILING DATE: 2002-09-18
PRIOR FILING DATE: 1097-09-17
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R APPLICATION NUMBER: 60/079689
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Publication No. US20030073189A1
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
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Watanbe, Colin
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|  | Length: Matches: Conservative: Mismatches: Indels: Gaps:                                   |
| 2001-03-09 NUMBER: 09/872035 2001-06-01 NUMBER: 09/918585 2001-07-30 NUMBER: 09/924419 2001-08-06 NUMBER: 09/929404 2001-08-09 NUMBER: 09/931836 2001-08-13 NUMBER: 09/941992 2001-08-16 NUMBER: 09/941992 2001-08-16 NUMBER: 09/941992 2001-08-16 NUMBER: 09/941992 2001-08-16 NUMBER: 09/941992 2001-08-16 NUMBER: 10/001054 2001-01-11-30 NUMBER: 10/081056 2002-01-15 NUMBER: 10/081056 2002-01-15 NUMBER: 10/081056 2002-01-15 NUMBER: 10/081056 2002-01-15 NUMBER: 10/081056 2002-01-15 NUMBER: 10/081056 2002-01-15   | 1.1e-138<br>1372.00<br>100.00%<br>: 99.62%<br>: 13.73%                                     |
| PILLING DATE: APPLICATION FILLING DATE: APPL | Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: |
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| US-09-964-956-13 |

| 194 GluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSerGluAlaAspGlyMet  |
|---|
| GAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCATG      |
| PhealaTyrValPheHisAspGluPheValAlaSerMetlleLysIleProSerAspThr      |
| Tredeeracererecardargargaerrecardecredargarraadarecerredacee      |
| PheThrllelleProAspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAsnPhe      |
| TTCACCATCATCCTGACTTTGATATCTACTATGTTTTTGCAGTGGCAACTTT              |
| ValTyrPheLeuThrLeuGlnProGluMetValSerProProGlySerThrThrLysGlu      |
| GTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACGAGGAG       |
| GlnValTyrThrSerLysLeuValArgLeuCysLysGluAspThrAlaPheAsnSerTyr      |
| CAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGAGGACACAGCCTTCAACTCCTAT   |
| ValGluValProIleGlyCysGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAla      |
| GTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC       |
| TyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAsp      |
| TACCTGTCCAAAGCGGGGGCGGTGCTTGGCAGGACCCTTGGAGTCCATCCA               |
| LeuLeuPheThrValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGluSer      |
| CTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCTGGATGAGTCG       |
| AlaLeuCysIlePheIleLeuLysGlnIleAsnAspArgIleLysGluArgLeuGlnSer      |
| GCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTCT      |
| ${\tt CysTyrArgGlyGlyThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCys}$ |

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Gurney,Austin
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Filvaroff, Ellen
Goddard, Audrey
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TITLE OF INVENTION: 2002-09-09
FRIOR APPLICATION NUMBER: US/00/2914
FRIOR FILING DATE: 1997-09-17
FRIOR APPLICANTION NUMBER: 60/063046
FRIOR FILING DATE: 1997-10-24
FRIOR PELING DATE: 1997-10-24
FRIOR PELING DATE: 1998-03-27
FRIOR PELING DATE: 1998-03-27
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FRIOR APPLICANTION NUMBER: 60/089801
FRIOR PELING DATE: 1998-06-02
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                                                       GlyValSerAspMetValArgGlyIleProValPheThrGluAspArgAspArgMetThr
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Matches:
Conservative:
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin
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Percent Similarity:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACTDS ENCODING THE SAME
TITLE OF INVENTION: ACTDS ENCODING THE SAME
FILE REPERENCE: P3630R108B
CURRENT APPLICATION NUMBER: US/10/245,055
CURRENT FILING DATE: 2002-09-16
PRIOR PAPLICATION NUMBER: 00/059114
PRIOR APPLICATION NUMBER: 60/059114
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-00-17
PRIOR PAPLICATION NUMBER: 60/063046
PRIOR PILING DATE: 1997-10-24
PRIOR PLING DATE: 1997-11-10
PRIOR PLING DATE: 1997-11-10
PRIOR PLING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-27
PRIOR PLING DATE: 1998-05-22
PRIOR PLING DATE: 1998-05-22
PRIOR PLING DATE: 1998-05-22
                                                                                                                                                                                                                                                                                                                                                          314 TyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAsp
                        LeuLeuPheThrValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGluSer
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
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PRIOR APPLICATION NUMBER: 60,089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60,090557
PRIOR FILING DATE: 1998-06-24
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
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Wood, William
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APPLICANT: Zhang, Zemin
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C10
CURRENT APPLICATION NUMBER: U5/10/238,370
CURRENT FILING DATE: 2002-07-18
PRIOR FILING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 60/06699
PRIOR FILING DATE: 1998-05-22
PRIOR PELICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
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Matches:
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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100.00%
99.62%
13.73%
                                                    Wood, William
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US-10-238-370-91
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Query Match:
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Pred. No.:
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LENGTH: 2597
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Mismatches:
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Matches:
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 PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 116
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                                 ORGANISM: Homo Sapien
US-10-245-055-91
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                  SEQ ID NO 91
LENGTH: 2597
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APPLICANT: TORGY SHERME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630RTC72
CURRENT FILING DATE: 10202-09-16
PRIOR APPLICATION NUMBER: 10/19792
PRIOR PLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1097-09-17
PRIOR FILING DATE: 1097-09-17
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Filvaroff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher.
Gurney, Austin
Smith, Victoria
sequence 91, Application US/10245147; publication No. US20030073193A1; GENERAL INFORMATION:
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Watanbe, Colin
Wood, William
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ORGANISM: Homo Sapien
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PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
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PRIOR APPLICATION NUMBER: 60/087607
PRIOR APLICATION NUMBER: 60/089601
PRIOR FILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Sitch, Victoria
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Search completed: June 28, 2003, 19:18:57 Job time: 749 secs

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(without alignments) 5754.618 Million cell updates/sec 1 MKAMPWNWTCLLSHLLMVGM.....QKLAYKLEQVITLMSLDSNK 1896 June 28, 2003, 04:29:14 ; Search time 5336 Seconds OM protein - nucleic search, using frame\_plus\_p2n model US-09-964-956-13 9990 score: Scoring table: Title: Perfect sc Sequence: Run on:

16154066 seqs, 8097743376 residues BLOSUM62
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Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
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32308132 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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-NO\_MMAP -LARGEQUERY -NGS\_SCORES=0 -WAIT -DSPBENCK=100 -LONGLOG
-DEV\_INMOGUT=120 -WARN\_INMOGUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7

EST:\* Database

gb\_est4:\*
gb\_est5:\*
em\_estfun:\* em\_estom:\* em\_esthum:\* em\_estin: \*
em\_estmu: \*
em\_estov: \* em\_estro:\* em\_htc:\* em\_estba:\* gb\_est1:\*
gb\_est2:\*
gb\_htc:\* \$:ssb\_db gb\_est3: em\_estpl:

em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_vrt:\* em\_gss\_fun:\* em\_gss\_pln:\* em\_gss\_mam:

em\_gss\_other: em\_gss\_pro:\* em\_gss\_rod:\* em\_gss\_mus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description    | US H<br>US H<br>GENC<br>GENC<br>GENC<br>GENC<br>GENC<br>GENC<br>GENC<br>GENC | BQ434703 AGENCOURT AL134799 DKF2D547C BG294786 602391607 BB656076 BB656076 BI159919 602916727 BQ684665 AGENCOURT BQ684665 AGENCOURT BQ683335 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ686140 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT BQ678617 AGENCOURT | BQ947921 AGENCOURT<br>BQ720660 AGENCOURT<br>BQ441249 UT-M-EXO-<br>B1824913 603032430<br>BQ073659 AGENCOURT<br>BG825770 603747116<br>BF308474 601887611<br>BP30897297 AGENCOURT<br>BF312056 601897930<br>BE736103 601137485<br>BE294546 601173485<br>BQ180469 UT-M-EXO-<br>BE262288 601186342<br>BR3080469 UT-M-EXO-<br>BE262288 601186342<br>BB935540 UT-M-BH3-<br>BF309302 601887769  | mRNA linear HTC 07-AUG-2002, mRNA.  niata; Vertebrata; Euteleostomi; urognathi; Muridae; Murinae; Mus. Institutes of Health, Mammalian |
|----------------|--|--|--|--|
| B ID           | 1100 1400<br>4   | Α.   | 14 BQ947921<br>14 BQ742660<br>14 BQ44249<br>13 B1824913<br>12 B625770<br>12 BF306474<br>12 BF306474<br>12 BF312056<br>12 BF73103<br>14 BQ97297<br>16 BE73103<br>17 BE7311719<br>18 BF311719<br>18 BF317719<br>18 BF317719<br>18 BF317719<br>19 BF309302  | ALIGNMENT 4120 bp 4120 bp 7934 Chordata; Cra Rodentia; Sci ))  |
| Length DB      | 147<br>100<br>100<br>88<br>96  | ,882/78884<br>11999887988  | 906<br>904<br>904<br>909<br>909<br>900<br>900<br>900<br>900<br>900<br>900  | us,<br>c<br>c<br>us<br>me<br>Eut<br>11 t<br>7, R.  |
| Query<br>Match | 13.<br>13.<br>14.<br>17.   |  |  | 362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362   |
| Score          | 4000444444   | 10000000000000000000000000000000000000   | 01010.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>001000.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>001000.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>001000.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>001000.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>001000.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>001000.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>001000.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>001000.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>00100.5<br>0010 | Z X  |
| Result<br>No.  | 10 m 4 m 0 r m 0 r   | 112<br>112<br>114<br>116<br>116<br>117<br>118<br>118<br>118<br>118<br>118<br>118<br>118<br>118<br>118  | 0.<br>00000000000000000000000000000000000  | RESULT 1 BC036274 LOCUS DEFINITION ACCESSION VERSION VERSION VERYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOHNNAL                 |

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1033 alPheGlnTyrValGluAspProThrIleValArgIleGluProGluTrpSerIleValS 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysGluHisIleAsnIle------CysGluValLeuAsnAlaThrGluMetThrC 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1132 snLysThrAsnPheThrTyrTyrProAsnProValPheGluAlaPheGlyProSerGlyI 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luLysProCysThrVal---ThrValSerAspValGlnLeuLeuCysGluSerProAsnL 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ProGlnIleArgAlaLySHisGlyGlyL 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                  994 ysLeuPheHisArgArgSerProSerTyrIleValCysAsnThrThrSerSerAspGluV 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LeuValGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ACGGGTGGCGTCAAAAGCAGGTCAACAAGCTCATCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1019 TCTTGTCTCCTGCT--------GTCCCGAAGAGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaGlyValGluCysSerProLeuValAspGlyTyrIleProAlaGluGlnIleValCys
                                                                                                                                                  GluMetGlyGluAlaLysProSerGlnHisAlaGlyPheValGluIle--CysValAlaV
                                                                                                                                                                                                                                                                                                                    ysGlnAlaProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGluArgProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1152 leLeuGluLeuLysProGlyThrProIleIleLeuLysGlyLysAsnLeuIleProProV
                                             ACTATCCATGGGTCCAATCTGGGTGTCAAAGCAGATGACGTC---AAGAAGATAACTGTG
                                                                                                                 GCTGGCCAGAACTGTGCCTTTGAACCAAGAGGGTACTCCGTATCCACCGGGTTGTGT
                                                                                                                                                                                alCysArgProGluPheMetAlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrL
                                                                                                                                                                                                                                                      AAACTCGGCCA---TTCACCGCCCAC---GTCCAGTTCACTTATCAACAACCCCAGCCTC
                                                                                                                                                                                                                                                                                          euSerAspLeuLysProSerArgGlyProMetSerGlyGlyThrGlnValThrIleThrG
                                                                                                                                                                                                                                                                                                                                                                976 lyThrAsnLeuAsnAlaGlySer-----AsnValValWalMetPheGlyLysGlnProC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     662 GTGAAGTG---ACAAAGTTTGGAGCACAGCTACAGTGTGTCACAGGTCAACAGTTGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1014 alLeuGluMetLysValSerValGlnValAspArgAlaLysIle---HisGlnAspLeuV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           719 CAGGCCAGGTGACACTAGAAATCTACTATGGGAGCTCCAGAGTGCCCAGGCCCCGGCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             779 CTTTCACCTACTGCGAGAACCCCATGATACGAGCCTTTGAGCATTGAGAAGCTTTGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAGCGTGTGACGGTCGAGGGCATGGAGTACGTGTTCTACAATGACACCAAGGTCGTCT
           AAGCCGGAGTCTTTGAGTATGTGGCAGACCCCACCTTTGAGAACTTC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1172 alAlaGlyGlyAsnValLysLeuAsnTyrThrVal----
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                                                                                                                                                                                                                                                                                                                                 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 10 Row: j Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor metastatized to lung. Tumor
                                                                                                                                                                                                                                                X., Hulyk, S.W., Hale, S.M.,
S., Martin, R.G., Muzny, D.M.
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerSerSerValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIleAsnAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              837 HisCysProAlaGlnGluSerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AGCAATGTCACTTCTGAGTGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGACACCTTCTCTTTTAGGACCCCAAAGCTATCCTATGATGGTAATGAG-----ACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCCTCTTCACCTGTATGTTAAGTCCTTTGGCAAG----AACATTGACAGCAAGCTACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnLysValHisLeuTyrLysCysGlyAlaMetArgGluSerCysGlyLeuCysLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone_lib="NoI_CGAP_LU29" /lab_host="DH10B"
                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                           This clone has the following problem: no 5' EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4120
444
204
403
141
33
                                                                                                                                                                                                             Web Site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyl
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart:
Richards, S., Gibbs, R.A.
                                                       http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCMV-SPORT6"
1166 c 1151 g 850 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/map="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1-4120)
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/tissue_type="Mammary t
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54.36%
37.25%
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                                                       NIH-MGC Project URL: h
Contact: MGC help desk
                                                                                                                                                                                                Center code: BCM-HGSC
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| 185 GGGACTTGATACTTCACGGACATACTGCGGACTCTCACTGCTCACTGGACCTCGG. 244  1416 ASDLEUGIUSETLYSASDHISPTOLYSLEULEULEUATGATGTACTCGGTAGCTCAG. 244  245 TATGTTGCCAAGACCCCAAGCTGATGCTGCGCAGGACAGACGTGGACGTAGAA 298  1436 LysMetleuThrashTpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGly 145  1456 LysMetleuThrashTpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGly 145  1456 GluProLeuPheScarGCATCTGCCTCTACACCTTTGTGGGACTCTGTGGGA 358  1456 GluProLeuPheScarLeuPheCysAlaIleLysGlnGlnMetGluLysGlyProlleAsp 147  1476 GluProLeuPheScarCTCACCACTGGGGATTAAGCATCTAGGGACTCCTGTGGGA 358  259 AAGCTGCTGTATATGCTCTTCAGAGGGATTAAGCATCAAGTGGACAAGGGTCCCGTGGAC 418   | ASPTYLLSTALLINGSCAAATACACTCTGAATGACAACGCCTGCTCGCTGGTGGTGGTGGAGGGGTGGGAGGGGTGGAGGGGGGGG   | 1553 LeuGluTrpargGlnGlySerGlyAlaArgMetlleLeuGlnAspGluAspTlehrThr 1572  1573 LeuGluTrpargGlnGlySerGlyAlaArgMetlleLeuGlnAspGluAspTlehrThr 1572  1573 LystleGluAsnAspTrpLyBArgLeuAsnThrLeuAlaHisTyrGlnValProAspGly 1592  1574 LystleGluAsnAspTrpLySArgLeuAsnThrLeuAlaHisTyrGlnValProAspGly 1592  1575 LystleGluAsnAspTrpLyBArgLeuAsnThrLeuAlaHisTyrGlnValProAspGly 1592  1576 GAACTCCAGGGTCTGGGAGGCTCTGAATACATGCAATGCAATGCAATGGA 778  1577 GAACTCCAGGGTCTGTGGAGGCTCTGAATACATGCAATGTACAAGGTCCCAGTGGA 778  1578 SerValValAlaLeuValSerLySGlnValThrAlaTyrAsnAlaValAsn 1609  1579 GCAACGTGGCCTTGTCCCTGCCTCACCAAGCATATTCTTAGG   | 1650 LysMetTrpHisLeuValLysAsnHisGluHisGlyAspGlnLysGluGlyAspArgGly   1669   15: |
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| 4  | 00 00 00 00 00 00 00 00 00 00 00 00 00   | 90 A A A A A A A A A A A A A A A A A A A   | 00 O O O O O O O O O O O O O O O O O O   |
| LOCUS  BC026974  Mus musculus, clone IMAGE:5364076, mRNA.  BC026974.  BC026974.  BC026974.  BC026974.  BC026974.  BC026974.  BC026974.  BC026974.  BC026974.  BC026974.  BC026974.  BC026974.  BC026974.  BC026974.  BC026974.  BC026974.  GC02697 | USA  REMARK OCHACL: MGC help desk CONTACT: MGC help desk CONTACT: MGC help desk Email: cgapbar remail.nih.gov Tissue procurement: The Cepko Laboratory CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. Web site: Ntp://www.hgsc.bcm.tmc.edu/Cdna/ COntact: amg@bcm.tmc.edu COntact: amg@bcm.tmc.edu Gunaratne, P. H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Robis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A. | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 53 Row: g Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis This clone has the following problem: incomplete processing. This clone has the following problem: incomplete processing.  FEATURES  1.2779  Ab_xref="taxon:10090" /clone="IRAGE:5546776" /tissue_type="Epy, retina, mouse strain C57Bl\6" /tlone="IRAGE:549, retina, mouse strain C57Bl\6" /tlone="IRAGE:549, retina, mouse strain C57Bl\6" /lab_host="BASE COUNT" /note="vector: pCMV-SPORT6" /note="vector: pCMV-SPORT6" /note="vector: pCMV-SPORT6" /note="vector: pCMV-SPORT6" | Alignment Scores:     8.63e-156  |

| BASE COUNT 250 a 308 c 303 g 198 t  | Scores: 1.33e-152 Length:   | Score: 1357.50 Matches: 278 Percent Similarity: 89.29% Conservative: 22 Best Local Similarity: 82.74% Mismatches: 30 Query Match: 13.59% Indels: 6 | 13 Gaps:<br>6-13 (1-1896) x BMS47417 (1-1059)                                 | Qy 1256 ValLeuIlealaTyrLysArgLysSerArgGluSerAspLeuThrLeuLysArgLeuGln 1275                              | Oy 1276 MetGlnMetAspAsnLeuGluSerArgValAlaLeuGluCysLysGluAlaPheAlaGlu 1295 | Qy 1296 LeuGlnThrAsplleHisGluLeuThrSerAspLeuAspGlyAlaGlyIleProPheLeu 1315<br>  | Oy 1316 AspTyrArgThrTyrThrMetArgValLeuPheProGly1leGluAspHisProValLeu 1335<br> | Oy 1336 ArgaspLeuGluValProGlyTyrArgGlnGluArgValGluLysGlyLeuLysLeuPhe 1355 | Oy 1356 AlaGlnLeuIleAsnAsnLysValPheLeuLeuSerPheIleArgThrLeuGluSerGln 1375  | 1376 ArgSerPheSerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGln | 4 4 . | 1416  | LysMetLeuThrasnTrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGly                   | Qy 1456 GluproLeuPheSerLeuPheCysAlaIleLysGlnGlnMetGluLysGlyProIleAsp 1475                               | Qy 1476 AlaileThrGlyGluAlaArgTyrSerLeuSerGluAspLysLeuIleArgGlnGlnIle 1495 |  | OY 1516 ProValLySIleLeuAsnCysAspThrIleThrGlnValLySGluLySIleLeuAspAla 1535   | Oy 1536 IlePheLysAsnVal-ProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTr 1555   |
|---|---|--|---|--|---|--|---|---|--|---|-------|---|--|---|---|--|---|---|
| Db 1181 AACAGCCTGCCGCTAAGGTTCTGGATCAACATCATCAAGAACCCACAGTTTGTGTTCGAT 1240 | Qy 1761 IleHisLysAsnSerIleThrAspAlaCysLeuSerValValAlaGlnThrPheWetAsp 1780 ::: | Qy 1781 SerCysSerThrSerGluHisArgLeuGlyLysAspSerProSerAsnLysLeuLeuTyr 1800<br>  | Qy 1801 AlaLysAspileProSerTyrLysAsnTrpValGluArgTyrTyrSerAspileGlyLys 1820<br> | 1821 MetProAlalleSerAspGlnAspWetAsnAlaTyrLeuAlaGluGlnSerArgMetHis IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | 1841 MetAsnGlupheAsnThrMetSerAlaLeuSerGluIlePheSerTyrValGlyLysTyr         | 1861 SerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysGlyLysGlnLysLeuAla 1  1861 In ::::::::    :::     :::     1541 InTGACCAGATCATCATGCCTGGAGGAGGAGGAGGAGGAAAANGCAGGAGGA | 1881 TYTLYSLeuGluGlnVal 1886<br>  |   | LOCUS BM54/41/ DEFINITION AGENCOURT_6507625 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5724374 ACCESSION BM547417 | ,   |       | TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) of Factorian Strausberg, Ph.D. COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs remail.nih.gov | = Technologies, Inc.<br>I.M.A.G.E. Consortium (LLNL)<br>ijoscience Corporation | Cound through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Plate: LiAM12713 row: column: 15 | FEATURES Location/qualifiers  Source 11059 /organism="Homo sapiens"       | /db_xref="taxon'9606"<br>/clone="ltaxon'9606"<br>/clone_lib="NHLMGE:5724374"<br>/clone_lib="NHLMGC_125"<br>/cat_="DH10B" | // Anote="Organ: Ovary (pool of 3); Vector: pcMV-SPORT6; Site_1: EccRV (destroyed); Site_2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned /Forpv site is destroyed unon allocational incore | size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036." |

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AL529477 LTL_NFL001_NBC4 Homo sapiens cDNA clone CS0DD006YE12 5
prime, mRNA sequence.
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                                                                                                                                             .510 AlaAsnSerProGluValProValLysIleLeuAsnCysAspThrIleThrGlnValLys 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                         560 TCCTCCACCTCACCAAG---TCCCTCAGCAGAGAACAAGCATGCTGCGCAGGCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 GAGAATGCACCTGAGGTGCCGGTGAAGGGCTGGACTGTGACACGGTCACCCAGGCCAAG
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Mammalia, Eutheria, Primates; Catarrhini, Hor
( bases 1 to 980)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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AGENCOURT_6490555 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5587657
         pargGlnGlySerGly-AlaArgMetile-LeuGlnAspGluAspIleThrThrLysile 1574
||||||||||||
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Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12357 row: i column: 02
High quality sequence stop: 676.
                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1027)
NIH-WCC http://mgc.nci.nih.gov/.
Nathonal Institutes of Health, Mammalian Gene Collection (MGC)
                                                             GluAsnAspTrp----LysArgLeuAsnThrLeuAlaHis 1586
                                                                           1027
270
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/db_xref="taxon:9606"
/clone="IMAGE:5587657"
/clone_lib="NIH_MGC_125"
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                                                                                                                                                                       5', mRNA sequence.
BM544169
BM544169.1 GI:18775199
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87.02%
79.65%
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ProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGlySerGly 1560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contact:
    nisc_mgc@ndgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C.,
Dietrich,N.L., Guan,X., Gupta,J., Ho.S.-L., Karlins,E., Legaspi,R.
Lim,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,E.E., Snyder,B., Stantipop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
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Strausberg.R.
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 28 Row: i Column: 23
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Submitted (30-UDL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                         660 GC-CGCTACTCCCTGAGCGAGGACAAGCTCATCCGGCAGCAGTAGAGTACAAGACCCTG
                                                                                                                                                                                                                                 .501 ValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLysIleLeu
                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing DNA Sequencing Center (NISC).
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Contact: MGC help desk
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/sex="male"
/tissue_rype="neuroblastoma cells"
/tissue_rype="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@ilfetech.com URL:
http://fulllength.lnvitrogen.com"
3 others
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Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
                                                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www
Location/Qualifiers
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ORF
This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency
                                                                        is clone has the following problem: frame shifted.
Location/Qualifiers
1. .261
1. .261
/organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4121608"
/tissue_type="Muscle, rhabdomyosarcoma"
/lab_nost="NHH_MGC_17"
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Indels:
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12.74%
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Best Local Similarity:
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Kargil, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka, T.S., Carter, M.G. and Ko, M.S.H.
Verification and initial annotation of NIA mouse 15K cDNA clone set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG086250 627 bp mRNA linear EST 26-JAN-2001
H3123F01-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3123F01-5', mRNA sequence.
BG086250
                               Please
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361 GTCACAGCATACAATGCAGCCAATAACTCCACTGTATCTAGGACATCAGCAAGTAGATAT 420
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                                                                                                                     1662 AspGlnLysGluGlyAspArgGlySerLysMetValSerGluIleTyrLeuThrArgLeu
                                                                                                                                                                                           1642 ThrProAspLeuGluSerGlyValLysMetTrpHisLeuValLysAsnHisGluHisGly
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 627)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone set has been freely distributed to the community. Visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3123 row: F column: 01 Seq primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                         721 ACCAAACAGGGGGGACAAAGCATGGGGATTCCTTGATCCTTCAGGTGGAGGGCCCCC
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/clone_lib="NIA Mouse 15K cDNA Clone Set"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .627
/organism="Mus musculus"
/strain="C57BL/63"
/db_xref="niaeS7:H3123F01-5"
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Other_ESTs: H3123F01-3
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/dev_stage="embryo, stage 31-32"
/lab_host="DH10B (phage-resistant)"
/note="Norgan: whole embryo; Vector: pCMV-SPORT6; Site_l:
NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. 1gor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NGI-CGPB clone distribution information can by
www-bio.lnh.gov/bbrp/image/image.html
Plate: LiAn12311 row: a column: 09
High quality sequence stop: 553.
Location/Qualifiers
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                Xenopodinae; Xenopus.
1 (bases 1 to 878)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgTyrSerLeuSerGluAspLysLeuIleArgGlnGlnIleAspTyrLysThrLeuVal
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:5569808"
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Unpublished (1997)
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            Xenopus laevis
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL at:

Clone distribution: NGT-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence start: 2

High quality sequence start: 2

High quality sequence stop: 797.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapabs-remail.nih.gov

Cissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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5'-TCGACCCAGGGTCG6-3' and
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/dev_stage="adult, 16 yr"
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AGENCOURT_8470039 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGES:6195860 5', mRNA sequence.
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1 (bases 1 to 918)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1994)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
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            ThralaHisArgGlySerAlaLeuProLeuAlaIleLysTyrMetPheAspPheLeuAsp
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Homo sapiens cDNA clone IMAGE:6156354
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                                   u-VallysAsnHisGluHis-GlyAspGlnLysGluGlyAspArgGlySer-LysMetVa 1673
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/do_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="InAGE:6156354"
/clone="lip="NIH_MGC_71"
/tissue_type="lelomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: sal1; Cloned unidirectionally. Primer: Oligo dT.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 844)
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National Institutes.of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information car found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov hcolumn: 19 plate: LLAM13500 row: h column: 19 plate: LLAM13500 row: h column: 19 High quality sequence stop: 597.
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Tissue Procurement: ATCC
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AGENCOURT_7909800 NIH_MGC_71
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Alignment Scores:

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AGENCOURT_8072266 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089613
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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717

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AL134739 762 bp mRNA linear EST 25-FEB-2000 DKFZp547C1590_rl 547 (synonym: hfbrl) Homo sapiens cDNA clone DKFZp547C1590 5', mRNA sequence.
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1 (bases 1 to 762)
Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.).
EST (Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                              Email: poustka@mping-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from 5. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2): Email 8.wiemann@dkfz- heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin.
6, 14059
                                                             No sl sequence available.
This clone (DKFXp547Cl500) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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Department Lehrach
Max-Planck Institute for Molecular Genetics
Innestrasse 73, 14195 Berlin, Germany
Far: +49-30-84131128
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/tissue_type="brain"
/dev_stage="fetal"
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/lab_host="DH10B (phage-resistant)"
/note="Corgan: skin: Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oilgo-dr priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GCACGAGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1641 IleThrProAspLeuGluSerGlyValLysMetTrpHisLeuValLysAsnHisGluHis 1660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1661 GlyAspGlnLysGluGlyAspArgGlySerLysMetValSerGluIleTyrLeuThrArg 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CCCTACTCCCAGGGCCCAAGGCCGGGACATGGACTGGAGTGGCGCCAGGGCCGCATG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 TACGAGAGCATGCTGCGCCACGCCAGACAGCCCGGCGCTGCGCTCGCGCTCGCGCCCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaArgMetIleLeuGlnAspGluAspIleThrThrLysIleGluAsnAspTrpLysArg
              NIH-WGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                     pe
                                                                                           Email: capbs.remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information con http://image.lln.gov k column: 22
http://image.lln.gov k column: 22
High quality sequence stop: 625.
High quality sequence stop: 625.
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Matches:
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                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6089613"
/clone_lib="NIH_MGC_112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-964-956-13 (1-1896) x BQ878090 (1-851)
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73.87%
10.81%
  (bases 1 to 851)
                                                         Unpublished (1999)
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Score: Pred.

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Alignment ORIGIN

BASE COUNT

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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
Cona Library Preparation: Life Technologies, Inc.
Cona Library Preparation: Life Technologies, Inc.
Cona Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0374 row: m column: 01
High quality sequence stop: 712.
                                                                                                                                                                                                                                                                                                                                                           /tissue_type="retina"
//lab_host="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pcNNv-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Full-length clones and constructed by Life Technologies.
Note: this is a NH_MGC Library."
                                                    Craniata; Vertebrata; Euteleostoml;
Sciurognathi; Muridae; Murinae; Mus
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211
16
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4503720"
                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_94"
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                                                      Chordata;
GI:13055976
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1072.00
91.53%
85.08%
10.73%
                                         Mus musculus
Eukaryota; Metazoa;
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Query Match:
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                     Sall
                   Site_1: NotI; Site_2: 136 t
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Matches:
Conservative:
Mismatches:
Indels:
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                      /note="Vector: pAMP1;
225 c 228 g
         /lab_host="X1-2blue"
                                                                                                                                                                                   US-09-964-956-13 (1-1896) x AL134739
                                                                                        7.45e-119
1077.00
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Query Match:
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 612)
Arakawa.T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
D., Shibata,K., Shinagawa,A., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Taqawa,A., Taqawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Taqawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB656076 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130060F15 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                    CysSerThrSerGluHisArgLeuGlyLysAspSerProSerAsnLysLeuLeuTyrAla 1801
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                                       HisLysAsnSerIleThrAspAlaCysLeuSerValValAlaGlnThrPheMetAspSer 1781
                                                                                                                                                                                                                          CysLeuProLeuArgPheTrpValAsnMetIleLysAsnProGlnPheValPheAspIle 1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              URL:http://genome.gs.gsc.riken.go.jp,
URL:http://genome.gs.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
W., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
aggist., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                  1722 GluGlnAlaAspLysHisGlyIleHisAspProHisValArgHisThrTrpLysSerAsn 1741
                                                                                                                                                         Contact: Yoshliide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
Fax: 81-45-503-9216
CTAGCCACCAAGGCCACCCTGCAGAAATTTGTGGACGACTTGTTTGAGACCTTGTTCAGC 420
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                                                                                                                                                                                                                                                                                                                                       Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
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Unpublished (2001)
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JOURNAL
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KEYWORDS
SOURCE
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Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [6] and with a primer [6] and with a primer [6] and with a primer [6] and with a primer [6] and was gagadadacceccecaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrccaacrcca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1123 AspAsnValGlnSerLeuLeuLleLeuAsnLysThrAsnPheThrTyrTyrProAsnPro 1142
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                                                                                                                                                                                     with
. 11 (2), 281-289 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RIKEN full-length enriched, 12 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
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                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site_1: SalI; Site_2: BamHI; cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      612
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
/lab_host="DH10B"
         Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="D130060F15"
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                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .612
nonredundant cDNA library.
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<sup>1243</sup> Alavalalagly: 1246

completed: June 28, 2003, 15:57:58 Search comp Job time :